University of São Paulo
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Multi-omics approaches for understanding spinetoram resistance in *Spodoptera frugiperda* (Lepidoptera: Noctuidae)

Rubens Hideo Kanno

Thesis presented to obtain the degree of Doctor in Sciences. Area: Entomology

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Bachelor in Agronomic Engineering

Multi-omics approaches for understanding spinetoram resistance in *Spodoptera frugiperda* (Lepidoptera: Noctuidae

versão revisada de acordo com a resolução CoPGr 6018 de 2011

Advisor:
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“Success consists of going from failure to failure without a loss of enthusiasm.”

Winston Churchill

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RESUMO

Abordagens multi-ômicas para compreender a resistência de *Spodoptera frugiperda* (Lepidoptera: Noctuidae) a spinetoram

A resistência a inseticidas é um dos principais desafios em programas de manejo de pragas. A lagarta-do-cartucho, *Spodoptera frugiperda* (Lepidoptera: Noctuidae), é uma praga polífaga com alto risco de evolução de resistência a inseticidas. A resistência de *S. frugiperda* ao spinetoram já foi reportada, no entanto, informações sobre as bases moleculares da resistência ao spinetoram e os possíveis custos adaptativos associados a ela não foram elucidados. O uso de abordagens multi-ômicas tem fornecido informações sobre os mecanismos de resistência e processos de adaptação. Assim, para apoiar os programas de manejo de resistência a inseticidas e compreender a resistência *S. frugiperda* a spinetoram, este estudo teve como objetivos: i) caracterizar as bases moleculares da resistência de *S. frugiperda* a spinetoram utilizando o método de *bulk segregant analysis* combinada com sequenciamento de DNA e RNA, ii) avaliar o custo adaptativo associado à resistência de *S. frugiperda* a spinetoram comparando vários parâmetros biológicos e por meio de tabelas de vida de fertilidade das linhagens resistentes, suscetíveis e heterozigotas quando alimentadas com plantas de milho, soja e algodão, iii) caracterizar e quantificar as proteínas das linhagens de *S. frugiperda* resistente e suscetível a spinetoram quando alimentadas com plantas de milho, soja e algodão mediante uso de cromatografia líquida acoplada à espectrometria de massa (LC-MS), e iv) identificar os metabólitos associados à resistência de *S. frugiperda* a spinetoram por meio da metabolômica baseada em cromatografia gasosa acoplada à espectrometria de massa (GC-MS). A análise de mapeamento genômico possibilitou a identificação de uma deleção de três nucleotídeos na subunidade α6 do receptor nicotínico de acetilcolina (nAChR α6), e a análise do transcritoma demonstrou a superexpressão de genes do citocromo P450, transportadores ABC e proteínas cuticulares que podem estar envolvidos na resistência a spinetoram. Com base nos paramêtros biológicos, há custo adaptativo associado à resistência de *S. frugiperda* a spinetoram quando as lagartas se alimentam de plantas de soja e algodão, ao passo que não foi observado custo adaptativo em plantas de milho. O estudo de proteômica demonstrou que as plantas hospedeiras são fatores significativos na expressão proteica das linhagens resistente e suscetível de *S. frugiperda* a spinetoram, sendo que a maioria das proteínas diferencialmente expressas entre essas duas linhagens é específica para cada planta hospedeira. A análise de enriquecimento demonstrou que as proteínas diferencialmente expressas estão relacionadas a processos metabólicos, celulares, de desenvolvimento e regulação biológica. Um total de 86 metabólitos foram detectados por meio da metabolômica baseada em GC-MS, dos quais 20 metabólitos foram diferencialmente abundantes entre as linhagens resistente e suscetível a spinetoram. Os metabólitos diferenciais foram principalmente aminoácidos, carboidratos, ácidos dicarboxílicos e ácidos graxos e foram enriquecidos em vias relacionadas ao metabolismo de cisteína e metionina, metabolismo do ácido linoléico e biossíntese de aminoacil-tRNA. O uso de abordagens multi-ômicas permitiu um entendimento amplo e integrado dos mecanismos moleculares associados à inseticidas e à adaptação a plantas hospedeiras em *S. frugiperda*, fornecendo uma perspectiva holística desses dois processos adaptativos.

Palavras-chave: Lagarta-do-cartucho, Espinosinas, Genômica, Transcritômica, Proteômica, Metabolômica

ABSTRACT

Multi-omics approaches for understanding spinetoram resistance in *Spodoptera frugiperda* (Lepidoptera: Noctuidae)

Insecticide resistance is one of the main challenges in pest management programs. The fall armyworm, *Spodoptera frugiperda* (Lepidoptera: Noctuidae), is a polyphagous pest with a high risk of resistance evolution to insecticides. Resistance of *S. frugiperda* to spinetoram has been reported, however, information about the molecular basis of spinetoram resistance and the possible fitness costs associated with it is not elucidated. The use of multi-omics approaches has provided insights into resistance mechanisms and adaptation processes. Thus, to support the insecticide resistance managament programs and understand the spinetoram resistance in *S. frugiperda*, this study aimed to: i) characterize the molecular basis of spinetoram resistance in *S. frugiperda* employing the bulk segragant analysis combined with DNA and RNA sequencing, ii) assess the fitness costs of spinetoram resistance in *S. frugiperda* by comparing several biological parameters and constructing fertility life tables for resistant, susceptible, and heterozygous strains feeding on plants of corn, soybean, and cotton plants, iii) characterize and quantify the proteins of spinetoram-resistant and susceptible strains of *S. frugiperda* when fed on corn, soybean and cotton plants using liquid chromatography mass spectrometry (LC-MS), and iv) identify the metabolites associated with spinetoram resistance in *S. frugiperda* using metabolomics-based gas chromatography mass spectrometry (GC-MS). The genome mapping analysis led to the identification of the deletion of three nucleotides in the subunit α6 of the nicotinic acetylcholine receptor (nAChR α6), and the transcriptome analysis showed up-regulation of some cytochrome P450, ABC transporters and cuticle proteins genes that could be involved in spinetoram resistance. Based on life history traits, there are fitness costs associated with spinetoram resistance in *S. frugiperda* when the larvae feed on soybean and cottons plants, but not on corn plants. The proteomics study showed that the host plants are significant factors in shaping the protein expression of spinetoram-resistant and susceptible strains, with majority of the differentially expressed proteins between these two strains being specific to each host plant. Enrichment analysis showed that the differential expressed proteins were related to metabolic, cellular, developmental, and biological regulation processes. A total of 86 metabolites were detected using GC-MS based metabolomics, of which 20 metabolites were differentially abundant between the spinetoram-resistant and susceptible strains. The differential metabolites were mainly amino acids, carbohydrates, dicarboxylic acids and fatty acids and they were enriched in pathways related to cysteine and methionine metabolism, linoleic acid metabolism and aminoacyl-tRNA biosynthesis. The use of multi-omics approaches allowed a comprehensive and integrated understanding of the molecular mechanisms underlying insecticide and host plant adaptation in *S. frugiperda*, providing a holistic perspective on these two adaptive processes.

Keywords: Fall armyworm, Spinosyns, Genomic, Transcriptomic, Proteomic, Metabolomic

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1. INTRODUCTION

Insecticide resistance in crop pests represents one of the major constraints to agricultural production (Onstad and Knolhoff, 2023). The widespread use of synthetic insecticides imposes a strong selection pressure, resulting in the evolution of many cases of resistance. So far, there are more than 600 species of arthropod pests that have evolved resistance to at least one insecticide (Sparks et al., 2020). The loss of effectiveness of the current and newly developed insecticides due to insect resistance impacts the pest management programs, limiting the control options and decisions of growers to minimize the damage caused by insect pests (Sparks et al., 2020).

The fall armyworm, *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae), is one of the most important pests in agriculture production systems. It is a polyphagous pest that can feed on more than 350 host plants, including economically important crops such as corn, soybean, and cotton (Montezano et al., 2018). The distribution of *S. frugiperda* was restricted to tropical and subtropical regions of the Americas until 2016 when it was reported as an invasive pest in Africa (Goergen et al., 2016). To date, this pest has spread in many countries of Africa, Asia and Oceania (Baloch et al., 2020). One of the greatest concerns, in addition to the high economic losses caused by *S. frugiperda*, is the ability of this pest to evolve resistance to insecticides and Bt plants.

Chemical insecticides are a key component to manage *S. frugiperda* in agriculture systems (Burtet et al., 2017; Van den Berg and du Plessis, 2022). Although the advent of Bt crops provided effective control and reduced the use of synthetic insecticides against *S. frugiperda* (Fatoretto et al., 2017; Van den Berg and du Plessis, 2022), the widespread use of this technology with a low adoption of insect resistance management strategies favored to evolution of Bt resistance for this pest (Huang, 2021; Yang et al., 2022). Therefore, the use of synthetic insecticides has increased due to the resistance cases of *S. frugiperda* to Bt crops. This has contributed to the evolution of *S. frugiperda* resistance to different groups of insecticides (Bolzan et al., 2019; Carvalho et al., 2013; Diez-Rodríguez and Omoto, 2001; Garlet et al., 2021; Muraro et al., 2021; Nascimento et al., 2022, 2016), including the insecticides of the spinosyn group (Lira et al., 2020; Okuma et al., 2018).

The spinosyns are a group of insecticides that are effective against a broad range of insect pests (Crouse et al., 2001). These insecticides act on the insect nervous system as allosteric modulators of nicotinic acetylcholine receptors (Crouse et al., 2001; Sparks et al., 2012). Currently, there are two commercially available active ingredients: spinosad and

spinetoram. Spinosad, a naturally occurring mixture of spinosyns A and D, was the first spinosyn insecticide to be launched (Sparks et al., 2012). Spinetoram, the second spinosyn insecticide introduced to the market, is a mixture of synthetically modified metabolites (spinosyn J and L) and has shown positive toxicological attributes compared to spinosad (Dripps et al., 2008). Spinosyn insecticides have been an important tool in integrated pest management programs due its novel mode of action and highly favorable environmental and toxicological profiles (Salgado and Sparks, 2005). However, resistance cases have been reported for the spinosyn insecticides in many species of insect pests (Sparks et al., 2012), including the reports of *S. frugiperda* resistance for both spinosad (Okuma et al., 2018) and spinetoram (Lira et al., 2020).

The resistance of *S. frugiperda* to spinosyn insecticides has been characterized as autosomal, incompletely recessive and polygenic (Lira et al., 2020; Okuma et al., 2018). In addition, the resistant strains selected by Okuma et al. (2018) and Lira et al. (2020) presented high levels of resistance (resistance ratio >890-fold). To effectively address the evolution of spinosyn resistance in *S. frugiperda*, it is essential to understand the molecular mechanisms involved, the relationship between the adaptations to environmental factors and insecticide resistance, and the potential fitness costs associated with both adaptation processes.

The evolutionary process of insecticide resistance usually involves physiological and biochemical changes that are genetically inherited by insect pests to overcome xenobiotics compounds (Hawkins et al., 2019). Such adaptive mechanisms involve changes at genomic and transcriptomic levels in response to selective pressure. Studies on the molecular mechanisms of insecticide resistance have identified target site insensitivity and metabolic detoxification as the main resistance mechanisms in insects (ffrench-Constant, 2013; ffrench-Constant et al., 2004; Li et al., 2007). Identification of resistance mechanisms is fundamental to understanding the evolutionary process of insecticide resistance and how these genes are spread in natural populations.

In a similar way, herbivorous insects have to evolve numerous traits that enable them to adapt to host plants, which includes fitness variations and physiological mechanisms to overcome plant defense mechanisms (Etges, 2019). The interaction between host plant adaptation and insecticide resistance may influence the insect response in these two adaptation processes due to an overlap in some metabolic pathways involved in both processes (Alyokhin and Chen, 2017). This can be more challenging to polyphagous species, which must have a greater capacity to cope with the diverse plant secondary compounds from different host plants (Alyokhin and Chen, 2017; Dermauw et al., 2018). The study conducted

by Dermauw et al. (2013) demonstrated that the transcriptional response of *Tetranychus urticae* changed according to the host plant, and most of genes with altered expression belonged to known detoxification enzymes. A similar scenario may occur for *S. frugiperda*, especially in regions where the agricultural landscape is characterized by the succession and overlapping of different crops. Although the ability of *S. frugiperda* to cope with xenobiotics such insecticides and plant toxins has been described (Amezian et al., 2021), studies covering the molecular basis and the fitness effects of the interaction between these two factors remain incipient.

The next-generation high-throughput sequencing technologies have been an important tool in insecticide resistance studies (Pittendrigh et al., 2014). The use of genomic and transcriptomic sequencing enabled the identification of genetic polymorphisms and differential gene expression between resistant and susceptible strains (Ingham et al., 2021). In addition to genomic and transcriptomic analysis, mass spectrometry-based omics technologies such as proteomics and metabolomics can provided a comprehensive understanding of biological processes at protein and metabolite level (Griffiths and Wang, 2009). The study of insecticide resistance along with these omics approaches can also provide insights into questions about adaptation to changing environments, sources of adaptive variation and origins of novel traits (Hawkins et al., 2019).

The high degrees of polyphagia of *S. frugiperda*, the recent report of spinetoram resistance in a field-collected population, and the availability of omics approaches provide a unique opportunity to understand the evolution of spinosyn resistance in *S. frugiperda* by identifying the molecular mechanisms and exploring factors that could magnify the fitness costs. Thus, the objectives of this study were to use genomics, transcriptomics, proteomics, and metabolomics approaches to identify at molecular level the resistance mechanisms and the possible effects of plants of corn, soybean, and cotton on the fitness costs associated with spinetoram resistance in *S. frugiperda*.

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2. GENOMIC AND TRANSCRIPTOMIC ANALYSIS OF SPINETORAM RESISTANCE IN *Spodoptera frugiperda* (LEPIDOPTERA: NOCTUIDAE)

Abstract
The evolution of resistance to insecticides poses a major threat to pest management programs. Understanding the molecular mechanisms underlying insecticide resistance is essential to design sustainable resistance management programs. The fall armyworm, *Spodoptera frugiperda* (J. E. Smith), is an important insect pest of many crops and has a remarkable ability to evolve resistance to insecticides. In this study, we characterize the molecular basis of spinetoram resistance in *S. frugiperda* employing the bulk segregant analysis (BSA) combined with DNA and RNA sequencing. Crosses between a spinetoram-resistant and susceptible strains of *S. frugiperda* were performed and the resulting progeny was propagated for eight generations, following a selection by spinetoram to form the selected and unselected strains. The genome mapping analysis led to the identification of the deletion of three nucleotides in the subunit α6 of the nicotinic acetylcholine receptor (nAChR α6). The transcriptome analysis showed up-regulation of some cytochrome P450, ABC transporter and cuticle proteins genes involved in spinetoram resistance. In addition, the combined genomic and transcriptomic approaches with BSA allowed the identification of the target site insensitivity as spinetoram resistance mechanism in *S. frugiperda*.

Keywords: fall armyworm; spinosyn; DNA-Seq; RNA-Seq; bulk segregant analysis

2.1. Introduction

Insect pests can cause significant damage to agricultural crops, reducing production and threatening the food supply. Chemical insecticides have been one of the main strategies used to minimize the impact of insect pests on agricultural crops. However, the widespread use of these chemical compounds has led to the evolution of insect resistance to many groups of insecticides (Sparks et al., 2020). The emergence of highly resistant populations to insecticides poses a challenge to many pest management programs, threatening the effectiveness of the currently available insecticides and thus impacting the decisions for pest control options (Sparks et al., 2021). Therefore, resistance management strategies are needed to preserve the lifetime of current and newly developed insecticides.

The fall armyworm, *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae), is one of the most damaging pests of cultivated crops. The importance of this pest has been increasing worldwide because it has been reported as an invasive pest in many countries of the African, Asian and Oceanian continent (Baloch et al., 2020; Goergen et al., 2016). Due to its high degrees of polyphagia, this pest can be found causing severe damage in agricultural crops such as maize, soybean, cotton, sorghum and rice (Montezano et al., 2018). The control of *S. frugiperda* relied mostly on the use of insecticides, which inevitably resulted in the

evolution of resistance to many groups of insecticides (Bolzan et al., 2019; Carvalho et al., 2013; Diez-Rodríguez and Omoto, 2001; Garlet et al., 2021; Lira et al., 2020; Muraro et al., 2021; Nascimento et al., 2022, 2016).

The rapidly evolution of insecticide resistance in *S. frugiperda* poses a threat to the sustainability of currently available insecticides for its control. Spinetoram is a spinosyn-based insecticide with neurotoxic effects that acts as an allosteric modulator of nicotinic acetylcholine receptors, registered for *S. frugiperda* control (Dripps et al., 2008; Salgado and Sparks, 2005). This insecticide is a mixture of synthetically modified metabolites (spinosyn J and L) of the actinomycete soil bacterium *Saccharopolyspora spinosa* and has demonstrated positive toxicological attributes compared to its predecessor spinosad (Crouse et al., 2001; Dripps et al., 2008; Salgado and Sparks, 2005). Spinosyn insecticides have been an important tool in pest management programs due to their high efficacy against insect pests and low toxicity to beneficial and non-target organisms (Dripps et al., 2011; Salgado and Sparks, 2005). However, resistance cases for this group of insecticides have been reported for many insects pests (Sparks et al., 2012), including the recent reports for *S. frugiperda* (Lira et al., 2020; Okuma et al., 2018).

The resistance mechanisms of spinosyn insecticides have been studied in several insect pests. Most of the studies have associated target site insensitivity of the nicotinic acetylcholine receptor (nAChR) with spinosyn resistance. Point mutations, deletions, exon skipping, mis-splicing and truncated proteins involving the α6 subunit of the nAChR have been reported in spinosad-resistant strains of *Drosophila melanogaster* (Perry et al., 2007), *Plutella xylostella* (Baxter et al., 2010; Rinkevich et al., 2010), *Frankliniella occidentalis* (Puinean et al., 2013; Wan et al., 2018), *Frankliniella intonsa* (Hiruta et al., 2018), *Thrips palmi* (Bao et al., 2014) *Ceratitis capitata* (Ureña et al., 2019) and *Tuta absoluta* (Berger et al., 2016; Grant et al., 2019; Silva et al., 2016). However, some studies have shown that detoxification enzymes such as cytochrome P450 monooxygenases and esterases could also been involved in spinosad resistance (Bao et al., 2014; Herron et al., 2014; Rehan and Freed, 2014; Wang et al., 2009, 2006; Zhang et al., 2020). Most of these studies focused on the sequencing analysis of the nAChR α6 gene and the use of synergists that inhibits detoxification enzymes to investigate the possible mechanisms associated with spinosyn resistance.

The recent advance in genome/transcriptome sequencing technologies have provide a valuable tool for a better understanding of the molecular basis of insect resistance (Pittendrigh et al., 2014). These technologies allow for the surveying of changes in the entire genome and

transcriptome, enabling a more comprehensive analysis of the mechanisms responsible for insect resistance. In an attempt to elucidate the molecular mechanisms underlying spinosyn resistance in *S. frugiperda*, we employed bulk segregant analysis combined with DNA and RNA sequencing technologies to analyze and compare the changes at the genomic and transcriptomic levels between spinetoram-resistant and susceptible strains.

2.2. Material and Methods

2.2.1. Insect strains

Two strains of *S. frugiperda* were used to conduct this study: the laboratory susceptible strain (SS-Lab) and the spinetoram-resistant strain (RR). The laboratory susceptible strain was collected in Sete Lagoas, Minas Gerais State, Brazil and it has been maintained without selection pressure from any insecticides and Bt proteins for more than 20 years. The spinetoram-resistant strain was obtained from a field population collected in São Desidério, Bahia State, Brazil in 2018 and it presented a resistance ratio of 971-fold (Kanno et al., 2023). The reciprocal crosses between ♀ RR × ♂ SS-Lab and ♂ RR × ♀ SS-Lab were performed for bulk segregant analysis. The resulting F_1 progeny from both reciprocal crosses were inbred for 8 generations. All insects were reared on artificial diet (Kasten Jr et al., 1978) under laboratory conditions (25 ± 2 °C, 70% relative humidity and 14:10 (L:D) h photoperiod).

A subset of larvae from F_8 generation was selected at the discriminating concentration of 100 µg ml^{-1} of spinetoram, and the surviving individuals were considered as the selected strain (Sel). The remaining F_8 larvae formed the control unselected strain (Unsel). The Sel and Unsel strains were reared for one generation, and then the larvae from each strain were collected for DNA/RNA extraction. DNA was extracted from Sel, Unsel, RR and SS-Lab strains, while RNA was extracted from Sel, Unsel and SS-Lab strains.

2.2.2. Toxicological bioassays

Diet-overlay bioassay method was used to characterize the susceptibility of the Sel and Unsel strains to spinetoram. Six to eight concentrations logarithmically spaced were tested for each strain. The concentrations ranged from 1.8 to 180 µg ml^{-1} for Unsel strain and 32 to 1800 µg ml^{-1} for Sel strain. These different concentrations were obtained by the dilution

of the formulated insecticide (Exalt® 120 g a.i. l^{-1}, Dow AgroSciences, Franco da Rocha – SP) in distilled water with the addition of 0.1% (v/v) of the surfactant Triton X-100 (Sigma Aldrich Brasil Ltda). The bioassays were performed in 24 wells acrylic plates, with each well (1.9 cm^2 area) containing artificial diet. After the dilution, 30 µl of the insecticide solution was applied in each well. One early third instar-larvae was infested in each well. Approximately three replicates of 24 larvae were used for each concentration. The bioassay plates were kept under controlled conditions of 25 ± 2 °C, 70% relative humidity and a photoperiod of 14:10 (L:D) h. The mortality was assessed after 48 h, and larvae that did not showed coordinated movement when prodded were considered dead.

2.2.3. DNA/RNA extraction and sequencing

Total DNA and RNA was extracted from pools of ten fourth instar-larvae of *S. frugiperda* using the AllPrep DNA/RNA Mini Kit (Qiagen) according to the manufacturer's instructions. Four biological replicates were prepared for each strain. The integrity, quality and concentration of the DNA and RNA samples was checked using agarose gel electrophoresis and Qubit Fluorometer (Thermo Fisher Scientific). The prepared libraries were sequenced on an Illumina HiSeq 2500 platform using paired-end 150 bp reads.

2.2.4. Analysis of DNA reads and variant calling

The quality of the DNA reads was assessed with FASTQC (Andrews, 2010). The adapters and low-quality reads were removed using Trimmomatic v. 0.39 (Bolger et al., 2014). High-quality DNA reads were aligned to the reference genome of *S. frugiperda* (NCBI Accession Number PRJNA590312) using BWA with default parameters. The alignments files were processed using SAMTOOLS (Danecek et al., 2021). The SAM files were converted into BAM files and sorted using the *view* function, then the BAM files were sorted using the *sort* function and finally the BAM files from the same strain were merged using the *merge* function. Picard software was used to add read groups and mark duplicates into merged BAM files. Variant calling analysis was performed using freebayes (Garrison and Marth, 2012). The variants were annotated using SnpEff (Cingolani et al., 2012). Several criteria were considered for variant calling analysis: we remove i) reads with depth < 15; ii)

heterozygous alleles in the susceptible sample; iii) intron variants; iv) intergenic regions; v) low impact effects.

To perform the bulk segregant analysis (BSA), the final filtered variant calling file with SS-Lab and Sel samples was used to estimate the SNP index (alternative allele reads/total read depth) in the Mutplot software (Sugihara et al., 2022). Variants with SNP index ≥ 0.90 were considered homozygous following the criteria proposed by Abe et al. (2012). The variants associated with resistance require to present a SNP index ≥ 0.90 in RR and Sel samples.

2.2.5. Analysis of RNA reads

The quality of RNA sequencing reads was assessed using FASTQC (Andrews, 2010) and the adapters were removed using Trimmomatic v. 0. 39 (Bolger et al., 2014). The clean reads were directly mapped to the reference genome of *S. frugiperda* (NCBI Accession Number PRJNA590312) using HISAT2 alignment software (Kim et al., 2019). The aligned reads were counted with *featureCounts* (Liao et al., 2014). DESeq2 (Love et al., 2014) was used to assess the differentially expressed genes (DEG). The criteria for identifying differentially expressed genes were an adjusted p-value < 0.05 and relative expression log2FoldChange > 2 for up-regulated genes and log2FoldChange < -2 for down-regulated genes. GO enrichment analysis of the DEGs was performed using topGO package (Alexa and Rahnenführer, 2009) with Fisher test. KEGG enrichment analysis of the DEGs was performed using the *enrichKEGG* function from the clusterProfiler package (Yu et al., 2012) based on a hypergeometric test. All analyses were performed in the R Software (R Core Team, 2022).

2.2.6. Synergist bioassays

Synergist bioassays were performed with SS-Lab and RR strains to evaluate the effect of detoxification enzymes on spinetoram resistance. The synergists piperonyl butoxide (PBO, Sigma Aldrich), diethyl maleate (DEM, Sigma Aldrich) and S-S-S-tributyl phosphorotrithioate (DEF, Chem Service) were diluted in acetone, and 1 µl of the solution was applied onto the third instar larvae pronotum using a microapplicator (Bukard). The doses of synergists PBO, DEM and DEF were 0.1 µg, 1 µg and 0.32 µg per larva, respectively. The control treatment consisted of acetone alone. After 2h of synergist application, the larvae were

exposed to spinetoram in diet overlay bioassay method described previously. The tested concentrations of spinetoram ranged from 0.1 to 5.6 µg ml^{-1} for SS-Lab strain and 180 to 5600 µg ml^{-1} for RR strain.

2.2.7. Molecular analysis of nAChR α6 deletion and its association with spinetoram resistance

To examine the association of Y232del with spinetoram resistance in *S. frugiperda* we designed crosses between the SS-Lab and the RR strain for a genotyping assay. Initially, a single couple were established by the cross of one female individual from the SS-Lab strain with one male individual from the RR strain. Then, a backcross was established by crossing one male individual from the F_1 progeny with one female individual from the RR strain, which is the parental strain that was phenotypically more distinct from F_1 (Lira et al., 2020). 72 early third instar-larvae from this backcross were submitted to diet overlay bioassays performed in 24-well acrylic with a discriminating concentration of spinetoram (100 µg ml^{-1}). The evaluation of the bioassays was performed 48 h post-infestation to phenotypically identify the dead and alive individuals. Larvae that did not show coordinated movement were considered dead. The dead and alive larvae from the bioassays and the adults involved in the crosses were stored at -80 °C prior to DNA extraction.

DNA of individually dead and alive larvae from the bioassays and also of the adults of the SS-Lab strain, RR strain and F_1 progeny from crosses was extracted by using a modified CTAB protocol (Marín et al., 2021). The quality of DNA extraction was verified through a 1.5% agarose gel electrophoresis reaction. PCR was performed with 2.5 µl of 10X PCR Buffer Mg^{2+} Free, 1.75 µl of $MgCl_2$ at 25mM, 0.5 µl of dNTP Mix at 10 mM, 0.8 µl of forward and reverse primers at 10 uM, 0.3 µl of Taq DNA Polymerase at 5 units/µl and 2 µg of DNA, in a final volume of 25 µl. The forward (5' TTCACCATCATGATCAGGAGAC 3') and reverse (5' AGCGTGAGTTTCTCTCCG 3') primers were used for PCR to amplify a 129 bp region of the *S. frugiperda* nAChR α6 gene. The PCR amplification was performed in the following temperature cycling conditions: 1 cycle of 94ºC for 2 min followed by 35 cycles of 94ºC for 45 s, 58.5ºC for 30 s and 72ºC for 1 min, and a final step of 72ºC for 10 min. The PCR products were purified using the ExoSAP-IT™ PCR Product Cleanup Reagent (Thermo Fisher Scientific) and the purified fragments were quantified through a 3% agarose gel electrophoresis. The purified PCR fragments were sequenced using the Sanger method with the reverse primer. The sequencing was performed using the Applied Biosystems 3500

Genetic Analyzer equipment at Plant Breeding Laboratory – CENA/USP. The alignment of the sequences obtained from the Sanger sequencing was performed against the *S. frugiperda* nAChR α6 gene reference sequence available on NCBI (Gene ID: LOC118270232). A chi-square test was performed to examine the association between Y232del and survival to spinetoram exposure.

2.2.8. Complementation test

A complementation test was performed to verify if the three-nucleotide deletion of nAChR α6 gene, found in the spinetoram-resistant strain, is also present in a spinosad-resistant strain. For this, we used the spinosad-resistant strain (Spin-res) established by Okuma et al. (2018) which presents a resistance ratio of 890-fold. Reciprocal crosses between ♀ Spin-res × ♂ RR and ♂ Spin-res × ♀ RR were performed, generating the S1 and S2 progenies, respectively. The S1 and S2 progenies were maintained in 100 ml plastic cups containing artificial diet. At least 192 early third instar larvae from each parental strain, as well as from the S1 and S2 progenies were exposed to both spinetoram and spinosad insecticides in the diet overlay bioassays. The bioassays were performed in 24-well acrylic plates with the discriminating concentrations of 100 μg ml^{-1} and 1000 μg ml^{-1} of spinetoram and spinosad, respectively. The evaluation of the bioassays was performed 48 h post-infestation and larvae that did not show coordinated movement were considered dead. To confirm the presence of three-nucleotide deletion of nAChR α6 gene, 12 individuals from each of the S1 and S2 progenies and 10 individuals from each RR and Spin-res strains were submitted to a DNA sequencing using the Sanger method following the described procedure in section 2.2.7.

2.2.9. Statistical analysis

The mortality data from concentration-response curves were submitted to Probit analysis. The data were fitted to a generalized linear model with binomial distribution and probit as the function link. The LC_{50}s and the respective confidence intervals were estimate using the function *dose.p* from the MASS package (Venables and Ripley, 2002). The resistance ratio was calculated dividing the LC_{50} value of the tested strain by the LC_{50} value of the SS-Lab strain. Synergistic ratios were calculated by dividing the LC_{50} value of the control

(insecticide alone) by the LC_{50} value of the insecticide plus synergist treatment. All statistical analysis were performed in R Software (R Core Team, 2022).

2.3. Results

2.3.1. Toxicity of spinetoram to *Spodoptera frugiperda* strains

The LC_{50} of the SS-Lab strain was 0.81 μg ml^{-1}, whereas the RR and Sel strains presented a LC_{50} of 776.9 and 499.53 μg ml^{-1} respectively, resulting in a high resistance ratio of 971.12-fold for the RR strain and a resistance ratio of 624.37-fold for the Sel strain. The Unsel strain presented a LC_{50} of 6.53 μg ml^{-1}, resulting in a resistance ratio of 8.12-fold (Table 1).

Table 1. Susceptibility of *Spodoptera frugiperda* strains to spinetoram

Strain	*n*[a]	Slope (± SE)	LC_{50} (CI 95%)[b]	χ^2 (df)	Resistance ratio[c]
SS-Lab*	648	2.4 ± 0.2	0.8 (0.7 – 0.9)	9.1 (5)	-
RR*	693	2.6 ± 0.2	776.9 (685.7 – 880.3)	9.8 (5)	971.12
Sel	480	4.4 ± 0.6	499.5 (431.5 -578.2)	9.6 (4)	624.37
Unsel	552	1.8 ± 0.3	6.5 (4.4 – 9.6)	17.7 (5)	8.12

[a] number of larvae tested; [b] lethal concentration (μg ml^{-1}) of applied insecticide solution that kills 50% of the individuals; [c] Resistance ratio: LC_{50} of the tested strain/LC_{50} of the susceptible reference strain;*data from Kanno et al. (2023).

2.3.2. DNA sequencing analysis

DNA sequencing data was obtained by sequencing four samples from the SS-Lab and RR strains and two samples from the Sel and Unsel strains. The GC content ranged from 37 to 38% among all samples. The percentage of mappings in the reference genome of *S. frugiperda* ranged from 75.15 to 76.52% (Table 2).

Table 2. Summary of DNA sequencing

Sample	**Clean reads**	**GC content**	**Mapped ratio**
SS-Lab	610,578,483	37	76.03
RR	614,623,251	37	76.52
Sel	306,573,696	38	75.33
Unsel	223,832,174	38	75.15

2.3.3. Identification of SNPs and Indels associated with spinetoram resistance in *Spodoptera frugiperda*

The identification of genetic variants in the Freebayes software resulted in 29,163,352 variants, including 17,520,073 SNPs and 11,643,279 Indels. After the filtering process, nine SNPs and Indels presented a SNP index ≥ 0.90 in RR and Sel samples (Table 3). Among the variants, a deletion in the nicotinic acetylcholine receptor (nAChR) was identified.

Table 3. Nonsynonymous SNPs and Indels identified in the spinetoram resistant strain of *Spodoptera frugiperda*

ID	Reference	Alternative	Amino acid modification	Description
LOC118270232	GTACTACT	GTACT	Y232del	neuronal acetylcholine receptor subunit alpha-7-like
LOC118274764	CG	GA	R108S	trypsin, alkaline B-like
LOC118270596	C	T	R544K	uncharacterized LOC118270596
LOC118277248	A	C	K153N	zinc finger protein OZF-like
LOC118277371	A	T	R31Y	serine/threonine-protein kinase atg1-like
LOC118275334	TGA	TA	T92fs	keratin, type I cytoskeletal 10-like
LOC118269227	G	T	A243S	UDP-glucuronosyltransferase 2B10-like
LOC118275724	C	A	P493T	bile salt-activated lipase-like
LOC118278816	T	A	E208D	neurofilament heavy polypeptide-like

A high read depth was obtained in all sequenced samples. The SS-Lab strain presented a homozygous genotype for the reference allele and both RR and Sel strain presented a homozygous alternative allele. The Unsel strain presented this deletion in heterozygous form. The SS-Lab presented a SNP index of 0, while the RR and Sel strain presented a SNP index of 0.98 and 0.97, respectively. The SNP index of Unsel strain was 0.52.

This deletion corresponds to a region in exon 7 and results in a tyrosine amino acid predicted loss at the position 232 of nAChR α6 gene protein. The alignment of this region with the described nAChR α6 gene of other insect species demonstrated that the deletion of tyrosine amino acid occurs in a high conserved region across insect species (Fig. 1).

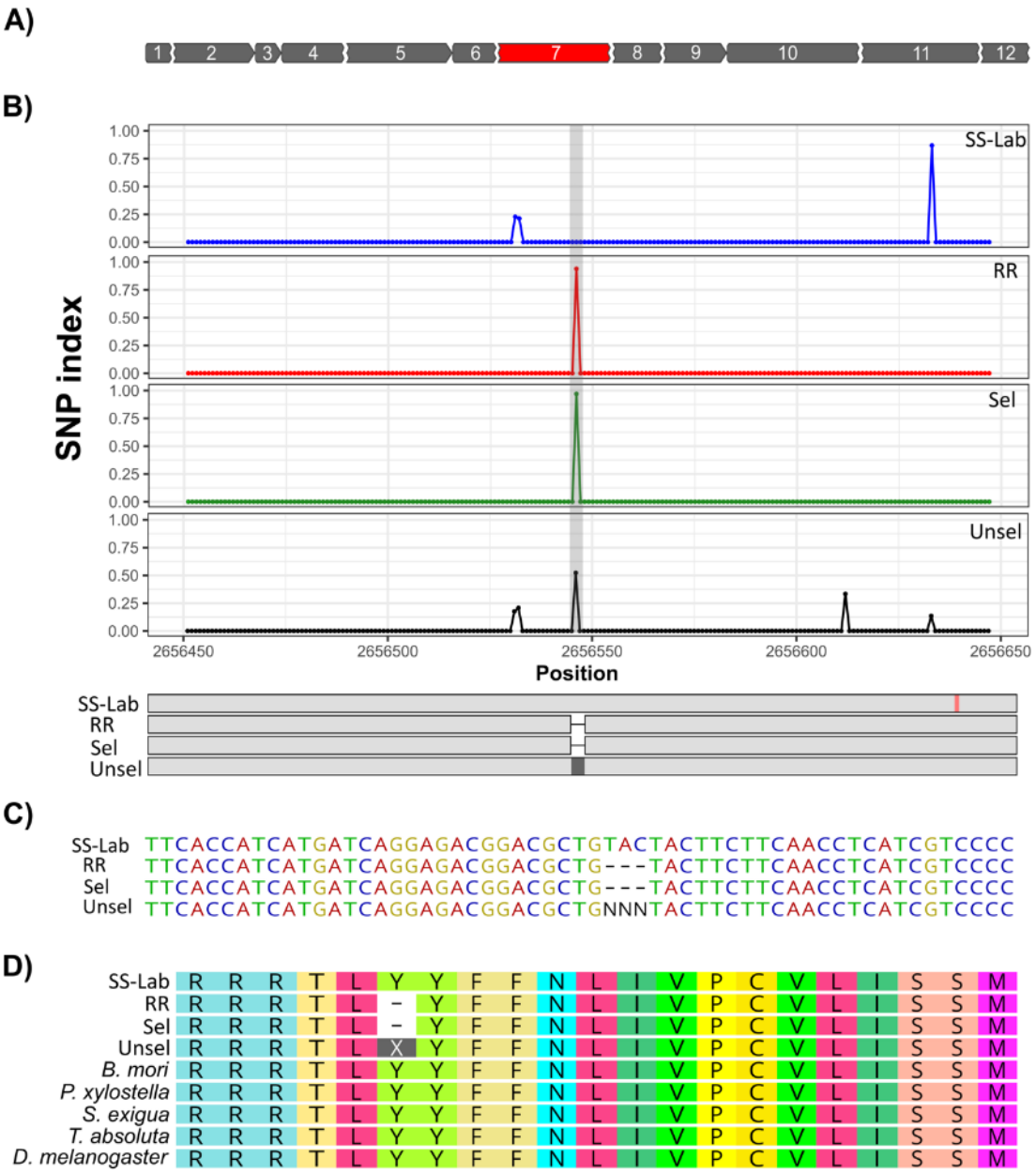

Fig. 1. Scheme of the deletion in the nAChR α6 gene of *Spodoptera frugiperda* strains. A) Exon structure of the nAChR α6 gene highlighting the exon 7. B) SNP index of the exon 7 for the SS-Lab, RR, Sel and Unsel strains. C) The triplet deletion presented in RR and Sel strains. D) Alignment of amino acids sequences of nAChR α6 of *S. frugiperda* strains with amino acids sequences of nAChR α6 from other insect species. The accession numbers of the shown sequences are: *Bombyx mori* (NP_001091842.2), *Plutella xylostella* (ADD69773.1),

Spodoptera exigua (QIC53910.1), *Tuta absoluta* (ALM23508.1) and *Drosophola melanogaster* (NP_723494.2).

2.3.4. RNA sequencing

The summary of Illumina sequencing of cDNA libraries is shown in Table 4. After removing the adapters and low qualities sequences, a mean of 17,925,160 clean reads were obtained for each library. The GC content for all libraries ranged from 45 to 46%. After the alignment, 85.54 to 86.76 % of the clean reads were mapped to reference genome of *S. frugiperda*.

Table 4. Summary of RNA sequencing on Illumina platform for *Spodoptera frugiperda* samples

Samples	Raw reads	Clean reads	GC content	Mapped ratio
SS-Lab 1	20,079,571	19,537,692	45	85.55
SS-Lab 2	18,879,975	18,290,122	46	85.50
SS-Lab 3	17,549,877	17,040,029	45	85.63
SS-Lab 4	19,764,274	19,273,147	46	85.55
Sel 1	17,169,398	16,480,144	46	85.77
Sel 2	18,491,405	17,809,257	46	85.54
Sel 3	21,388,898	20,640,215	46	82.95
Sel 4	18,290,402	17,617,702	46	86.23
Unsel 1	15,840,451	15,189,505	46	86.16
Unsel 2	18,213,018	17,566,502	46	85.61
Unsel 3	18,535,972	17,722,610	46	86.76
Unsel 4	18,567,786	17,935,002	46	86.35

2.3.5. Differentially expressed genes

The DEG analysis of the comparisons SS-Lab vs Sel, SS-Lab vs Unsel and Sel vs Unsel were performed on the 20,637 genes of the reference genome of *S. frugiperda*. Compared to the Sus transcriptome, a total of 2,688 DEGs were identified in the Sel strain, of which 1,470 were up-regulated and 1,218 were down-regulated (Fig. 2A and B; Appendix A). A similar number of DEGs were found in the comparison of the SS-Lab vs Unsel transcriptomes, a total of 2,565 DEGs were identified in the Unsel strain, including 1,376 up-

regulated and 1,189 down-regulated (Fig 2C and D; Appendix B). 16 DEGs were found in the last comparison (Sel vs Unsel), of which 9 were up-regulated and 7 were down-regulated in the Sel strain. (Fig 2E and F; Appendix C).

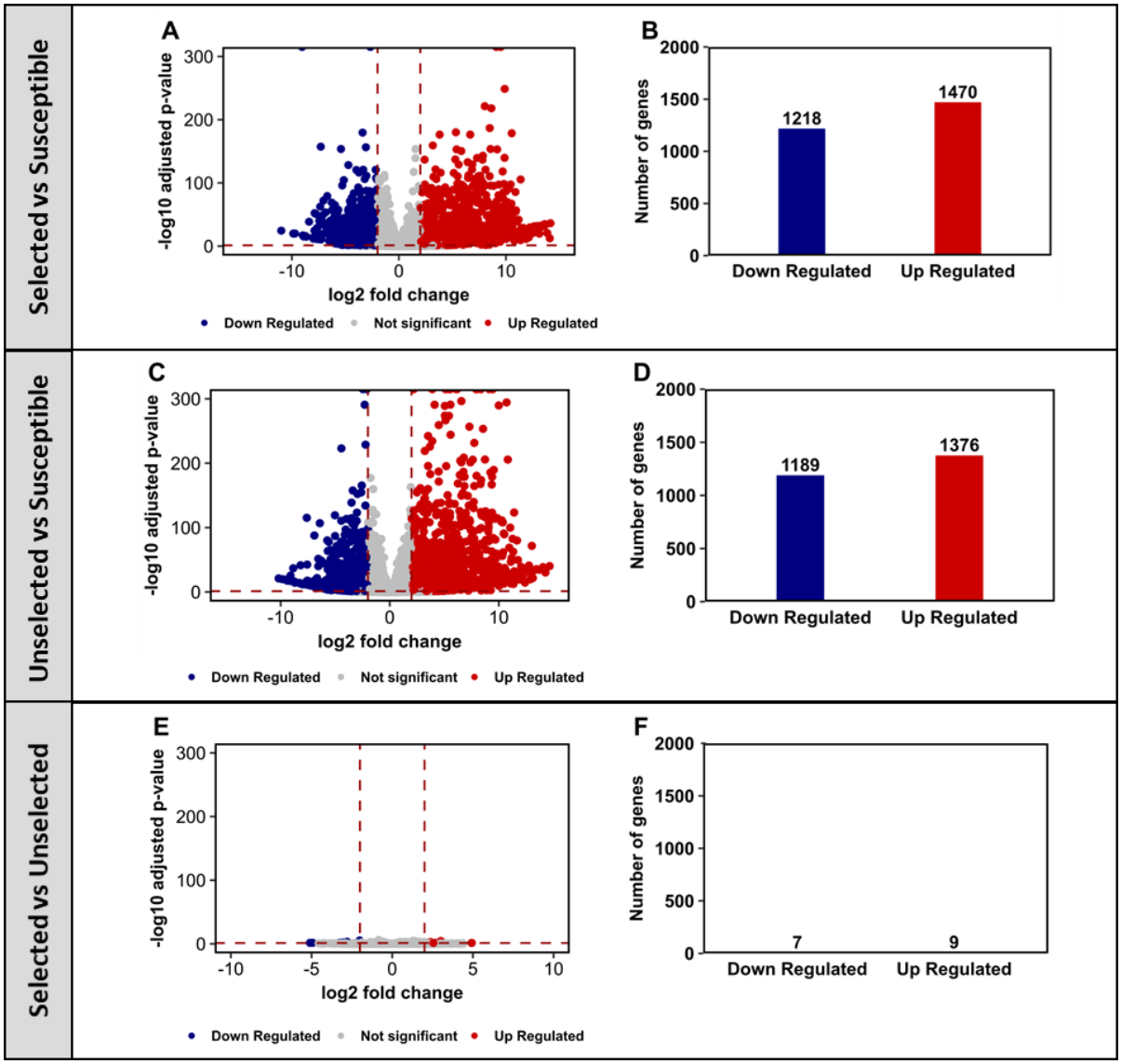

Fig. 2. Differentially expressed gene (DEG) analysis. A) Volcano plot of the DEGs for Sel vs SS-Lab; B) Number of up- and down-regulated DEGs for Sel vs SS-Lab; C) Volcano plot of the DEGs for Unsel vs SS-Lab; D) Number of up- and down-regulated DEGs for Unsel vs SS-Lab; E) Volcano plot of the DEGs for Sel vs Unsel; F) Number of up- and down-regulated DEGs for Sel vs Unsel.

2.3.6. GO and KEGG enrichment analysis of DEGs

Enrichment analysis assigned the identified DEGs into functional terms of GO. The 10 most enriched GO terms of the DEGs of each comparison (Sel vs SS-Lab, Unsel vs SS-

Lab and Sel vs Unsel) are shown in the Fig.3. The DEGs of Sel vs SS-Lab and Unsel vs SS-Lab comparisons were enriched in almost the same GO terms. For biological process, the most enriched terms include chitin-based cuticle development (GO:0040003), carboxylic acid metabolic process (GO:0019752) and small molecule metabolic process (GO:0044281). In molecular function category, the most enriched terms were related to cuticle structure (GO:0005214 – structural constituent of chitin-based cuticle, GO:0042302 – structural constituent of cuticle and GO:0008010 – structural constituent of chitin-based larval cuticle), oxidoreductase activity (GO:0016491) and catalytic activity (GO:0003824). The most enriched terms in the cellular component category were extracellular region (GO:0005576), extracellular matrix (GO:0031012) and extracellular space (GO:0005615).

The DEGs of the Sel vs Unsel comparison were enriched in terms of the biological process category that includes the cellular response to interferon-gamma (GO:0071346), response to interferon-gamma (GO:0034341) and fibroblast proliferation (GO:0048144). In the molecular function category, the DEGs were enriched in signaling receptor activator activity (GO:0030546), receptor regulator activity (GO:0030545), oxidoreductase activity, acting on NAD(P)H (GO:0016651) and structural constituent of ribosome (GO:0003735). The most enriched terms in cellular component category were lysosomal lumen (GO:0043202), organellar ribosome (GO:0000313) and mitochondrial ribosome (GO:0005761).

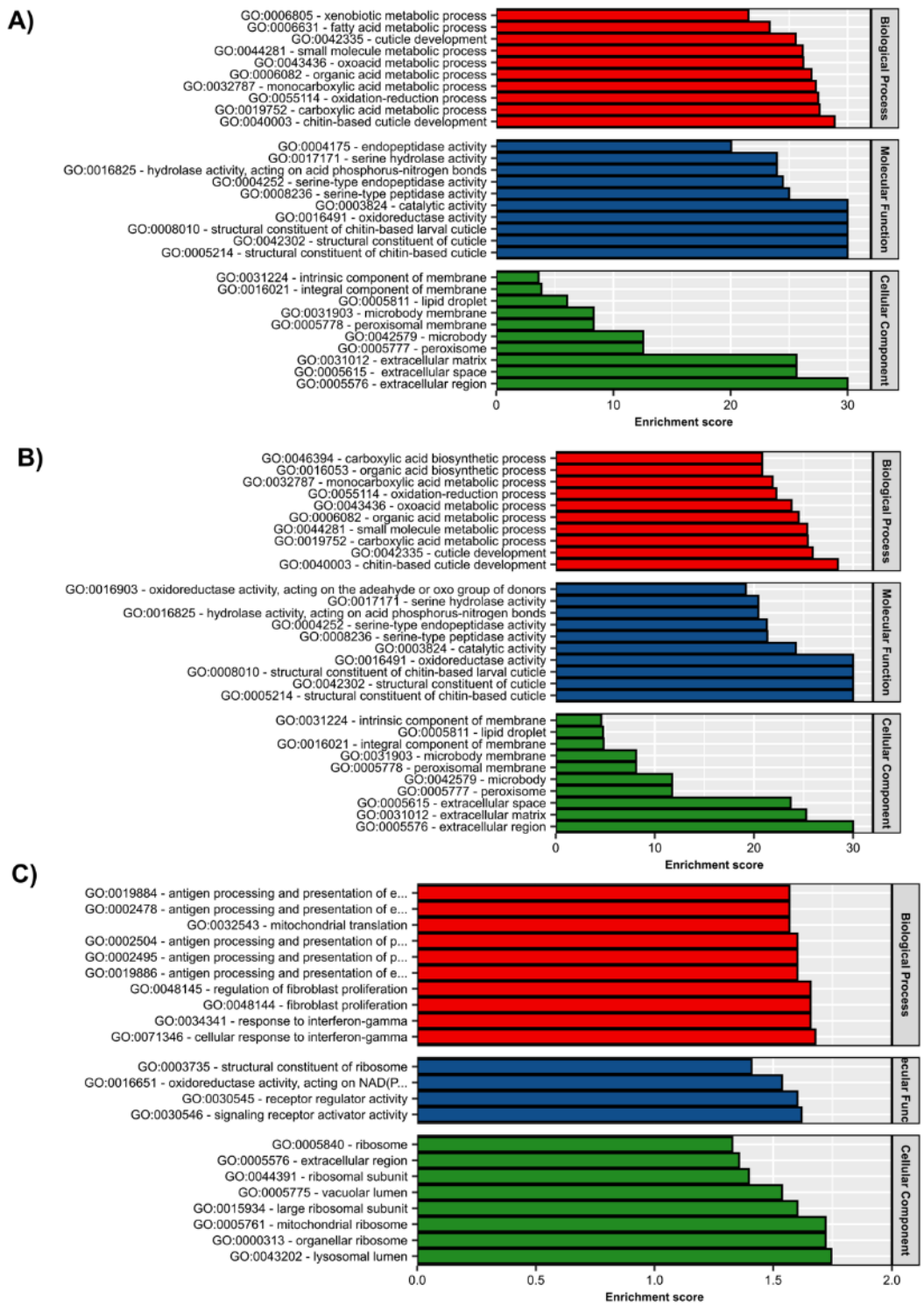

Fig. 3. Gene ontology enrichment analysis of the differentially expressed genes of A) Sel vs SS-Lab, B) Unsel vs SS-Lab and C) Sel vs Unsel

Based on the KEGG enrichment analysis, both DEGs of Sel vs SS-Lab and Unsel vs SS-Lab were enriched in almost the same pathways (Fig. 4). The majority of DEGs were enriched in metabolism pathways. The most enriched pathways included biosynthesis of

secondary metabolites, microbial metabolism in diverse environments and carbon metabolism. Pathways of biosynthesis of amino acid and ether lipid metabolism are also present in the top 10 enriched pathways. Antigen processing and presentation was the only enriched KEGG pathways were found in the DEGs of Sel vs Unsel.

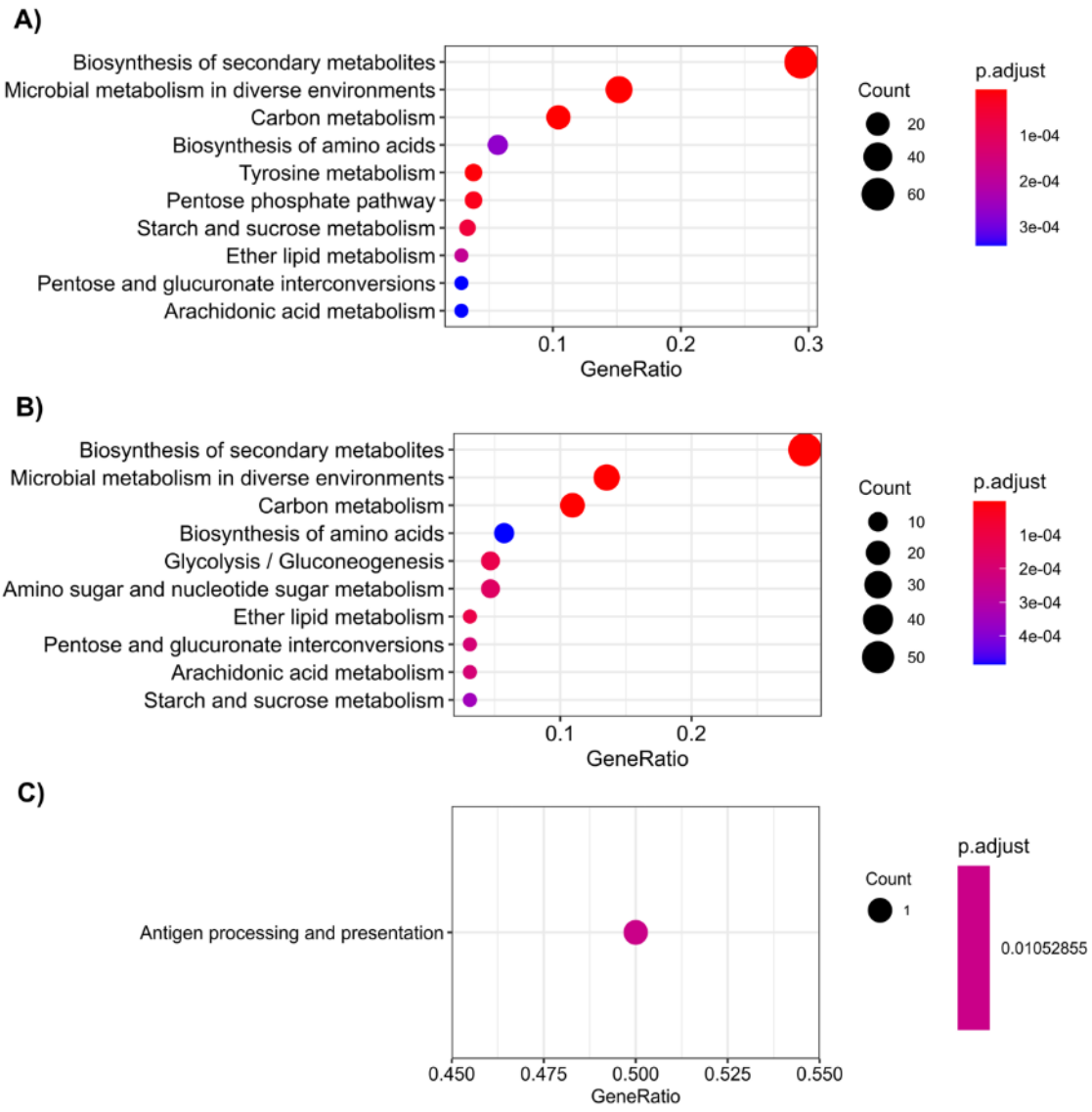

Fig. 4. KEGG enrichment analysis of the differentially expressed genes of A) Sel vs SS-Lab, B) Unsel vs SS-Lab and C) Sel vs Unsel

2.3.7. Expression patterns of insecticide detoxification related genes

The DEGs encoding potential enzymes involved in insecticide detoxification, which includes the cytochrome P450 monooxygenases (P450), carboxylesterases (CarE), glutathione

S-transferases (GST), ATP-binding cassette (ABC) transporter and UDP-glycosyltransferases (UGT) were obtained from the transcriptomes of Sel, Unsel and SS-Lab strains. Upon analyzing the DEGs, 86 P450s (Fig. 5), 18 CarEs (Fig. 6A), 19 GSTs (Fig. 6B), 5 ABC transporters (Fig. 6C) and 29 UGTs (Fig. 6D) were identified.

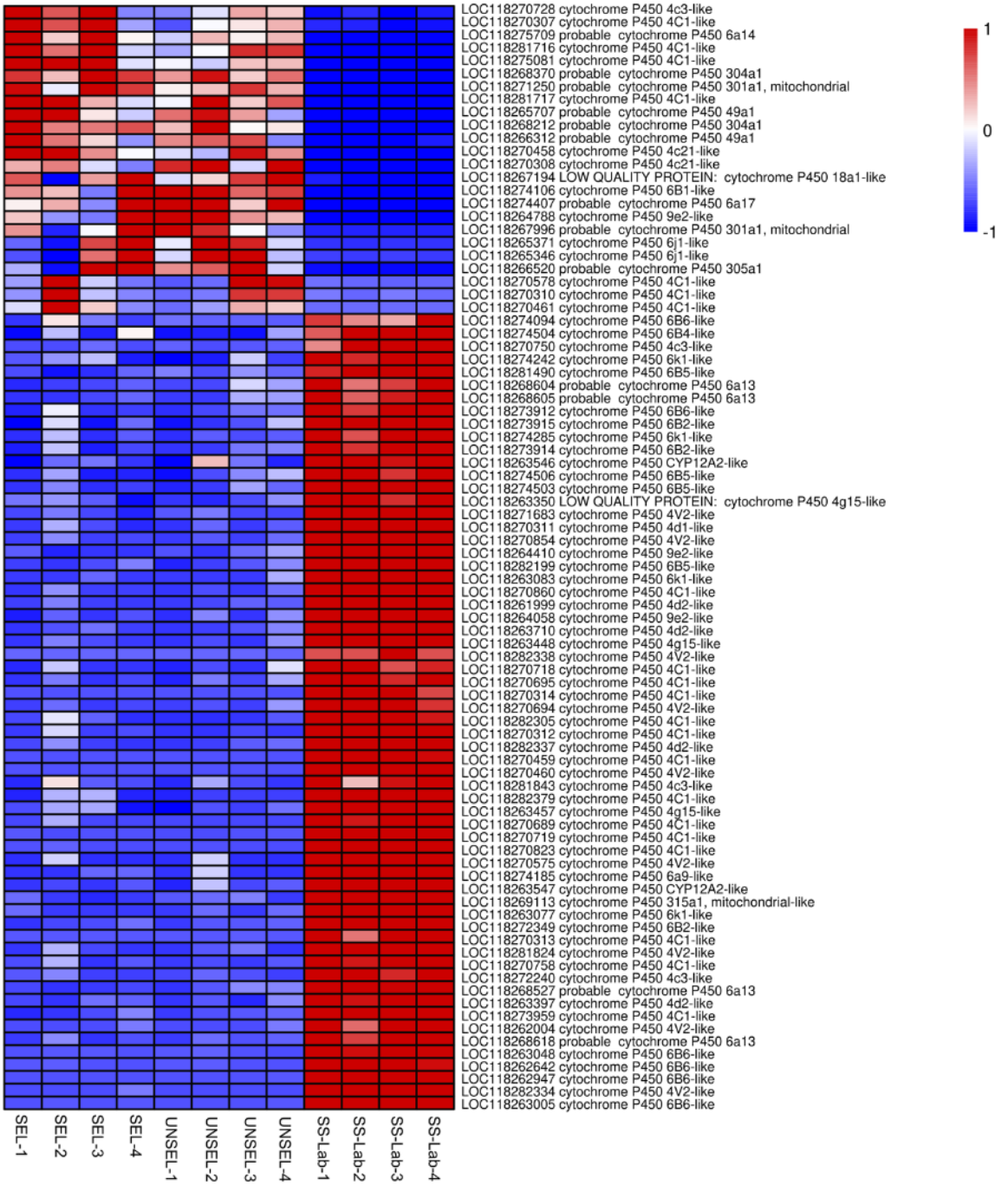

Fig. 5. Heatmap of differentially expressed cytochrome P450 genes.

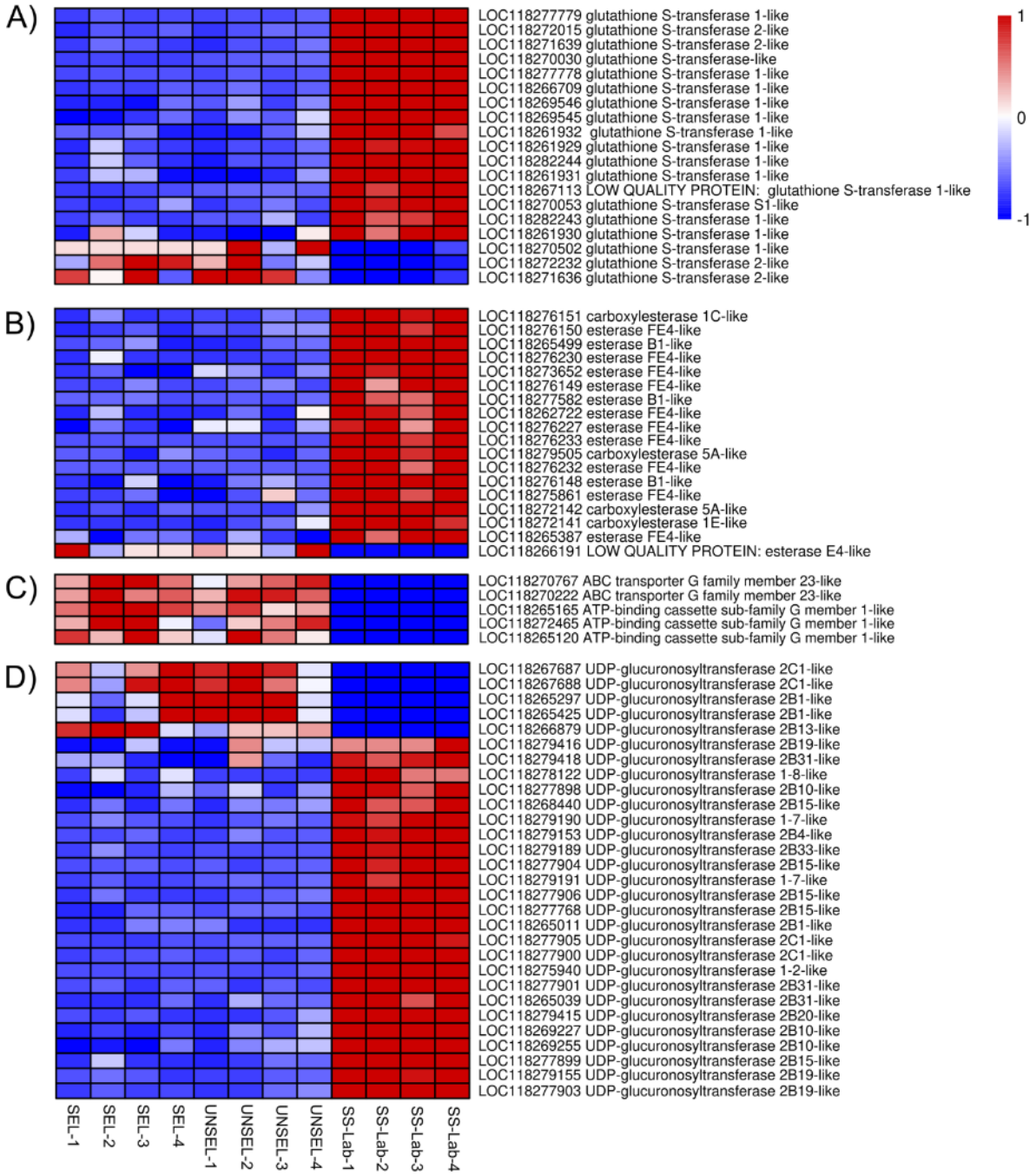

Fig. 6. Heatmap of differentially expressed A) Glutathione-S-transferases, B) Esterases, C) ABC transporters and D) UDP-glycosyltransferases genes.

The number of DEGs of each detoxification enzyme are presented in Table 5. Most of the detoxification genes are down-regulated in the Sel and Unsel strains compared to the SS-Lab strain. Among the P450 genes, 22 genes were up-regulated in Sel and Unsel strains compared to the SS-Lab strain, while 60 and 61 genes were down-regulated in Sel and Unsel strains, respectively. Most of the GST and CarE DEGs were down-regulated in Sel and Unsel

strains compared to the SS-Lab strain, with only 1 CarE and 3 GST genes up-regulated in the Sel and Unsel strains, respectively. Additionally, 5 and 3 ABC transporter genes were up-regulated in the Sel and Unsel strains compared to the SS-Lab strains. As for the UGT DEGs, 4 genes were up-regulated in Sel and Unsel strains compared to the SS-Lab strain. No detoxification enzymes were found in the Sel vs Unsel comparison.

Table 5. Differentially expressed genes of detoxification enzymes in each strain.

DEGs of detoxification enzymes	**Sel vs SS-Lab**		**Unsel vs SS-Lab**		**Sel vs Unsel**	
	Up-regulated	Down-regulated	Up-regulated	Down-regulated	Up-regulated	Down-regulated
P450 (86)	22	60	22	61	0	0
CarE (18)	1	17	1	13	0	0
GST (19)	3	14	3	16	0	0
ABC transporter (5)	5	0	3	0	0	0
UGT (29)	4	23	4	20	0	0

2.3.8. Synergist bioassays

The LC_{50} values of the SS-Lab strain with spinetoram plus the synergist treatment ranged from 0.68 to 0.72 μg ml^{-1}, whereas the LC_{50} value of spinetoram alone was 0.86 μg ml^{-1}. It resulted in a synergistic ratio of 1.19, 1.06 and 1.26-fold for PBO, DEM and DEF, respectively. For the RR strain, the LC_{50} values of spinetoram plus the synergist treatment ranged from 538.99 to 650.29 μg ml^{-1}, whereas the LC_{50} value of spinetoram alone was 727.97 μg ml^{-1}. The synergistic ratio for RR strain were 1.35, 1.11, 1.17-fold for PBO, DEM and DEF, respectively (Table 6).

Table 6. Synergist effect of PBO, DEM and DEF in spinetoram susceptible and resistant strains of *Spodoptera frugiperda*

Strain	Treatment	n[a]	Slope (± SE)	LC_{50} (CI 95%)[b]	χ^2 (df)	Synergistic ration[c]	Resistance Ratio[d]
SS-Lab	Spinetoram	452	3.10 (± 0.38)	0.86 (0.72 – 1.02)	8.91 (4)	-	-
	Spinetoram + PBO	503	1.94 (± 0.19)	0.72 (0.59 – 0.87)	6.88 (5)	1.19	-
	Spinetoram + DEM	498	2.19 (± 0.15)	0.81 (0.69 – 0.96)	4.63 (5)	1.06	-
	Spinetoram + DEF	431	2.99 (± 0.43)	0.68 (0.55 – 0.85)	9.38 (4)	1.26	-
RR	Spinetoram	525	2.50 (±0.26)	727.97 (604.42 – 876.77)	10.33 (5)	-	846.47
	Spinetoram + PBO	576	3.08 (±0.27)	538.99 (473.38 – 613.68)	6.30 (5)	1.35	748.59
	Spinetoram + DEM	451	2.75 (±0.40)	650.29 (512.26 – 825.51)	10.74 (4)	1.11	802.82
	Spinetoram + DEF	472	3.21 (±0.28)	621.62 (535.13 – 722.10)	4.71 (4)	1.17	914.14

[a] number of larvae tested; [b] lethal concentration (μg ml^{-1}) of applied insecticide solution that kills 50% of the individuals; [c] Synergistic ratio: LC50 of tested strain with insecticide alone/LC50 of the same strain with insecticide plus the synergist; [d] Resistance ratio: LC_{50} of the RR strain/LC_{50} of the SS-Lab strain.

2.3.9. Association of Y232del with spinetoram resistance in *Spodoptera frugiperda*

The nAChR α6 gene sequencing by the Sanger method confirmed the three-nucleotide deletion presence in the DNA sequence of RR strain individual. The DNA sequence of the SS-Lab strain individual did not present the three-nucleotide deletion. It was verified that the sequenced individual from F_1 progeny is heterozygous since it was detected two chromatographic peaks in some DNA positions during the sequencing (Fig. 7).

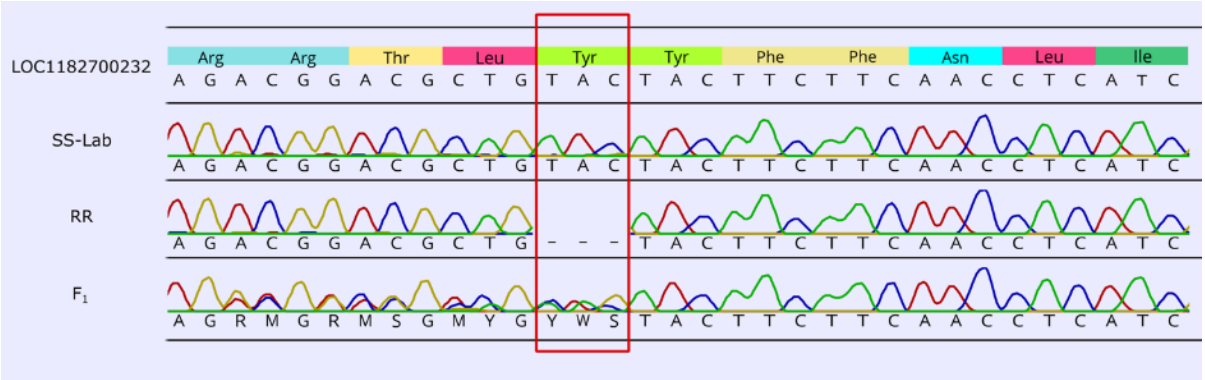

Fig. 7. Representative chromatograms from Sanger sequencing of the nAChR α6 PCR product from SS-Lab, RR and F_1 individuals. The red square represents the Y232del.

All 42 individuals (21 dead and 21 alive) from bioassays conducted with discriminating concentration of spinetoram were successfully genotyped. A significant association was observed between the insect genotype and its phenotype ($\chi^2 = 28.1$, df = 1, $p < 0.001$). All alive individuals presented a DNA sequence with the three-nucleotide deletion in homozygosis, while 85.71% of the dead individuals presented a DNA sequence with the deletion of three-nucleotide in heterozygosis (Fig. 8).

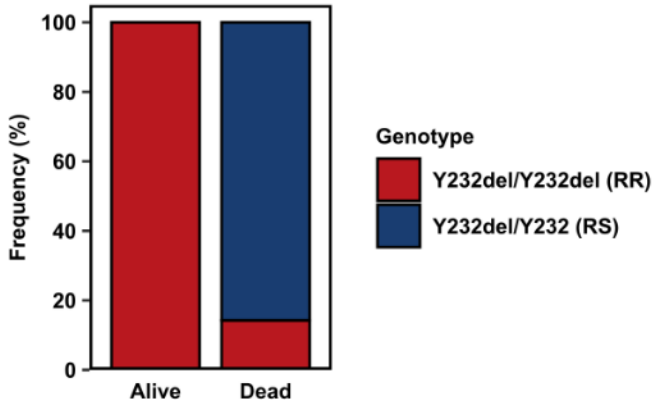

Fig. 8. Frequency of Y232del mutation in alive and dead individuals exposed to a discriminating concentration of spinetoram. *N* dead = 21, *n* dead = 21. A significant association was observed between the insect genotype and its phenotype by chi-square test (χ^2 = 28.1, df = 1, $p < 0.001$)

2.3.10. Complementation test

All strains showed a high survival rate in the spinetoram and spinosad bioassays performed for complementation test. There were no significant differences between the survival rates of the Spin-res, RR, S1 and S2 strains (F = 2.12; df = 3,72; p = 0.10 for strain; F = 1,54; df = 1,71; p = 0.21 for insecticide; F = 2.36; df = 3,68; p = 0.07 for interaction). The survival rate observed in spinetoram bioassays was 91.2, 96.6, 95.8 and 92.5 % to Spin-res, RR, S1 and S2, respectively. The survival rate observed in spinosad bioassays was 98.1, 95.8, 96.2 and 92.92 % to Spin-res, RR, S1 and S2, respectively (Fig. 9A). The Sanger sequencing demonstrated that all sequenced individuals from RR, Spin-res, S1 and S2 strains were homozygous for the deletion of three nucleotides in the nAChR α6 gene (Fig 9B)**.**

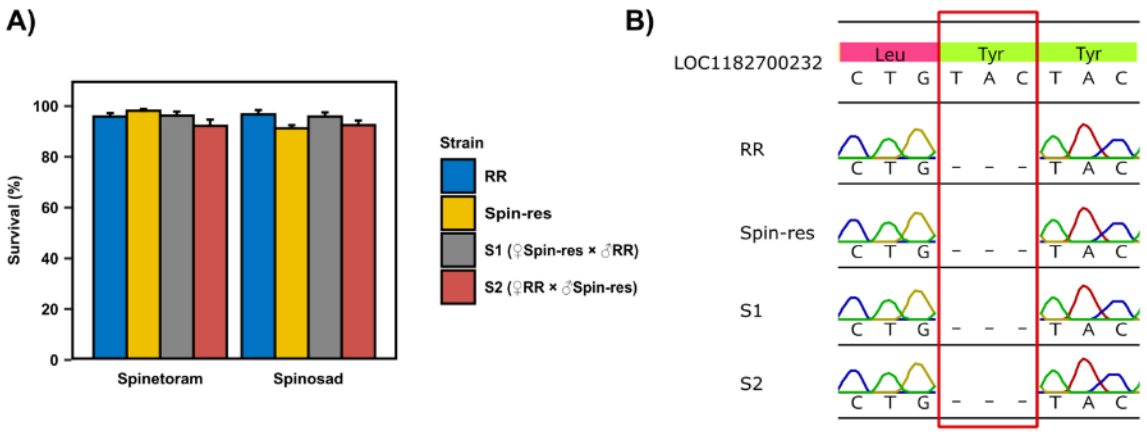

Fig. 9. A) Survival rates of RR, Spin-res and the reciprocal crosses (S1 and S2) in discriminating concentrations of spinosad and spinetoram. B) Representative chromatogram of from Sanger sequencing of the nAChR α6 PCR product from RR, Spin-res, S1 and S2 individuals. Red square represents the Y232del.

2.4. Discussion

Here we employed a DNA and RNA sequencing approach to identify the mechanisms of resistance that could be associated with spinetoram resistance in *S. frugiperda*. A robust investigation of the molecular mechanisms underlying insecticide resistance is essential to understand the how the insect pests have evolved such adaptive strategies to overcome these xenobiotics compounds. Insecticide resistance mechanisms are often complex and could involves a combination of multiple factors. The resistance levels could vary according to the combination of the modification in expression of different genes and/or mutations in target site of these compounds (Samantsidis et al., 2020).

The variant calling analysis provide evidence of 10 variants, including SNPs and Indels, with non-synonymous effect that could be associated with spinetoram resistance. Among them a triplet deletion (Y232del) was found in the nicotinic acetylcholine receptor subunit α6, the target site of spinosyn insecticides, resulting in a loss of a tyrosine amino acid in exon 7. In a similar way, Grant et al. (2019) found an F238del in spinosad resistant strain of *T. absoluta*, indicating that deletions in the nAChR α6 gene can be one of the mechanisms of spinosyn resistance in insect pests.

The modification in the nAChR α6 gene is consistent with the fact that changes in this gene are usually associated with spinosyn resistance as reported for other insect species. Point mutations in the nAChR α6 were associated with spinosad resistance in *D. melanogaster* (Perry et al., 2007), *P. xylostella* (Rinkevich et al., 2010), *F. occidentalis*

(Puinean et al., 2013), *T. palmi* (Bao et al., 2014), *T. absoluta* (Silva et al., 2016), *F. intonsa* (Hiruta et al., 2018) and *C. capitata* (Ureña et al., 2019). Mis-spliced transcripts of nAChR α6 producing truncated protein were reported for *P. xylostella* (Baxter et al., 2010). Truncated transcripts of nAChR α6 were also observed in *Bactrocera dorsalis* (Hsu et al., 2012), *F. occidentalis* (Wan et al., 2018) and *R. dominica* (Wang et al., 2018). Exon skipping and deletions were also associated with spinosad resistance in *T. absoluta* (Berger et al., 2016; Grant et al., 2019). It evidences that multiple and different changes in the nAChR α6 are associated with spinosyn resistance in insect pests.

The association between the Y232del and resistance of *S. frugiperda* to spinetoram was determined by performing backcrosses and genotyping the dead and alive individuals. The results from Sanger sequencing demonstrated that the Y232del co-segragates with spinetoram resistance in our bioassays, providing evidence of a causal role of this mutation in resistance. Complementation test also suggest that both spinosad and spinetoram resistance in *S. frugiperda* are conferred by the alleles at the same locus, and Y232del is also presented in the spinosad-resistant strain, confirming the presence of cross-resistance between these two insecticides as initially reported by Dourado (2009) and Lira et al. (2020).

Target-site modification are usually associated with fitness costs, since it can potentially alter the function of the protein and its interaction with other molecules (Kliot and Ghanim, 2012). A varying degree of fitness cost has been associated with spinosyn resistance (Sparks et al., 2012). A significant fitness cost was observed in a spinosad-resistant strain of *S. frugiperda* (Okuma et al., 2018), while the fitness of the spinetoram-resistant strain (RR) varied according to the host plant (Kanno et al., 2023). A more precise way to determine the effect of this deletion in spinosyn resistance in *S. frugiperda* is to introduce it in a susceptible individuals using genome editing techniques. Functional validation using CRISPR-Cas9 editing tools will be conducted in our future studies to determine the impact of this deletion in spinosyn susceptibility and if it carry some fitness costs in *S. frugiperda*.

The involvement of detoxification enzymes in the resistance of *S. frugiperda* to spinetoram was also investigated by performing a RNA-Seq analysis. To identify the DEGs that could possibly be involved as a resistance mechanism, we selected the DEGs annotated associated with the three phases of detoxification of xenobiotics. These group of enzymes included the P450s, CarEs, GSTs, and UGTs (Feyereisen, 2012; ffrench-Constant, 2013; Li et al., 2007; Lu et al., 2020; Nagare et al., 2021; Pavlidi et al., 2018). Our transcriptome analysis demonstrated that some subfamilies of CYP4, CYP6 and CYP9 were overexpressed in spinetoram resistant insects (SEL strain). Cytochrome P450 is often involved in phase I of

xenobiotic detoxification in insects, including a large set of insecticides (Feyereisen, 1999; Lu et al., 2020; Nauen et al., 2022; Stanley, 2017). Proteins related to phase II of detoxification, such as GSTs and UGTs also were up-regulated in insects resistant to spinetoram. Furthermore, proteins as ABC transporter C and G, responsible to transportation and elimination of products of metabolization of xenobiotics (phase III) were overexpressed in resistant strains (SEL strain). In *S. frugiperda*, several studies have shown the involvement of these enzymes in the detoxification process of insecticides and plant allelochemicals (Bai-Zhong et al., 2020; Carvalho et al., 2013; Giraudo et al., 2015; Hafeez et al., 2021; Israni et al., 2020; Nascimento et al., 2023, 2015; Silva-Brandão et al., 2021; Yu et al., 2003). For spinosyn resistance, some studies have associated the presence of detoxification enzymes with spinosad resistance in *S. litura* (Rehan and Freed, 2014), *S. exigura* (Wang et al., 2006), *Helicoverpa armigera* (Wang et al., 2009), *F. occidentalis* (Herron et al., 2014) and *T. palmi* (Bao et al., 2014).

Moreover, the synergist bioassays using inhibitors of detoxification enzymes such as P450s, show some increase in the susceptibility of the RR strain to spinetoram. However, previous studies showed that PBO, DEF and DEM did not have any significant effect on spinosad resistance in *T. absoluta* (Campos et al., 2014; Silva et al., 2016), *Musca domestica* (Shi et al., 2011), *F. occidentalis* (Bielza et al., 2007; Zhang et al., 2008), *P. xylostella* (Zhao et al., 2002). Our synergist bioassay results, along with the results of the transcriptome analysis, suggest that the few up-regulated detoxification enzymes can also be involved in *S. frugiperda* resistance to spinetoram.

Furthermore, our study identified up-regulation in some genes related to biogenesis, such as neurogenic proteins (LOC118267572; LOC118273655), structural component like neurofilament medium polypeptide (LOC118276446) and regulation of neural system, including neuroligin-4 (LOC118262827). These results demonstrate that the process of resistance of SEL strain to spinetoram may involve interactions and modifications at both structural and regulatory levels of the nervous system (Bolliger et al., 2008; Knight et al., 2011; Marro et al., 2019; Wilk et al., 1996; Zhou et al., 1997; Zhu et al., 2008). In addition, several cuticle proteins, larval and pupal cuticle proteins, were overexpressed in the SEL strain. These modifications suggests that structural change in insect tegument can slow cuticular penetration of insecticides (Balabanidou et al., 2018).

In summary, this study represents a crucial initial step towards enhancing our understanding of the molecular mechanisms of spinetoram resistance in *S. frugiperda.* We demonstrated that the deletion in the nAChR α6 gene along with up-regulation of some

metabolic resistance genes are probably the resistance mechanisms of spinosyns insecticides in *S. frugiperda*. The findings of this study will provide a basis for the development of molecular markers to detect spinetoram resistance in field populations of *S. frugiperda* to implement effective resistance management strategies.

2.5. Conclusions

- A three nucleotide deletion in the nAChR α6 gene was identified in the spinetoram-resistant strain of *S. frugiperda*;
- Up-regulation of some cytochrome P450, ABC transporter and cuticle protein genes were also associated with spinetoram resistance in *S. frugiperda.*

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3. FITNESS COSTS ASSOCIATED WITH SPINETORAM RESISTANCE IN *Spodoptera frugiperda* (LEPIDOPTERA: NOCTUIDAE) IS DRIVEN BY HOSTS PLANTS

Abstract
Insecticide resistance is usually associated with fitness costs. The magnitude of the fitness costs is affected by environmental and ecological factors. Here, we explored how host plants could affect fitness costs associated with insecticide resistance. Initially, spinetoram-resistant (RR) and susceptible (SS) strains of *Spodoptera frugiperda* (J. E. Smith) were selected using a F_2 screen from a population collected in São Desidério, Bahia State, Brazil. In addition to the RR and SS strains, fitness costs were also assessed for a heterozygous strain (RS). Life-history traits were evaluated to estimate population growth parameters of each strain feeding on corn, soybean, and cotton plants. The relative fitness of the RR strain was 1.06 higher compared to the SS strain on corn plants, while in soybean and cotton plants these values were 0.84 and 0.67 lower, respectively. The relative fitness of the RS strain was similar to the SS strain regardless of the host plant, suggesting a recessive fitness cost. No differences were found between the strains fed on corn plants. The larval development time was greater for the RR strain fed on soybean and cotton plants compared to the RS and SS strains. Low survival rate and fecundity of the RR strain were found when larvae fed on soybean and cotton plants. The results of this study showed that fitness costs of spinetoram resistance in *S. frugiperda* depend on the host plants that *S. frugiperda* larvae fed on. Such information can be used to design resistance management strategies considering the host plants of the agricultural landscape.

Keywords: fall armyworm; spinosyns; insect resistance management; relative fitness.

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3.1. Introduction

The fall armyworm, *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae), is recognized as one of the most important agriculturally damaging pests. Recently, the notoriety of this pest has increased because it has been reported as an invasive pest in many countries in Africa, Asia and Oceania (Goergen et al. 2016; Baloch et al. 2020; CABI 2021). *S. frugiperda* is a highly polyphagous pest with a wide range of host plant species (Montezano et al. 2018). The ability of this pest to explore different host plant species is one of the major factors in its success at colonizing new areas. The control of *S. frugiperda* relies mainly on the use of chemical insecticides, but the extensive use of this control tactic has resulted in resistance cases to many groups of insecticides (Diez-Rodríguez and Omoto 2001; Carvalho

et al. 2013; Nascimento et al. 2016; Okuma et al. 2018; Bolzan et al. 2019; Lira et al. 2020; Muraro et al. 2021; Garlet et al. 2021a), challenging the management of this pest.

The spinosyns are broad-spectrum insecticides derived from the natural fermentation of *Saccharopolyspora spinosa* (Sparks et al. 2001). This group of insecticides is represented by two chemical molecules, spinosad and spinetoram, that act as allosteric modulators of the nicotinic acetylcholine receptor (Crouse et al. 2001; Salgado et al. 2010; Dripps et al. 2011). These insecticides have demonstrated high efficacy against many insect pests (Salgado et al. 2010; Dripps et al. 2011). However, some insect species have already shown resistance to spinosyns (Sparks et al. 2012; Mota-Sanchez and Wise 2021) including *S. frugiperda* with a resistance ratio > 890-fold in Brazil (Okuma et al. 2018; Lira et al. 2020). The high levels of resistance that *S. frugiperda* shows for spinosyns indicates an elevated risk of resistance evolution in this pest and an urgency in implementing insect resistance management strategies.

One of the main insect resistance management strategies is based on the assumption of fitness costs associated with resistance (Roush and McKenzie 1987; Gassmann et al. 2009; Kliot and Ghanim 2012). The fitness costs of insecticide resistance can be understood as a significant disadvantage of resistant individuals compared with their susceptible counterparts in the absence of insecticides (Kliot and Ghanim, 2012). In general, fitness costs are associated with spinosyn resistance. A significant reduction in the survival rate to adulthood and a lower reproductive rate were found in a spinosad-resistant strain of *S. frugiperda* (Okuma et al. 2018). A fitness cost of spinosad resistance has also been reported for other pests such as *Chloridea virescens* (Fabricius) (Wyss et al. 2003), *Plutella xylostella* (Linnaeus) (Li et al. 2007b), *Helicoverpa armigera* (Hübner) (Wang et al. 2010), *Spodoptera litura* (Fabricius) (Rehan and Freed 2015), *Phenacoccus solenopsis* (Tinsley) (Afzal and Shad 2017) and *Ceratitis capitata* (Wiedemann) (Guillem-Amat et al. 2020). Spinetoram was introduced to the market more recently than spinosad, and so far only one study on the fitness costs associated with spinetoram resistance was reported in *Thrips hawaiiensis* (Morgan) (Fu et al. 2018); therefore, such information remains unknown for *S. frugiperda*.

The magnitude of fitness costs associated with insecticide resistance can be influenced by various environmental and ecological factors (Gassmann et al. 2009). Different host plant species and allelochemicals could play an important role in fitness costs (Carrière et al. 2004; Janmaat and Myers 2005; Bird and Akhurst 2007; Raymond et al. 2007, 2011; Wang et al. 2016; Chen et al. 2019; Santos-Amaya et al. 2022). The quality of the host plant can affect several insect development processes (Awmack and Leather 2002) and this is important

for population increase and outbreaks of insect pests, especially those that can feed on a large range of host plants (Kennedy and Storer 2000; Sivakoff et al. 2013). Therefore, it is essential to understand the interaction between the host plant and fitness costs associated with insecticide resistance to implement effective resistance management strategies.

Previous studies on the interaction between host plants and fitness costs have focused on Bt resistance (Janmaat and Myers 2005; Bird and Akhurst 2007; Raymond et al. 2007, 2011; Wang et al. 2016; Chen et al. 2018). To date, there is just one study conducted by Garlet et al. (2021b) exploring this interaction with chemical insecticide resistance. The recent documentation of spinosyn resistance in *S. frugiperda* (Okuma et al. 2018; Lira et al. 2020) and the broad host range of this pest provides us the unique opportunity to investigate the effect of different host plants on fitness costs associated with spinosyn resistance. Corn, soybean, and cotton are three of the most economically important crops in Brazil (Buainain et al. 2019), and their intensive cultivation offers an ideal scenario for the development of *S. frugiperda* populations throughout the year since this pest feeds on all three of those crops (Barros et al. 2010). In this context, we aimed to assess the fitness costs of spinetoram resistance in *S. frugiperda* by comparing several biological parameters and constructing fertility life tables for resistant, susceptible, and heterozygous strains feeding on plants of corn, soybean, and cotton plants. The findings of this study will contribute to the improvement of insecticide resistance management strategies of *S. frugiperda* and our understanding of how host plants can affect population growth in different agricultural landscapes.

3.2. Material and methods

3.2.1. Insect strains

The spinetoram-resistant strain (RR) of *S. frugiperda* was selected from a field population collected in São Desidério, Bahia State, in 2018. The F_2 screen method was used to obtain the resistant strain (Andow and Alstad 1998). To investigate the fitness cost of spinetoram resistance in strains with the same genetic background, a spinetoram susceptible strain (SS) was obtained from the same field population from which the resistant strain originated. The selection for susceptibility was conducted by establishing pair-mated adults from the field population. The larvae from the F_1 progeny of each couple were separated into two groups; one group was tested at the diagnostic concentration of 5.6 μg a.i. spinetoram/ml

(sufficient to kill the susceptible individuals) (Lira et al. 2020) and the other group remained to establish the susceptible strain if the respective progeny had a 100% mortality. The SS strain was not exposed to any insecticide after its establishment in the laboratory. Both strains was reared on artificial diet (Kasten Jr et al. 1978). The heterozygous strain (RS) was obtained by crossing RR females and SS males. Only one heterozygous strain was established because the inheritance pattern of spinosyn resistance in *S. frugiperda* is autosomal and both heterozygotes obtained from reciprocal crosses showed a similar mortality to spinosad and spinetoram (Okuma et al. 2018; Lira et al. 2020).

Concentration-response curves were performed to characterize the susceptibility of the SS and RR strains. In addition, a laboratory susceptible strain (SS-Lab), which was maintained in the laboratory for more than 25 years without the selection pressure of insecticides or Bt proteins, was used to validate the SS strain as a susceptible strain. Diet overlay bioassays were conducted in 24-well acrylic plates containing 1.25 ml of artificial diet in each well (1.9 cm^2 area). All strains were tested in eight logarithmically spaced concentrations (0.1 to 5.6 μg a.i. spinetoram/ml for the SS and SS-lab strains and from 180 to 5,600 μg a.i. spinetoram/ml for the RR strain). The different concentrations of spinetoram were obtained by diluting the formulated insecticide (Exalt® 120g a.i./l) in distilled water with the addition of 0.1% (v/v) of the surfactant Triton X-100 (Sigma Aldrich Brasil Ltda). In each well, 30 μl of the insecticide solution was applied. One early third instar larva was infested in each well after the insecticide solution dried. Mortality was assessed after 48 h following the same criteria described by Lira et al. (2020), and larvae that did not show coordinated movement when prodded were considered dead.

3.2.2. Fitness costs assessment bioassays

Fitness costs associated with spinetoram resistance in *S. frugiperda* were investigated on corn, soybean, and cotton plants. Plants of non-Bt hybrid corn (3700 RR2), non-Bt soybean (95R51), and non-Bt cotton (FM 944GL) were cultivated in 12l pots in a greenhouse. The SS and RR strains were reared for one generation on each host plant before the fitness costs bioassays to eliminate possible effects of changing the food source.

The bioassays were performed with leaves of corn from the V4 to V8 growth stages, leaves of soybean from V3 to V6, and leaves of cotton from the squaring phenological stage. The leaves of each plant were cut into pieces (approximately 4 cm^2) and placed over a gelled mixture of 2.5% agar-water in 16-well plastic trays (Advento do Brasil). One neonate (< 24 h

old) from each strain was infested in each well and reared until the 6th instar. Then, the larvae were transferred to another 16-well plastic tray containing vermiculite and leaves of the respective host plants for development until the pupal stage. The leaves were changed every day. For each strain, 160 larvae were tested (10 replicates of 16 larvae) per host plant. The following parameters were evaluated: duration and survival rates of the egg, larval, pupal, and egg-adult periods; pupal weight; sex ratio; male and female longevity; durations of the periods of preoviposition, oviposition, and postoviposition; fecundity; and fertility. To determine male and female longevity, duration of the preoviposition, oviposition, and postoviposition periods, fecundity, and fertility, 20 couples per strain were kept in PVC cages (10 cm diameter × 20 cm high) internally coated with paper for mating and oviposition. The adults were fed a 10% honey solution soaked into cotton. The embryonic period and survival were evaluated in 100 eggs of the second oviposition of each pair. All parameters were evaluated in daily observations. The bioassay trays and the insects were maintained in rearing rooms under controlled conditions of 25 ± 2 °C, 70% relative humidity and a photoperiod of 14:10 (L:D) h.

3.2.3. Statistical analysis

The mortality data of the concentration-response curves were fitted to a generalized linear model with a binomial distribution and probit as the function link. The LC_{50}s and the respective confidence intervals were estimated using the function *dose.p* in the MASS package (Venables and Ripley 2002).

The data from the fitness costs bioassays were analyzed using a generalized linear models (GLM) according to the distribution of the data. The pupal weight and fertility life table parameters data were fitted to a GLM with a Gaussian distribution; data on the development time of egg, larvae, pupae, and egg-adult period and the number of eggs were fitted to a GLM with a quasi-Poisson distribution; survival rates of egg, larvae, pupae, and the egg-adult period were fitted to a GLM with quasibinomial distribution. The fertility life table, which includes the net reproductive rate (total number of offspring that a female can produce during its lifetime – R_0), the mean length of a generation (mean time span between the birth of individuals of a generation and that of the next generation – T), the intrinsic rate of population increase (daily female offspring production per parental female – rm), and the finite rate of population increase (multiplication factor of the original population size at each time period – λ), was estimated using the *lifetable.r* procedure (Maia et al. 2014). The parameters of the life table were calculated using the formulas described by Maia et al. (2000). The net reproductive

rate was calculated as $R_0 = \sum lx.mx$, where lx is the probability of surviving to age x and mx is the mean number of female progeny per female of age x. The mean length of a generation was calculated as $T = \sum x.lx.mx / \sum lx.mx$. The intrinsic rate of population increase was calculated as $rm = \text{Ln}(R_0)/\text{T}$ and the finite rate of population increase was calculated as $\lambda = e^{rm}$. The relative fitness was calculated by dividing the *rm* values of the RR or RS strain by the *rm* value of the SS strain as proposed by Bird et al. (2020). The goodness of fit for all data was verified using the *hnp* package (Moral et al. 2017). Two-way ANOVA was performed to verify the effect of each factor (strain; host plant) and their interaction using a GLM for each evaluated parameter, followed by a multiple pairwise comparison (Tukey's test) using the *lsmeans* package. All statistical analyses were performed in R Software (R Core Team, 2020).

3.3. Results

3.3.1. Susceptibility of *Spodoptera frugiperda* strains to spinetoram

The SS and SS-Lab strains had a similar susceptibility to spinetoram (Table 7). The LC_{50} value of the SS strain was 1.0 µg ml-1, while the SS-Lab strain presented a LC_{50} of 0.8 µg ml-1, indicating a low variation of 1.2-fold. The LC_{50} value of the RR strain was 776.9 µg ml-1, which results in a resistance ratio of 971.12-fold when compared to the SS-Lab strain and a resistance ratio of 776.9-fold when compared to the SS strain.

Table 7. Susceptibility of *Spodoptera frugiperda* strains to spinetoram

Strain	n[a]	Slope (± SE)	LC_{50} (CI 95%)[b]	χ^2	df[c]	Resistance ratio [d]
SS-Lab	648	2.4 ± 0.2	0.8 (0.7 – 0.9)	9.1	5	-
SS	598	2.2 ± 0.2	1.0 (0.8 -1.2)	8.1	5	1.2
RR	693	2.6 ± 0.2	776.9 (685.7 – 880.3)	9.8	5	971.12

[a] number of larvae tested; [b] lethal concentration (µg ml^{-1}) of applied insecticide solution that kills 50% of the individuals; [c] degrees of freedom; [d] Resistance ratio: LC_{50} of the tested strain/LC_{50} of the susceptible reference strain.

3.3.2. Survival rate of *Spodoptera frugiperda* strains on corn, soybean, and cotton plants

The effects of strain, host plant, and their interaction on the survivorship of the egg stage were not significant (F = 2.64, df = 2, 87, p = 0.07 for strain; F = 2.76, df = 2, 85, p =

0.06 for host plant; F = 2.11, df = 4, 81, p = 0.08 for the interaction). A high survivorship of the egg stage (> 92%) was observed in all strains regardless the host plant (Fig. 10).

The larval stage was affected by strain, host plant and their interaction (F = 21.20, df = 2, 87, p < 0.05 for strain; F = 4.44, df = 2, 85, p < 0.05 for host plant; F = 12.24, df = 4, 81, p < 0.05 for the interaction). The SS and RS strains presented high survivorship (> 75%) on the three host plants and did not differ between them. A difference was observed in the survivorship of the larval stage of the RR strain on the different host plants. On corn plants, the RR strain had a larval survivorship of 90%, while on soybean and cotton plants the survivorship was 55% and 50.62%, respectively (Fig. 10).

No difference was observed in survivorship of the pupal stage among the SS, RS, and RR strains and among the three host plants evaluated (F = 2.10, df = 2, 87, p = 0.12 for strain; F = 1.19, df = 2, 85, p = 0.30 for host plant; F = 1.96, df = 4, 81, p = 0.10 for the interaction) (Fig. 10).

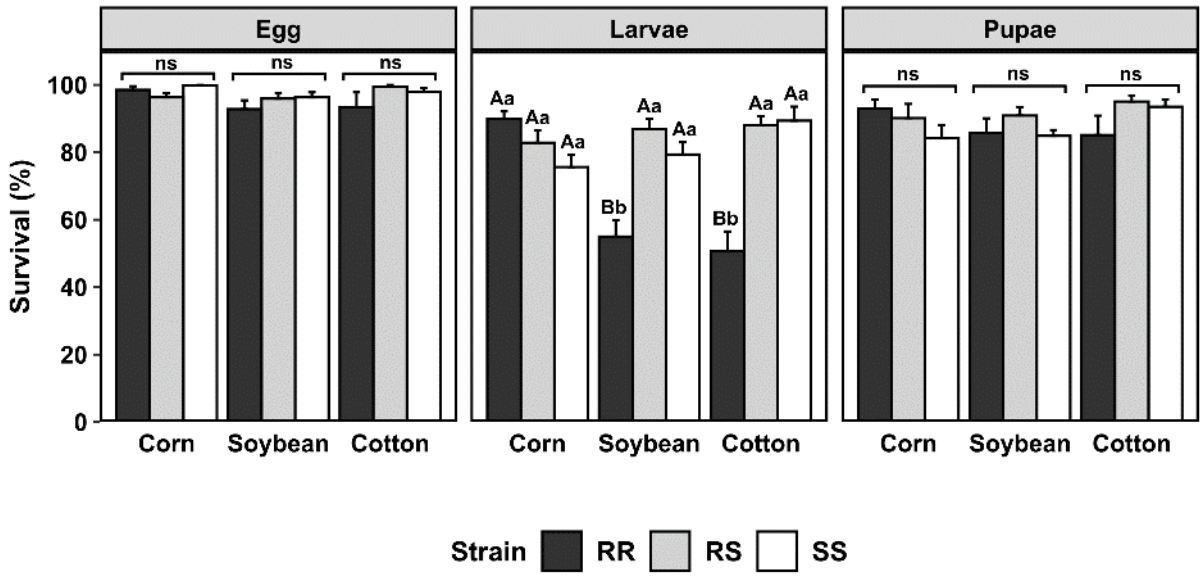

Fig. 10. Survival rates of different life stages of *Spodoptera frugiperda* strains on corn, soybean, and cotton plants. Bar height represents the mean of each treatment and error bars represent the standard error of the mean. Different lowercase letters indicate a significant difference between *S. frugiperda* strains on each host plant and uppercase letters indicate significant differences for the same strain on different host plants (Tukey's test, p < 0.05).

3.3.3. Development time of *Spodoptera frugiperda* strains on corn, soybean, and cotton plants

The effect of strain and the interaction between strain and host plant had significant effects on the duration of the egg stage ($F = 8.60$, $df = 2, 87$, $p < 0.05$ for strain; $F = 10.20$, $df = 4, 81$, $p < 0.05$ for the interaction). The effect of host plant was not significant ($F = 2.04$, $df = 2, 85$, $p = 0.13$). The duration of the egg stage ranged from 3 to 4 days in all strains evaluated. A difference among the three strains was only observed on soybean and cotton plants (Fig. 11).

The duration of larval stage was affected by the strain, host plant, and their interaction ($F = 8.93$, $df = 2, 87$, $p < 0.05$ for strain; $F = 948.44$, $df = 2, 85$, $p < 0.05$ for host plant; $F = 22.19$, $df = 4, 81$, $p < 0.05$ for the interaction). The longest duration of the larval stage was observed when the strains were reared on cotton plants. On cotton, the RR strain presented a larval stage duration of 30.36 days, differing from the SS and RS strains, which had durations of 25.74 and 25.93 days, respectively. No difference was observed among the strains when they were reared on corn and soybean plants. The larval stage was 3.55–3.74 days longer on soybean plants compared to corn plants (Fig. 11).

The strain, host plant, and their interaction had significant effects on the duration of the pupal stage ($F = 5.72$, $df = 2, 87$, $p < 0.05$ for strain; $F = 107.86$, $df = 2, 85$, $p < 0.05$ for host plant; $F = 13.72$, $df = 4, 81$, $p < 0.05$ for the interaction). A difference among the strains in the duration of the pupal stage was observed only on cotton plants; the SS strain had the shortest pupal stage duration (9.93 days), differing from RS and RR, which had durations of 10.76 and 11.31 days, respectively. The longest pupal stage duration of the strains among the plants was observed on soybean plants, with a duration ranging from 11.67 to 11.88 days among the strains (Fig. 11).

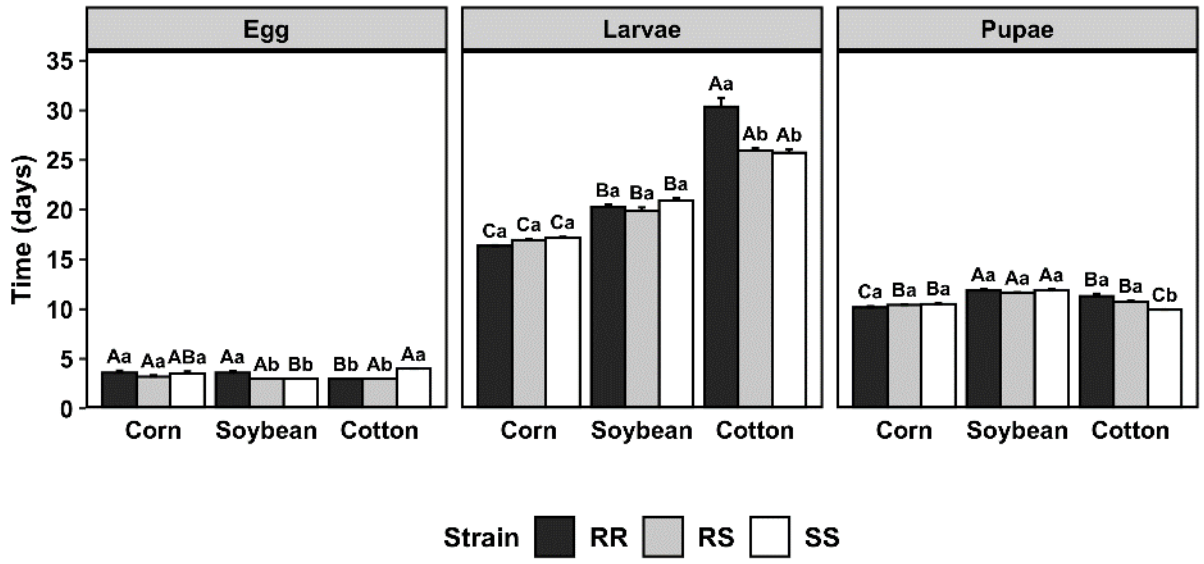

Fig. 11. Development time of different life stages of *Spodoptera frugiperda* strains on corn, soybean, and cotton plants. Bar height represents the means of each treatment and error bars represent the standard error of the mean. Different lowercase letters indicate a significant difference between *S. frugiperda* strains on each host plant and uppercase letters indicate significant differences for the same strain on different host plants (Tukey's test, $p < 0.05$).

3.3.4. Pupal weight and fecundity of *Spodoptera frugiperda* strains on corn, soybean, and cotton plants

The effects of strain, host plant, and their interaction had significant effects on pupal weight ($F = 14.05$, $df = 2, 87$, $p < 0.05$ for strain; $F = 52.57$, $df = 2, 85$, $p < 0.05$ for host plant; $F = 34.41$, $df = 4, 81$, $p < 0.05$ for the interaction). The difference in pupal weight among the strains was observed on soybean and cotton plants. On soybean plants, the SS strain had a pupal weight of 188.23 mg, differing from the RS and RR strains, which had pupal weights of 202.96 and 207.36 mg, respectively. On cotton plants, the RR strain had the lowest pupal weight (158.77 mg), differing from the SS (197.82 mg) and RS (193.82 mg) strains (Fig. 12A).

The fecundity of *S. frugiperda* was affected by strain, host plant, and their interaction ($F = 9.38$, $df = 2, 152$, $p < 0.05$ for strain; $F = 11.63$, $df = 2, 150$, $p < 0.05$ for host plant; $F = 6.65$, $df = 4, 146$, $p < 0.05$ for the interaction). The number of total eggs laid per female did not differ among SS, RS, and SS strains on corn plants. However, a large reduction was observed in the number of eggs laid by the RR strain when it was reared on soybean and cotton plants. The SS and RS strains reared on soybean and cotton had similar fecundities with no significant difference between them (Fig. 12B).

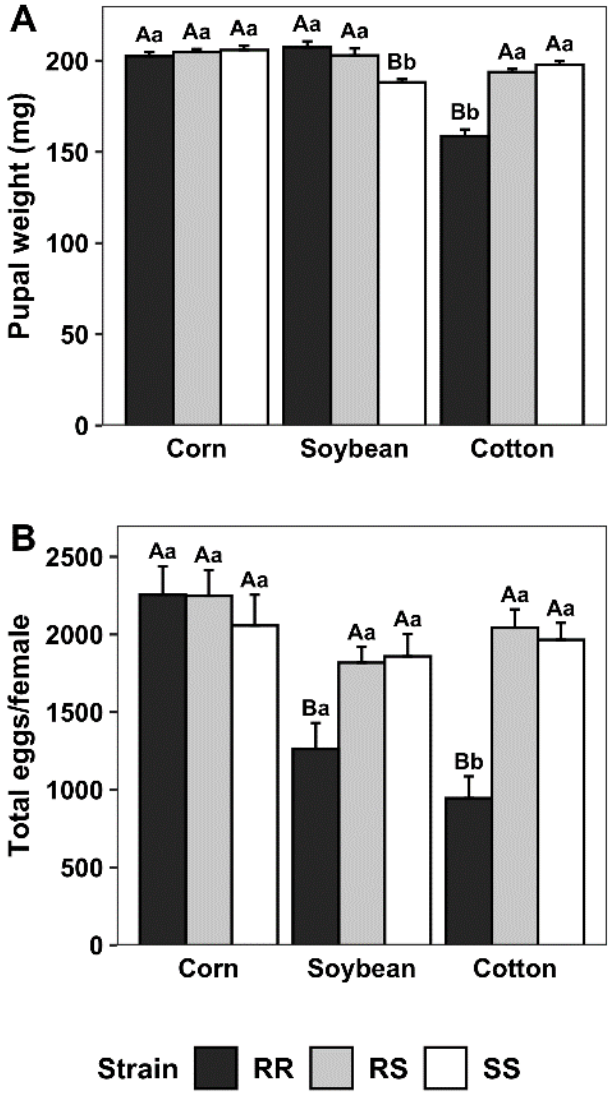

Fig. 12. Biological parameters of *Spodoptera frugiperda* strains reared on corn, soybean, and cotton plants: (A) Pupal weight and (B) Total number of eggs per female. Bar height represents the means of each treatment and error bars represent the standard error of the mean. Different lowercase letters indicate a significant difference between *S. frugiperda* strains on each host plant and uppercase letters indicate significant differences for the same strain on different host plants (Tukey's test, $p < 0.05$).

3.3.5. Population growth parameters of *Spodoptera frugiperda* strains on corn, soybean, and cotton plants

Differences in population growth parameters were observed when the SS, RS, and RR strains were reared on corn, soybean, and cotton plants (Table 8). The net reproductive rate (R_0) was affected by strain, host plant, and their interaction ($F = 43.36$, $df = 2, 154$, $p < 0.05$ for strain; $F = 33.46$, $df = 2, 152$, $p < 0.05$ for host plant; $F = 20.04$, $df = 4, 148$, $p < 0.05$

for the interaction). The R_0 values of the SS, RS, and RR strains reared on corn ranged from 699.74 to 836.98, with no significant differences among them. A difference among strains was observed on soybean and cotton plants. When reared on soybean plants, the RR strain presented a R_0 value of 239.33 while the R_0 values of the SS and RS strains were 580.02 and 637.84, respectively. On cotton plants, the RR strain showed a R_0 value of 144.90, differing from the SS and RS strains, which showed R_0 values of 786.30 and 813.85, respectively.

The mean length of a generation (T) was affected by strain, host plant and their interaction ($F = 49.46$, df = 2, 154, $p < 0.05$ for strain; $F = 1431.17$, df = 2, 152, $p < 0.05$ for host plant; $F = 61.59$, df = 4, 148, $p < 0.05$ for the interaction). On corn plants, the duration of a generation was similar for the RR and RS strains (35.82 days), but it was significantly shorter when compared to the SS strain (37.37 days). No differences were verified in generation time between the RR (42.02 days) and SS (41.01 days) strains on soybean plants, however these two strains differed from the RS strain (39.98 days). The longest durations of generations of the SS, RS, and RR strains were observed on cotton plants. The mean length of a generation of the SS and RS strains on cotton plants were 44.53 and 44.44 days, respectively, differing from the RR strain, which presented a duration of 49.74 days.

The effects of strain, host plant, and their interaction all had significant effects on the intrinsic rate of population increase (rm) ($F = 98.84$, df = 2, 154, $p < 0.05$ for strain; $F = 448.49$, df = 2, 152, $p < 0.05$ for host plant; $F = 61.05$, df = 4, 148, $p < 0.05$ for the interaction) and on the finite rate of population increase ($F = 94.48$, df = 2, 154, $p < 0.05$ for strain; $F = 452.26$, df = 2, 152, $p < 0.05$ for host plant; $F = 58.95$, df = 4, 148, $p < 0.05$ for the interaction). On corn plants, the SS strain presented the lowest intrinsic rate of population increase (0.1753) differing from the RR (0.1874) and RS (0.1878) strains. While on soybean and cotton plants, the lowest rm was observed in the RR strain, differing from the RS and SS strains. A similar pattern was verified for the finite rate of population increase (λ). The lowest finite rate of population increase was observed for the SS strain on corn, whereas the RR strain had the lowest finite rate of population increase on soybean and cotton plants. Differences in values of rm and λ for the RS and RR strains were observed across the host plants; the highest values were observed on corn plants, followed by soybean and cotton, whereas no difference was observed in the SS strain for these two parameters on soybean and cotton plants.

Considering the relative fitness (w) of the SS strain as a reference ($w = 1$), the relative fitness for the RR and RS strains on corn plants were 1.06 and 1.07, respectively. A decrease in the relative fitness were observed for the RR strain on soybean plants ($w = 0.84$)

and cotton (w = 0.67). However, the RS strain did not show any reduction in relative fitness when reared on soybean and cotton plants (w > 1 for both host plants). According to these results, the RR strain did not show a competitive disadvantage compared with the SS strain on corn plants. However, a reduction of the competitiveness of the RR strain was observed on soybean and cotton plants when compared to the SS strain. The RS strain did not demonstrate any disadvantages compared to the SS strain on the three host plants. This indicates that the fitness costs of spinetoram resistance in *S. frugiperda* are recessive independent of the host plant, since the fitness of the RS strain is similar to the fitness of the SS strain on the three host plants.

Table 8. Population growth parameters of *Spodoptera frugiperda* strains reared on corn, soybean, and cotton plants

Population growth parameters	Strain	Host plant		
		Corn	Soybean	Cotton
Net reproductive Rate - R_0 (♀/♀)	RR	822.78 ± 36.23 Aa	239.33 ± 31.38 Bb	144.90 ± 20.62 Bb
	RS	836.98 ± 62.36 Aa	637.84 ± 35.00 Aa	813.85 ± 47.51 Aa
	SS	699.74 ± 67.56 ABa	580.02 ± 44.88 Ba	786.30 ± 43.28 Aa
Mean length of a Generation - T (days)	RR	35.82 ± 0.15 Cb	42.02 ± 0.29 Ba	49.74 ± 0.17 Aa
	RS	35.82 ± 0.20 Cb	39.98 ± 0.19 Bb	44.44 ± 0.05 Ab
	SS	37.37 ± 0.45 Ca	41.21 ± 0.19 Ba	44.53 ± 0.20 Ab
Intrinsic rate of population increase - rm (♀/♀/day)	RR	0.1874 ± 0.001 Aa	0.1304 ± 0.003 Bb	0.1002 ± 0.003 Cb
	RS	0.1878 ± 0.002 Aa	0.1615 ± 0.001 Ba	0.1508 ± 0.001 Ca
	SS	0.1753 ± 0.003 Ab	0.1544 ± 0.002 Ba	0.1498 ± 0.001 Ba
Finite rate of population increase - λ (♀/♀/day)	RR	1.21 ± 0.001 Aa	1.14 ± 0.003 Bb	1.10 ± 0.003 Cb
	RS	1.21 ± 0.003 Aa	1.17 ± 0.002 Ba	1.16 ± 0.002 Ca
	SS	1.19 ± 0.003 Ab	1.16 ± 0.002 Ba	1.16 ± 0.002 Ba
Relative fitness (w) [a]	RR	1.06	0.84	0.67
	RS	1.07	1.04	1.01
	SS	1	1	1

Values represent means ± SE. Different lowercase letters indicate a significant difference between *S. frugiperda* strains on the same plants (columns) and uppercase letters indicates significant difference for the same strain on different plants (lines) (Tukey's test, $p < 0.05$).

[a] Relative fitness (w) = rm (RR or RS strain)/rm (SS strain)

3.4. Discussion

In this study, we demonstrated the effects of host plants on fitness costs associated with spinetoram resistance in *S. frugiperda* through the comparison of different biological parameters using strains with same genetic backgrounds. The concentration-response curves estimated a high resistance ratio for the resistant strain of *S. frugiperda* to spinetoram used in this study. A similarly high resistance ratio has also been reported for this pest to spinosad and spinetoram by Okuma et al. (2018) and Lira et al. (2020). The spinosyn insecticides are one of the chemical groups used to manage this pest in Brazil (Burtet et al. 2017). Thus, the increase in the number of highly resistant strains, selected in a short time, raises the hypothesis that the frequency of spinosyn resistance alleles in *S. frugiperda* populations in the field is rising, possibly due to an increase in the selection pressure exerted by these insecticides.

Fitness costs is one of the concepts that uphold enduring resistance management programs (Freeman et al. 2021). Our results showed that all strains (resistant, susceptible, and heterozygous) survived and completed their life cycles on corn, soybean, and cotton plants. Different patterns of development and life history traits were observed among the three evaluated host plants, indicating relevant fitness costs associated with spinetoram resistance in plants of soybean and cotton, but no significant fitness costs in corn plants. Different host plants can affect the magnitude of the fitness cost associated with insect resistance (Gassmann et al. 2009). Previous studies showed that plants of corn, soybean, and cotton affected the magnitude of fitness costs associated with Cry1F, chlorpyrifos and Cry1A.105 + Cry2Ab2 resistance in *S. frugiperda* (Jakka et al. 2014; Garlet et al. 2021b; Santos-Amaya et al. 2022). Similar results were also observed in other insect pest such as *H. armigera*, *P. xylostella* and *Trichoplusia ni* (Hübner) when feeding on different food sources (Bird and Akhurst 2007; Raymond et al. 2011; Wang et al. 2016). However, the fitness costs of Vip3A resistance in *S. frugiperda* was not evident on different host plants (Chen et al. 2019), suggesting that the magnitude of fitness costs on different host plants is not always apparent, and it should be studied for each resistance case.

The variation in fitness costs on different host plants could be related to plant defense compounds and their nutritional quality that alters food conversion efficiency, which in turn can affect the development time and fecundity of insect pests (Awmack and Leather 2002). Although *S. frugiperda* is a highly polyphagous pest, corn and other grass plants appear to be the most suitable host plants for *S. frugiperda* (Barros et al. 2010; Silva et al. 2017). In our

study we hypothesized that the slow development of *S. frugiperda* strains on soybean and cotton plants could be related to the secondary compounds present on these plants. A study conducted by Peruca et al. (2018) demonstrated that secondary compounds of soybean plants impair the development of *S. frugiperda*. The lower fitness on cotton plants could be related to gossypol, a polyphenolic aldehyde, that affects larval development as demonstrated in Bt-resistant strains of *Pectinophora gossypiella* (Saunders) (Carrière et al. 2004; Carrière et al. 2019; Williams et al. 2011).

Another hypothesis for the lower fitness of the RR strain on plants of soybean and cotton is the interaction between the resistance mechanisms of spinosyn resistance in *S. frugiperda* and the mechanisms of adaptation to the plant defense compounds of soybeans and cotton. Insects exploit different strategies to overcome plant secondary compounds. The main mechanism of insect adaptation to synthetic and natural xenobiotics is the increased metabolic capability of detoxification (Li et al. 2007a; Schuler 2011; Feyereisen 2012; Heidel-Fischer and Vogel 2015; Lu et al. 2020; Vandenhole et al. 2020). Since the process of synthesizing detoxification enzymes is very costly, it demands an energy reallocation from other biological functions, resulting in a lower fitness (Kliot and Ghanim 2012). The spinosyns resistance mechanisms have been studied for several species of insect pests. Target site insensitivity has been associated with spinosyn resistance in most cases (Perry et al. 2007; Baxter et al. 2010; Hsu et al. 2012; Silva et al. 2016; Zimmer et al. 2016; Wan et al. 2018; Wang et al. 2020a, 2020b; Zuo et al. 2020). However, some studies showed that metabolic detoxification enzymes could also be involved in spinosyn resistance (Wang et al. 2009; Sial et al. 2011; Rehan and Freed 2014). At the moment, the mechanism underlying spinosyn resistance in *S. frugiperda* is still unknown. Multi-omics approaches will be considered in our future studies to identify the molecular mechanism associated with spinosyn resistance in *S. frugiperda* and understand the interaction between the mechanism of insecticide resistance and the mechanism of host plant adaptation.

From a practical perspective, no significant fitness costs associated with spinetoram resistance on corn plants means that removing the selective pressure from the environment would not result in a decrease of spinetoram resistance allele frequency on corn plants since there is no competitive disadvantage between resistant and susceptible individuals. On the other hand, a negative impact was verified on the life history traits of the RR strain on soybean and cotton plants, which had a significant reduction in the survival and reproductive rates compared to the other strains. This information could be exploited to design effective resistance management strategies. For example, a seasonal removal of spinosyn insecticides in

the control of *S. frugiperda* and an adoption of insecticides with different modes of action in a rotation scheme, or another control tactic, would aid in maintaining the resistance to spinetoram at low frequencies.

In conclusion, we showed that the rate of spinetoram resistance evolution in *S. frugiperda* might be dependent on the host plant. When feeding on corn plants, resistance may evolve more rapidly than when feeding on soybean and cotton plants. The shorter development time on corn plants increases the number of generations of the pest, consequently increasing the frequency of resistance alleles in the field. On soybean and cotton plants, the frequency of resistant individuals tends to be lower due to the presence of a fitness cost. Despite the competitive disadvantage of resistant individuals on soybean and cotton plants, an attention should be given to the heterozygous individuals because their performance is similar to the susceptible individuals regardless the host plant. The heterozygous individuals are the main carriers of resistance alleles and their competitiveness guarantees the permanence of resistance alleles in the field (Roush and Daly 1990). The information provided here supports the design of effective IRM strategies, highlighting the importance of not only the biological aspects of the pest, but also the host plants that are part of the agricultural system where the pests are found.

3.5. Conclusions

- The fitness costs associated with spinetoram resistance in *S. frugiperda* varied with the host plant;
- No fitness costs associated with spinetoram resistance were observed in corn plants;
- Significant fitness costs associated with spinetoram resistance were observed in soybean and cotton plants.

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4. PROTEOMIC ANALYSIS OF SPINETORAM RESISTANCE AND HOST PLANT INTERACTIONS IN *Spodoptera frugiperda* (LEPIDOPTERA: NOCTUIDAE)

Abstract
Insecticide resistance and host plant adaptation in insects are both complex evolutionary processes. The fall armyworm, *Spodoptera frugiperda* (J. E. Smith), is a polyphagous pest with a high risk of insecticide resistance evolution. In this study, a comparative proteomic analysis was conducted to identify the molecular and physiological responses spinetoram-resistant and susceptible strain of *S. frugiperda* feeding on corn, soybean, and cotton plants by using liquid chromatography tandem mass spectrometry (LC-MS/MS). A total of 3267 proteins were identified from the LC-MS/MS analysis. Our results show that the host plant is a significant factor in shaping the protein abundance of resistant and susceptible strains. Most of differentially abundant proteins between the spinetoram-resistant and susceptible strains were specific to each host plant. Enrichment analysis showed that the differentially abundant proteins were related to metabolic, cellular, developmental, and biological regulation processes. The protein-protein interaction analysis that showed interactions were associated with gene regulation and epigenetic processes. The proteins that were differentially abundant between the spinetoram-resistant and susceptible strains, regardless of the host plant were related to energy production and cellular metabolism. The results of this study contribute for the understanding of the molecular mechanisms underlying spinetoram resistance and host plant adaptation in *S. frugiperda*.

Keywords: fall armyworm; spinosyns; LC-MS/MS; insecticide resistance; adaptation.

4.1. Introduction

Adaptation of insects to a particular host plant involves different evolutionary processes to face a wide variety of host plant defenses. To protect themselves against the herbivore attack of insects, plants have developed a variety of defensive strategies, either by the physical or chemical barriers (War et al., 2012). These chemical barriers includes the production of secondary compounds that may affect the insect growth and development (Awmack and Leather, 2002). Insects, in turn, have evolved multiple mechanisms to cope with chemical defenses of the plants (Heidel-Fischer and Vogel, 2015). This greater ability of insects to rapidly adapt to different environmental conditions, such as adaptation to feed on different host plants or survive exposure to pesticides, could be one of the main factors that explain the evolutionary success of insect pests. These adaptation process can be more challenging for generalist insect species that have to overcome a wide spectrum of chemical barriers posed by the different host plants (Dermauw et al., 2018).

The fall armyworm, *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae), is an economically important pest that poses a serious threat to agriculture. Recently, the

notoriety of this pest has increased because it has been reported as an invasive pest in many countries of the Africa, Asia and Oceania (Baloch et al., 2020; Goergen et al., 2016). The fall armyworm can fed on more than 350 host plants, including economically crop plants such as corn, soybean and cotton (Montezano et al., 2018). Chemical insecticides have been widely used for the control of this pest (Van den Berg and du Plessis, 2022). However, the evolution of resistance of *S. frugiperda* to the main chemical groups of insecticides has been reported due to the intensive use of this control tactic (Bolzan et al., 2019; Carvalho et al., 2013; Diez-Rodríguez and Omoto, 2001; Garlet et al., 2021; Lira et al., 2020; Muraro et al., 2021; Nascimento et al., 2022, 2016; Okuma et al., 2018). Given that, *S. frugiperda* could serve as model to study the interaction between host plant and insecticide adaptations because it is a good representative of a generalist insect and has the remarkable ability to evolve resistance to insecticides.

Spinosyn insecticides are used against a broad range of insect pests, acting as allosteric modulators of the nicotinic acetylcholine receptor causing hyper excitation of the insect nervous system and thus leading to involuntary muscle paralysis and death (Crouse et al., 2001; Salgado and Sparks, 2005). Spinetoram is semi-synthetic spinosyn insecticide derived from the modified metabolites (spinosyns J and L) of the bacterium *Saccharopolyspora spinosa* and exhibited improved insecticidal activity compared to spinosad (Dripps et al., 2008; Salgado and Sparks, 2005). The favorable environmental profile such as low toxicity to non-target organisms and high efficacy of insect control made these insecticides an important tool in pest management programs (Dripps et al., 2011; Salgado and Sparks, 2005). However, the widespread use of spinosyn insecticides has increased the selection pressure leading to resistance evolution of many insect pests (Sparks et al., 2012), including *S. frugiperda* (Lira et al., 2020; Okuma et al., 2018).

Insecticide resistance and host plant adaptation are both evolutionary phenomena that arises from complex mechanisms resulting from genetic mutations and changes in gene expression (Alyokhin and Chen, 2017; Després et al., 2007; Hawkins et al., 2019). These mechanisms are often shared between these two processes, as many of the genes responsible for host plant utilization are also responsive to chemical insecticides (Vogel et al., 2014). This link was demonstrated in a study by Dermauw et al. (2013), which observed an increased transcriptional responses in *Tetranychus urticae* when reared on tomato plants. Furthermore, several of these altered expressed genes were associated with detoxification enzymes, leading to a reduction in susceptibility to pesticides. Similarly, microsomal oxidases and cytochrome P450 enzymes were involved in the response of *S. frugiperda* to different host plant and their

allelochemicals (Giraudo et al., 2015; He et al., 2023; Yu, 1982). Although the effect of different host plants has been evaluated in life history traits of resistant strain of *S. frugiperda* to spinetoram (Kanno et al., 2023), there is no information about the molecular basis of adaptation of these host plants in the resistance of *S. frugiperda* to spinetoram.

Significant progress has been made in expanding our understanding of these adaptation processes, however the majority of the research have primarily focused in the use of genomic and transcriptomic approaches (Alyokhin and Chen, 2017; Després et al., 2007; Etges, 2019; Heidel-Fischer and Vogel, 2015; Vogel et al., 2014). These studies sometimes overlook the post-transcriptional modification and protein-protein interactions. Proteomic analysis is a powerful tool to investigate the molecular mechanisms of insect adaptation in a more accurately way since the proteins are the primary functional molecules involved in the different physiological processes (Aslam et al., 2017). To date, there is no proteomic analysis data investigating the interaction of host plants and insecticide adaptation in *S. frugiperda*. Understanding how host plant affect protein expression in insect pests enables the development of effective insect resistance management strategies that consider the potential influence of host plants on insecticide resistance and other adaptive traits. In this context, we conducted a comparative proteomic analysis to identify the molecular and physiological responses of spinetoram-resistant and susceptible strain of *S. frugiperda* feeding on corn, soybean, and cotton plants by using liquid chromatography tandem mass spectrometry (LC-MS/MS).

4.2. Material and Methods

4.2.1. Insect strains

The spinetoram resistant (RR) and susceptible (SS) strain of *S. frugiperda* were used in this study. These two strains were obtained from a field population collected in São Desidério, Bahia State, Brazil in 2018 (Kanno et al., 2023). The RR strain presented a resistance ratio of 776.9-fold compared to SS strain. Both strains were reared in artificial diet (Kasten Jr et al., 1978) under laboratory conditions of 25 ± 2 °C, 70% relative humidity and 14:10 h (L:D) photoperiod.

4.2.2. Sample collection

The RR and SS strains were reared in leaves of non-Bt plants of corn (3700 RR2), soybean (95R51) and cotton (FM 944GL). All plants were cultivated in 12l pots in a greenhouse. Leaves of each plant were collected and placed into a gelled mixture of 2.5% agar-water in 16-well plastic trays (Advento do Brasil). Neonate larvae (<24h old) from RR and SS strains were infested in each well and reared until the fourth instar. Newly and fresh leaves were replaced every day. Seven pools of five fourth instar larvae from each strain were collected per host plant. The larvae were frozen in liquid nitrogen and then stored at -80ºC for the protein extraction.

4.2.3. Protein extraction

Approximately 150 mg of tissue samples were crushed using a TissueLyser (Qiagen, Hilden, Germany) with tungsten carbide beads. The samples were homogenized in 800 µL of protein extraction buffer (0.5M TrisHCl, pH 7.5; 0.1M KCl; 0.05M EDTA; 0.7M sucrose; 2% (v/v) β-mercaptoethanol; 2mM PMSF; 1% (w/v) PVPP). After the homogenization, 800 µL of saturated phenol with 10 mM TrisHCl pH 8.0 was added to the samples. The samples were homogenized using an orbital shaker (150 rpm) for 30 min at 4ºC and the phases were separated by centrifugation (10000g, 30min, 4ºC). The supernatant was recovered to new tubes and 800 µL of the extraction buffer was added in each sample. This procedure was repeated three more times. Proteins were precipitated in 1.6 mL of 0.1 M ammonium acetate in methanol and kept at -20ºC overnight. Then, the samples were centrifugated (16000g) for 30 min at 4ºC. The pellet was washed two times with 1.6 mL of 0.1 M ammonium acetate in methanol and once in 1.6 mL in acetone 100%, incubated at -20ºC for 1h and centrifugated (16000g) for 30 min at 4ºC. The pellet was dried and resuspended in 400 µL of solubilization buffer (7M Urea, 2M Thiourea, 10 mM DTT and 0.01% (w/v) Triton X-100). The proteins were desalted in 50 mM ammonium bicarbonate buffer using an Amicon 3 kDa filter (Millipore).The Bradford method was used to quantify the protein concentration (Bradford, 1976). The quality of protein samples was also verified using a 12% polyacrylamide gel stained with Comassie Blue G250 and bovine serum albumin was used as an internal standard.

4.2.4. Protein sample preparation and analysis with LC-MS

The proteins were solubilized in a solution of 0.2% of RapiGest SF (Waters) and incubated at 80ºC for 15 min. Then, 2.5 µL of 100 mM dithiothreitol (BioRad) was added in each sample and incubated at 60ºC for 30 min, followed by the addition of 2.6 µL of 300mM of iodoacetamine (GE). The samples kept at room temperature in the dark for 30 min. The proteins were enzymatically digested with trypsin (Promega) at 1:100 (w/w), and the sample were incubated at 37ºC for 16h. After the digestion, 10 µL of 5% trifluoroacetic acid (v/v) was added to each sample and incubated at 37ºC for 90 min to hydrolyze the RapiGest. Then, the samples were centrifugated at 16000g for 30 min at 6ºC, and the supernatant was transferred to new tube. The samples were vacuum dried using a SpeedVac (Eppendorf) and desalted using the ZipTip Reversed-Phase Zip-Tip C18 (Millipore) according to the manufacturer's instructions. The peptides were resuspended in 0.1% formic acid. The sequencing of the peptides was performed on a NanoElute system (Bruker Daltonik) coupled to a timsTOF Pro mass spectrometer (Bruker Daltonik).

4.2.5. Data processing and analysis

Raw data were processed with MaxQuant (Tyanova et al., 2016) and Perseus (Tyanova and Cox, 2018) software using the protein FASTA file of *S. frugiperda* (NCBI Accession Number PRJNA590312) to identify and quantify the proteins in each sample. Statistical analysis was performed using MetaboAnalysts 5.0 (Pang et al., 2022). The data were log-transformed and pareto-scaled for further analysis. Principal Component Analysis (PCA) was performed to classify the sample groups. Two-way ANOVA was used to verify the effect of host plant, strain and their interaction on protein abundance. Pairwise analysis using volcano plot was conducted to identify the differentially abundant proteins in each host plant. The criteria to identify the differentially abundant proteins were adjusted p-value < 0.05 and fold change $\geq |2.0|$. Venn diagram was used to identify the common and exclusively differentially abundant proteins in each host plant.

Functional analysis of the differential abudant proteins was conducted using the database of Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG). Annotation of the proteins into GO and KEGG database was made using the software EggNOG-mapper v2 (Cantalapiedra et al., 2021). GO enrichment analysis of the higher and lower abundant proteins was performed using the package topGO (Alexa and Rahnenführer,

2009) with Fisher exact test. The results from enrichment analysis were reduced and visualized using REVIGO (Supek et al., 2011). KEGG enrichment analysis of the higher and lower abundant proteins was performed using the function *enrichKEGG* from the package clusterProfiler (Yu et al., 2012). All enrichment analysis were performed in the R software (R Core Team, 2023).

Protein-protein interaction analysis was performed in STRING (Szklarczyk et al., 2015) using the differential abundant proteins that were exclusively in each host plant. The entire proteome of *S. frugiperda* (NCBI Accession Number PRJNA590312) was uploaded to compute the interaction network. The minimum require interaction score was set to 0.7 (high confidence). Gene ontology enrichment analysis was performed only for the proteins that presented some interaction using the package topGO as described earlier.

4.3. Results

4.3.1. Overview of *Spodoptera frugiperda* proteome

In total, 3267 proteins of *S. frugiperda* were identified from LC/MS analysis. The average of protein sequence coverage was 28.76%. The number of proteins that presented sequence coverage >20% was 1835 (56.16%), indicating a high confidence of the identified proteins (Fig. 13A). The distribution of the number of unique peptides showed that 2948 proteins were identified by at least two unique peptides, accounting for 90.23% of the total number of identified proteins (Fig. 13B). The molecular weight of the proteins ranged from 6.35 to 1917.4 kDa, with the majority (82.73%) ranging between 10-100 KDa (Fig. 13C).

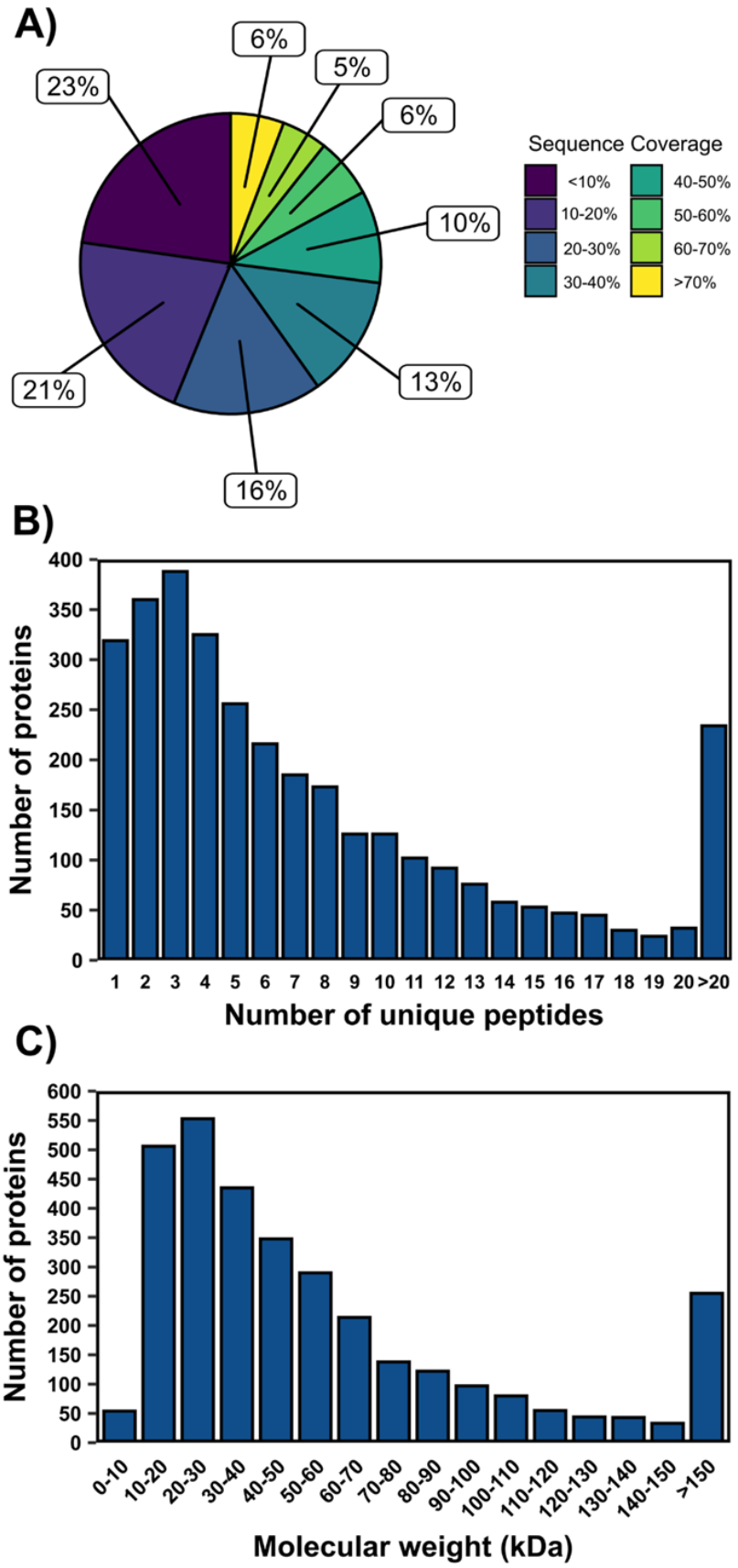

Fig. 13. Distribution of A) protein sequence coverage, B) number of unique peptides and C) molecular weight of the identified proteins of *Spodoptera frugiperda*.

The functional annotation from the 3267 identified proteins in the different databases showed that 2459 (75.26%), 2175 (66.57%) and 2932 (89.74%) proteins were annotated into the GO, KEGG and COG databases, respectively (Fig. 14).

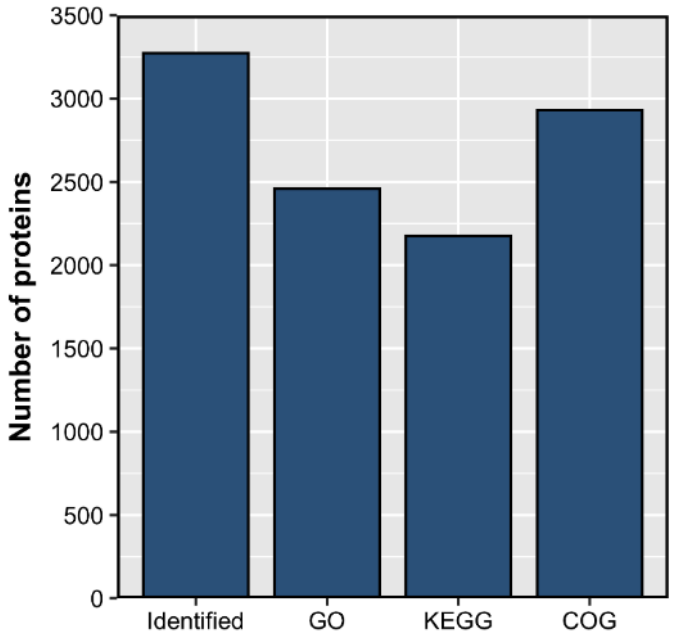

Fig. 14. Number of identified proteins of *Spodoptera frugiperda* annotated in the different databases.

Annotation into GO database was used to predict the functional categories of the proteins. The 2459 annotated proteins were classified in 67 GO terms distributed into the three major categories: Biological process (27 terms), molecular function (22 terms) and cellular component (18 terms) (Fig. 15). In the biological process category, the main GO terms are cellular process (87.9%), metabolic process (75.3%) and biological regulation (64.7%). In the molecular function category, the main GO terms are binding (68.5%), catalytic activity (41%) and structural molecule activity (10.6%). Cell (89.4%), cell part (89.4%) and organelle (77%) were the main GO terms in the category of cellular components.

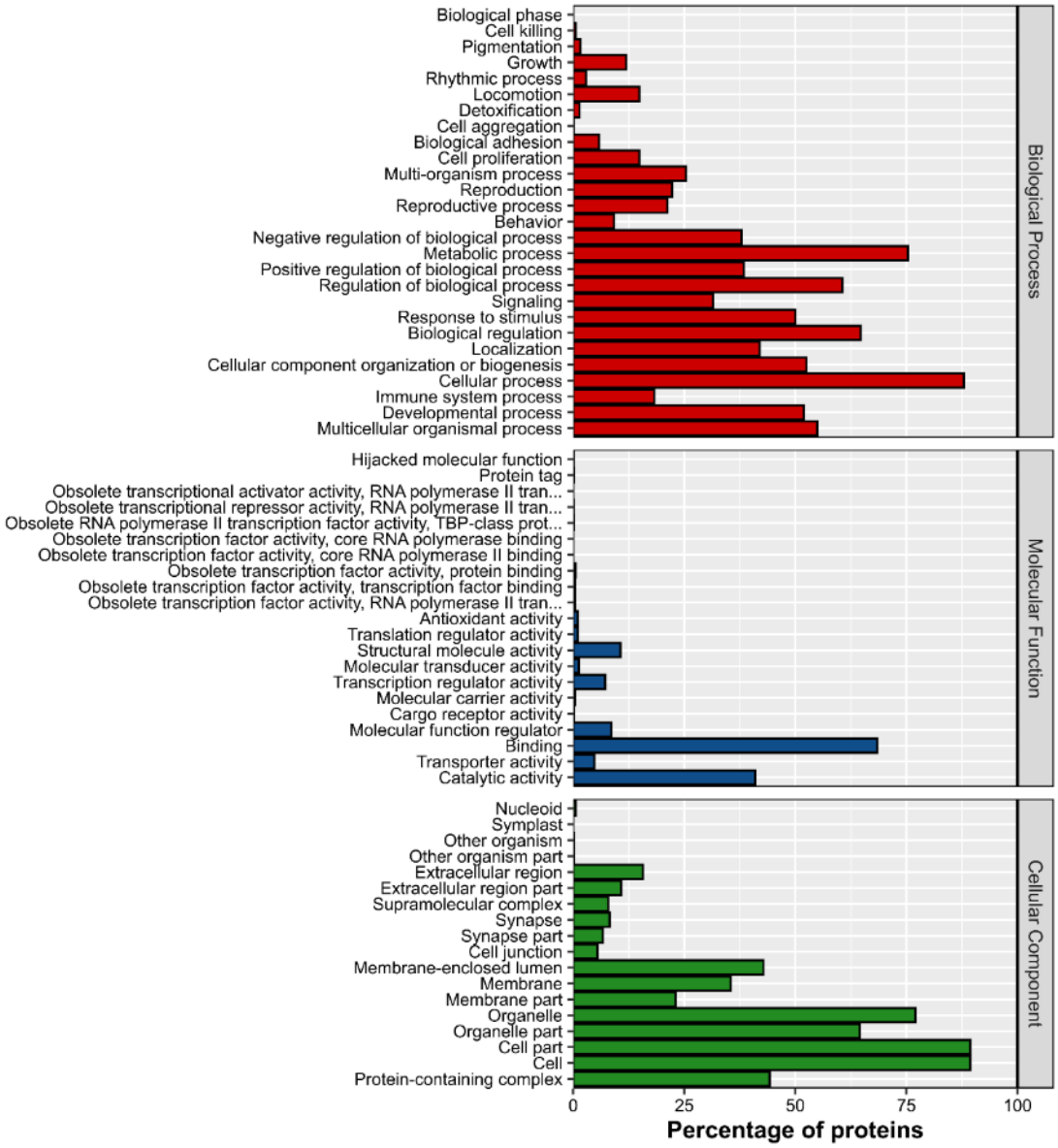

Fig. 15. Distribution of Gene Ontology terms in biological process, molecular function and cellular component of the identified proteins of *Spodoptera frugiperda*.

The COG database was also used to predict and classify the functionality of the proteins. A total of 2932 proteins were annotated and classified into COG functional classes (Fig. 16A). A high number of proteins were classified in “Function unknown” (724 proteins), followed by “Postranslational modification, protein turnover, chaperones” (368 proteins), “Signal transduction mechanisms” (283 proteins) and “Translation, ribosomal structure and biogenesis” (208 proteins). The potential metabolic pathways involved in a specific protein was predicted by the annotation in the KEGG database. A total of 2175 proteins were assigned to 46 biological pathways (Fig. 16B). The three most highly represented pathways

were “Global and overview maps” (860 proteins), “Neurodegenerative disease” (732 proteins) and “Signal transduction” (537 proteins).

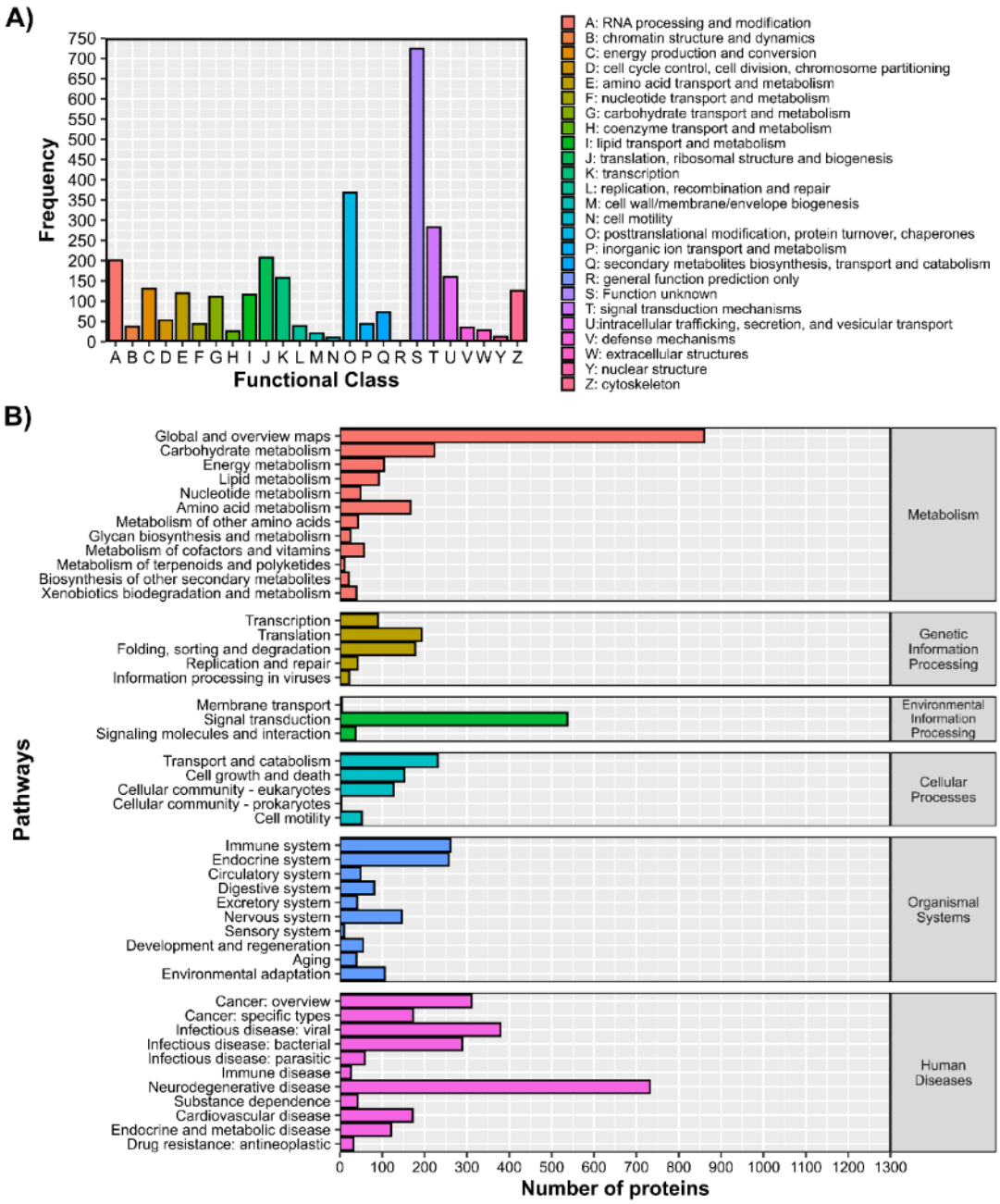

Fig. 16. Classification of the identified proteins of *Spodoptera frugiperda* in the following databases: A) Clusters of Orthologous Groups of proteins (COG) and B) Kyoto Encyclopedia of Genes and Genomes (KEGG)

4.3.2. Proteome changes of *Spodoptera frugiperda* strains in response to host plants

The Principal Component Analysis (PCA) showed a distinction in the protein profile of the resistant and susceptible strains in corn, soybean, and cotton plants. The first two principal components PC1 and PC2 explained 29.6 and 13.4% of the total variation, respectively (Fig. 17A). The two-way ANOVA showed that most of the proteins were significantly affected by the host plant, strain, and their interaction. Most of the proteins were exclusively affected by the host plant (48.6%) and only 67 (2.3%) and 62 (2.1%) proteins were exclusively affected by the strain and by the interaction of host plant and strain, respectively. There were 660 proteins that were simultaneously affected by the host plant, strain and their interaction (Fig. 17B).

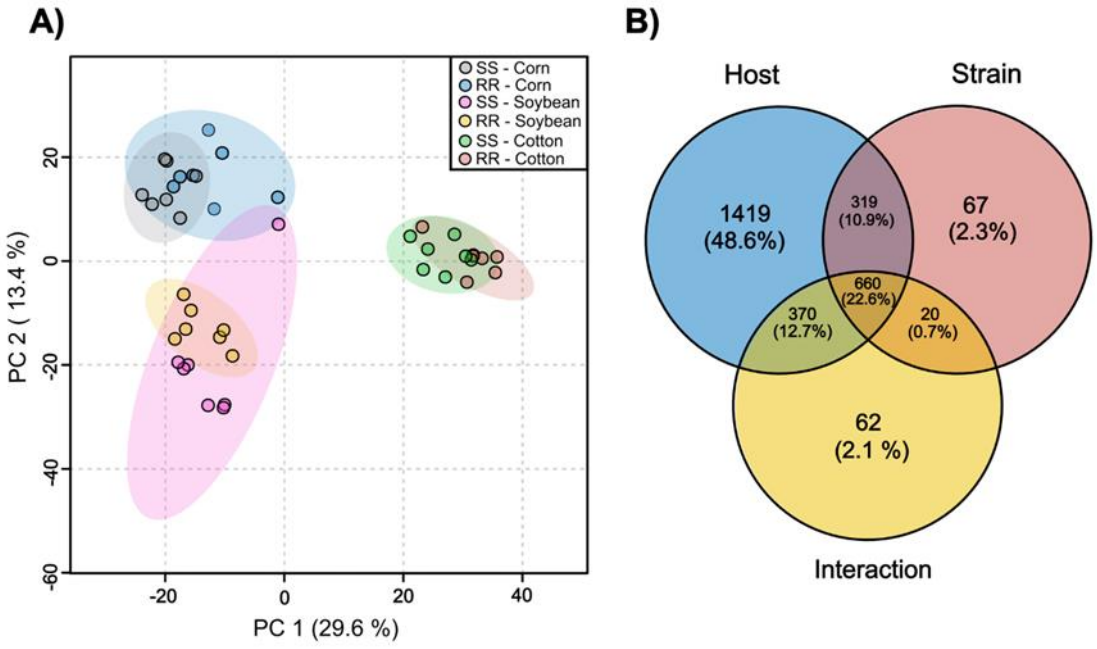

Fig. 17. A) Principal Component Analysis (PCA) of *Spodoptera frugiperda* resistant and susceptible samples. B) Venn diagram showing the number of significant proteins for "Host", "Strain" and "Host vs Strain interaction" obtained by two-way ANOVA.

Volcano plots were used to further determine which proteins are differentially abundant between resistant and susceptible strains in each host plant (Fig. 18). A total of 257 differentially abundant proteins were identified between resistant and susceptible strains in corn plants, of which 180 proteins presented an decreased abundance and 77 proteins

presented a increased abundance. When the resistant and susceptible strains fed on soybeans plants, there were 359 differentially abundant proteins, including a reduced abundance of 169 proteins and increased abundance of 190 proteins. There were 310 differentially abundant proteins between the strains when fed on cotton plants, of which 122 proteins were less abundant and 188 proteins were more abundant in the resistant strain compared to the susceptible strain.

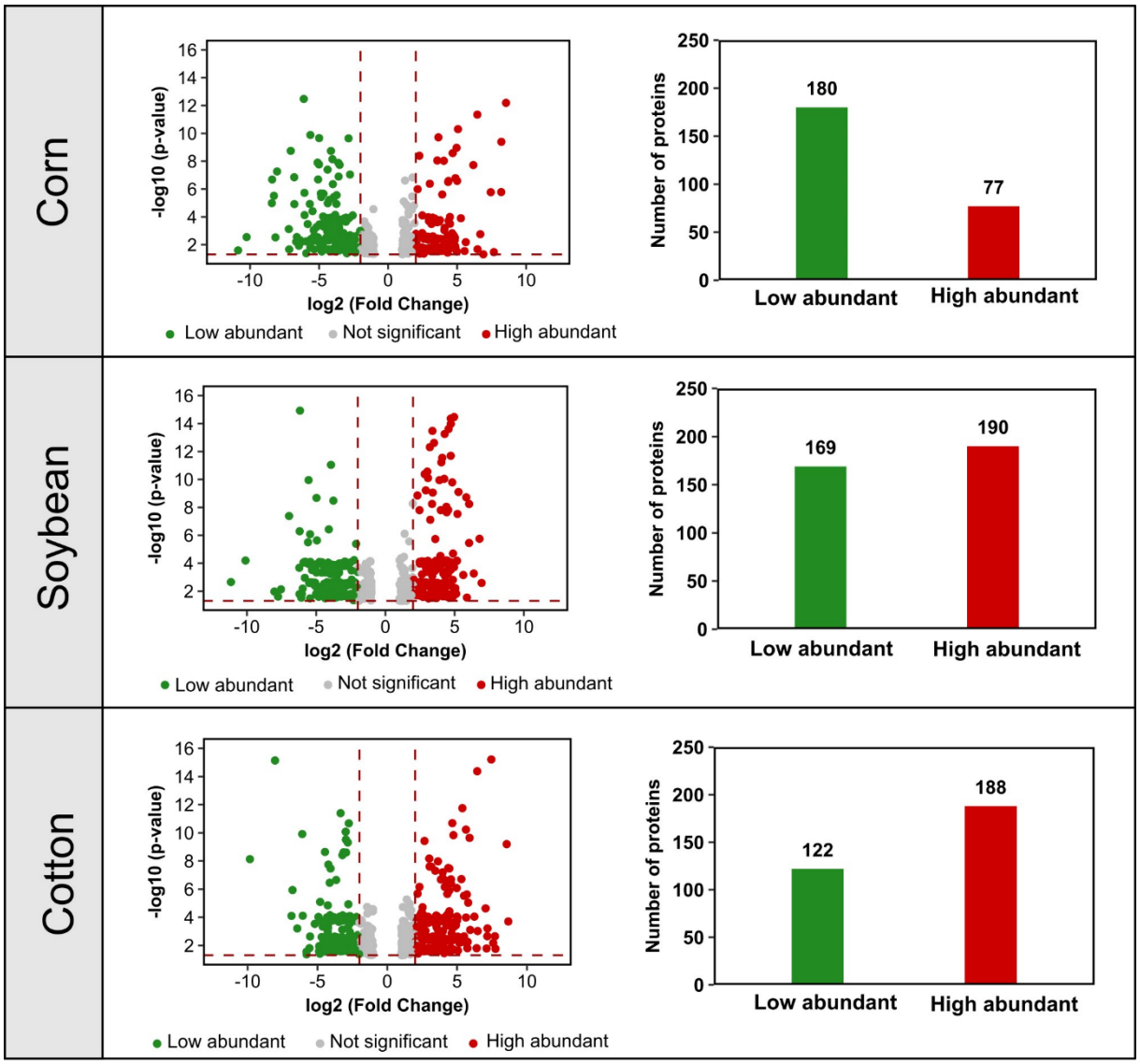

Fig. 18. Number of differential abundant proteins of *Spodoptera frugiperda* strains when feeding on plants of corn, soybean, and cotton.

All differentially abundant proteins were analyzed using the Venn diagram to identify the common and exclusively differential abundant proteins in each host plants (Fig. 19). The greater part of differentially abundant proteins were exclusively for each host plant

(Appendix D, E, F). There were 178, 254 and 225 differentially abundant proteins exclusively in corn, soybean, and cotton, respectively. Only 17 proteins were common in the comparison of resistant and susceptible strain in the three host plants (Appendix G).

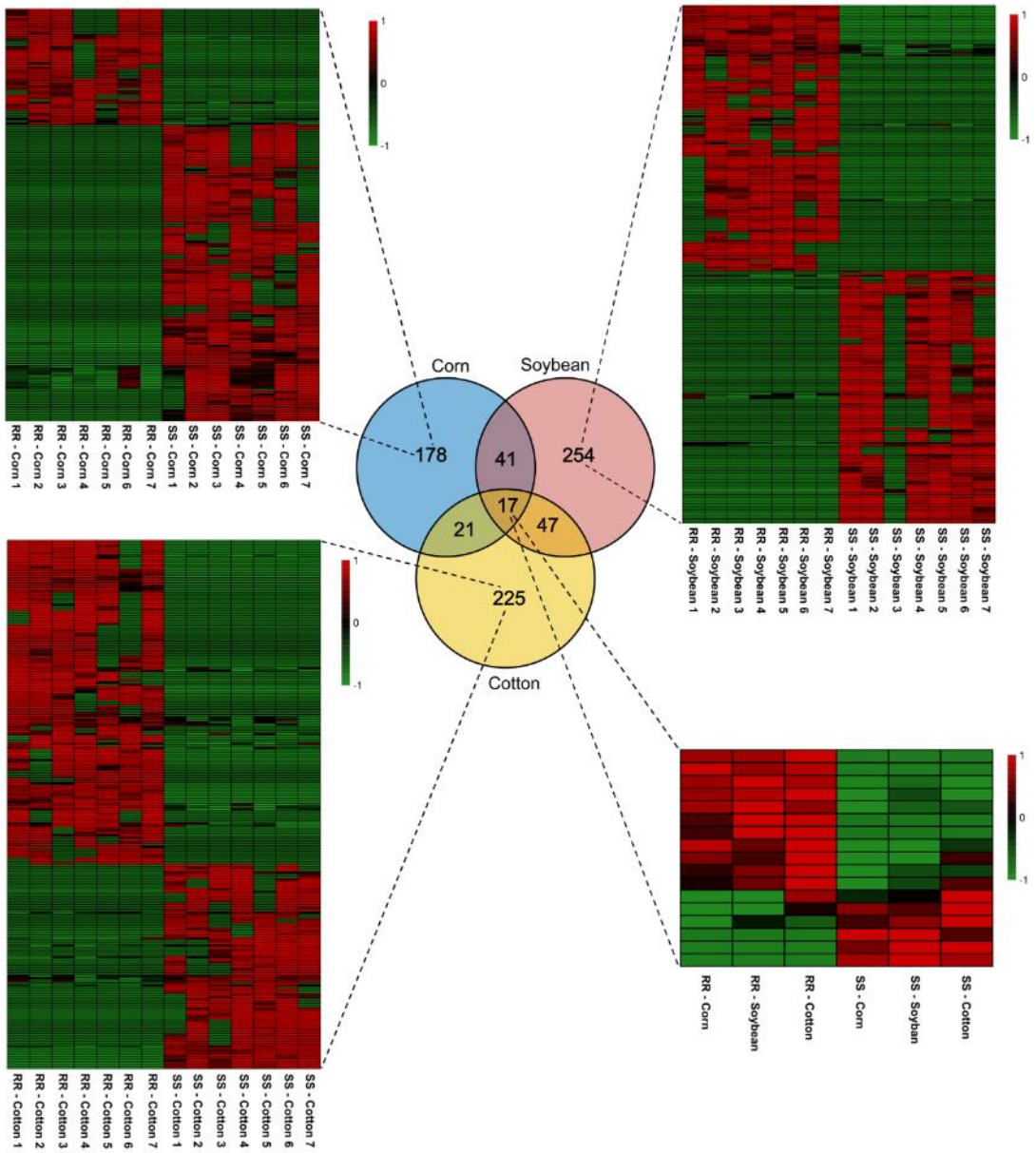

Fig. 19. Venn diagram and heatmaps showing the common and the exclusively proteins that were differentially abundant between the resistant and susceptible strains of *Spodoptera frugiperda* when feeding on corn, soybean and cotton plants.

4.3.3. Functional analysis of the differentially abundant proteins

Gene ontology enrichment analysis was performed to obtain a more detailed understanding about the biological process of the exclusively differentially abundant proteins between resistant and susceptible strain in each host plants. Enrichment analysis of GO terms showed 21 significant terms for the high-abundant proteins in corn, which includes small molecule catabolic process (GO:0044282), small molecule metabolic process (GO:0044281) and apoptotic signaling pathway (GO:0097190) as the representative terms of the GO clusters (Fig. 20A). For the low-abundant proteins in corn, there were 32 significant terms for biological process, including histone modification (GO: 0016570), protein-DNA complex subunit organization (GO: 0071824) and embryonic morphogenesis (GO:0048598) as the representative GO terms (Fig. 20B).

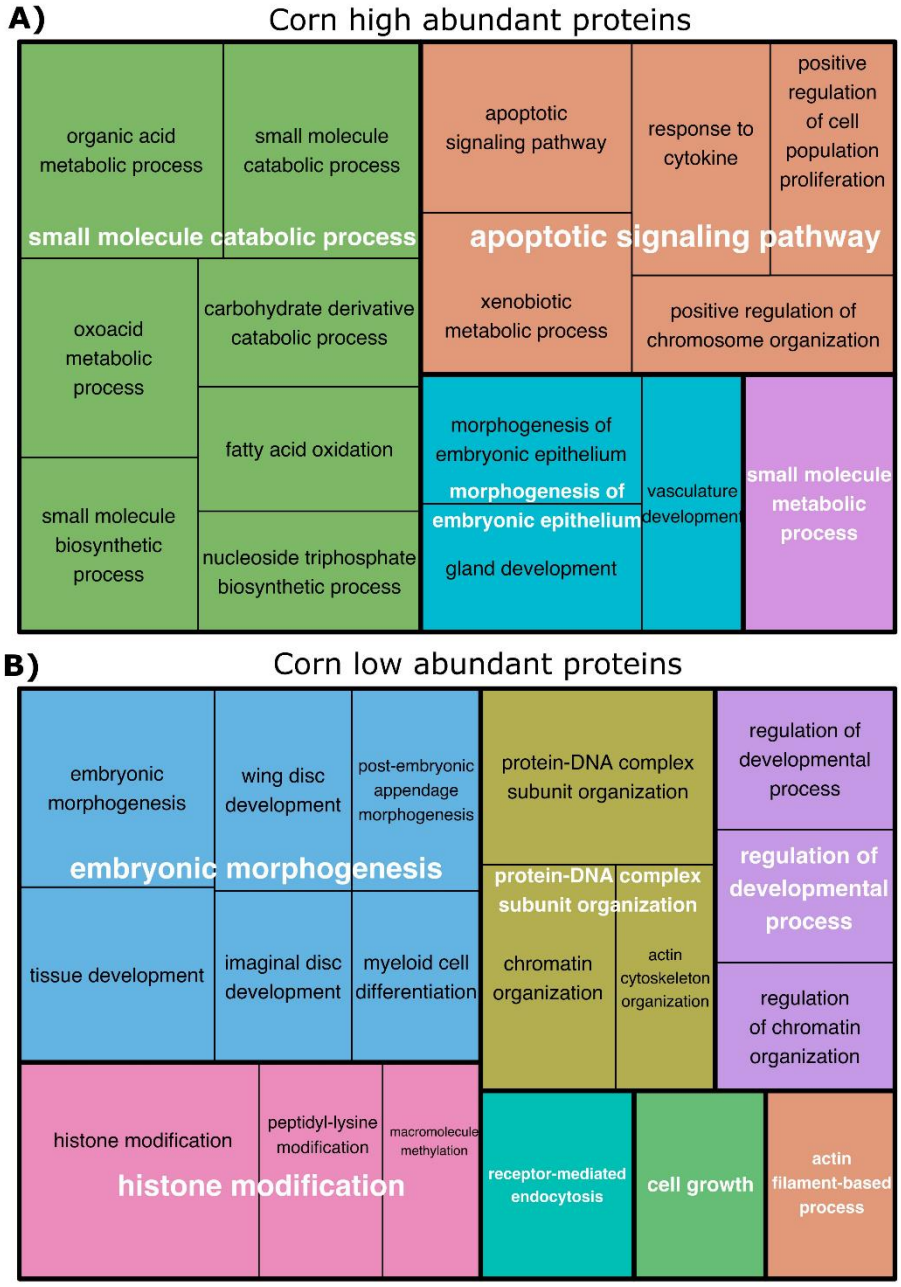

Fig. 20. Treemap representation of the overrepresented Gene Ontology terms from A) high-abundance and B) low-abundance proteins of *Spodoptera frugiperda* strains when feeding on corn plants.

In soybean plants, there were 49 and 31 significant terms in high-abundance and low-abundance proteins, respectively. The representative terms for the high-abundance proteins in soybean plants includes the positive regulation of transcription by RNA polymerase II (GO:0045944), transcription by RNA polymerase II (GO:0006366) and chromatin organization (GO:0006325) (Fig. 21A), while the low-abundance proteins were enriched in GO terms related to cellular and metabolic process (GO:0006807 – nitrogen

compound metabolic process, GO:00334660 – ncRNA metabolic process, GO:0065003 – protein-containing complex assembly, GO:0097190 – apoptotic signaling pathway) and also response to stimulus (GO:0050896) (Fig. 21B).

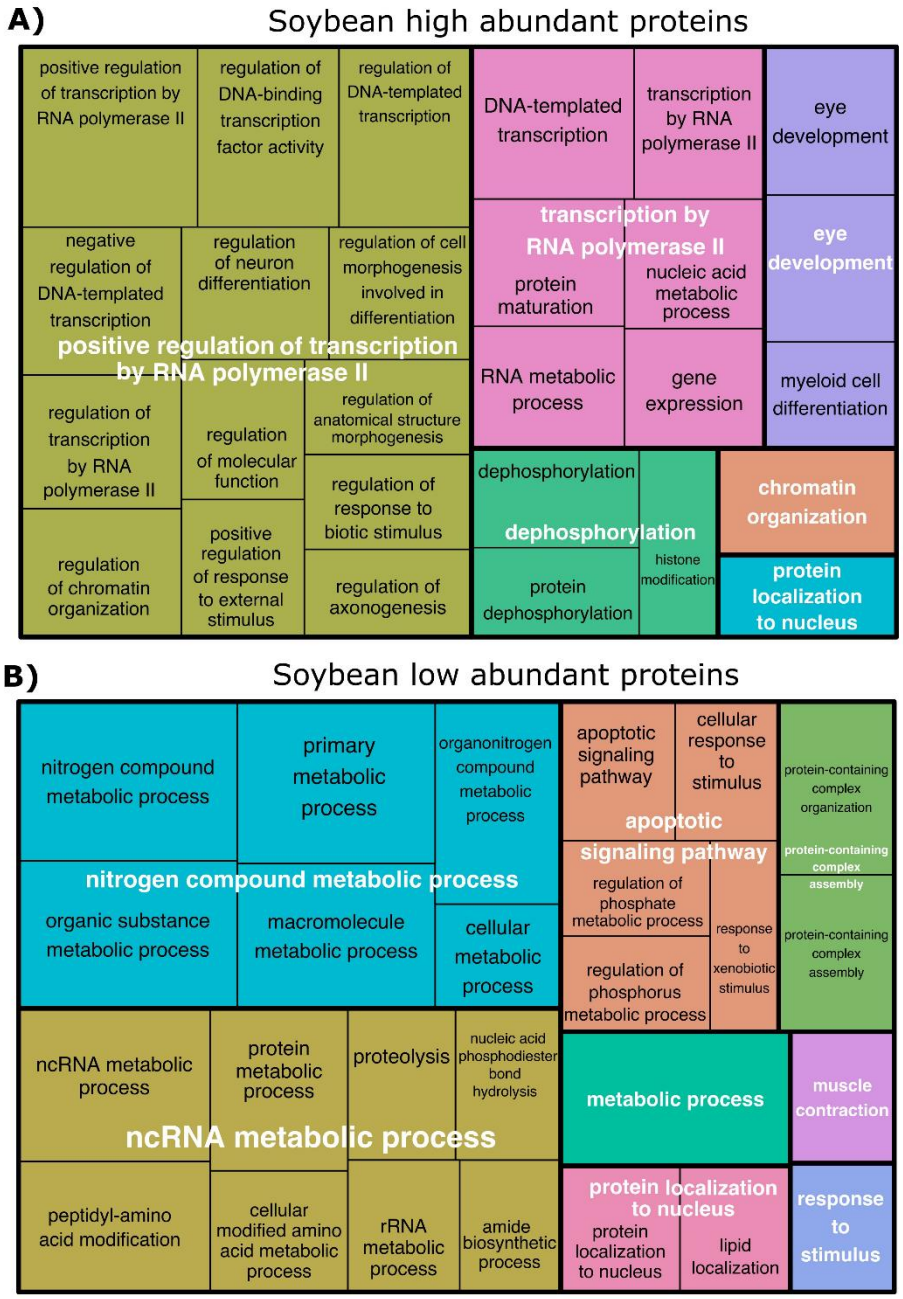

Fig. 21. Treemap representation of the overrepresented Gene Ontology terms from A) high-abundance and B) low-abundance proteins of *Spodoptera frugiperda* strains when feeding on soybean plants.

Enrichment analysis for the high-abundance proteins in cotton plants showed 33 significant terms, including small molecule metabolic process (GO:0044281), response to

xenobiotic stimulus (GO:0009410), immune effector process (GO:0002252) (Fig. 22A). For the low-abundance proteins, there were 73 significant enriched terms including positive regulation of biological process (GO:0048518), biological regulation (GO:0065007) and developmental process involved in reproduction (GO:0003006) (Fig. 22B).

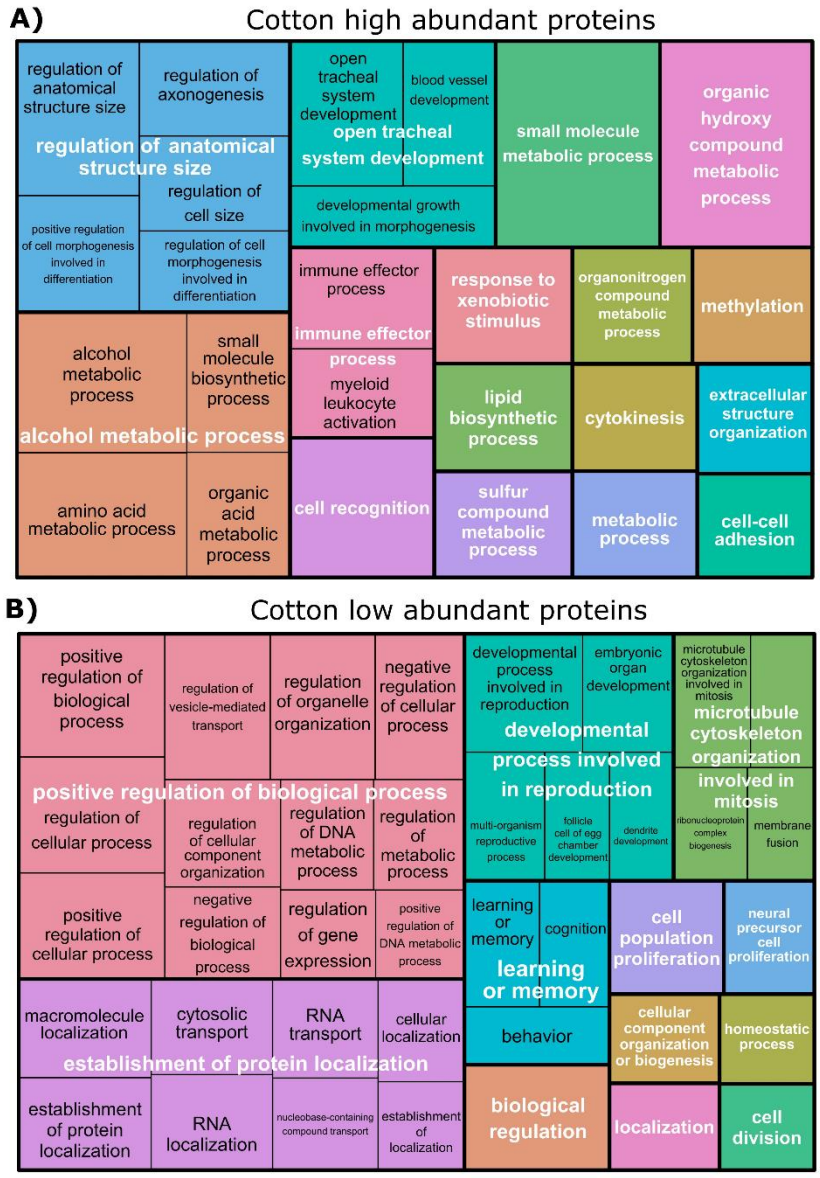

Fig. 22. Treemap representation of the overrepresented Gene Ontology terms from A) high-abundance and B) low-abundance proteins of *Spodoptera frugiperda* strains when feeding on cotton plants.

The enrichment analysis for the proteins that were common in the comparison of resistant and susceptible strain in the three host plants showed six significant terms in which glucose homeostasis (GO:0042593) and monocarboxylic acid biosynthetic process (GO:0072330) were the representative terms (Fig. 23).

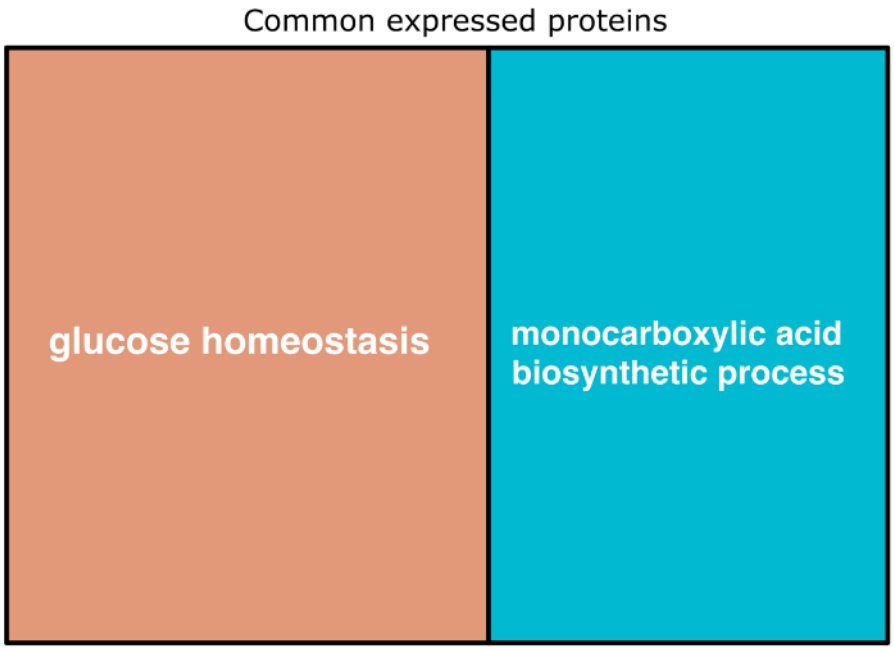

Fig. 23. Treemap representation of the overrepresented Gene Ontology terms from the proteins were common in the comparison of the spinetoram-resistant and susceptible strains of *Spodoptera frugiperda* in the three host plants.

In the enrichment analysis of the differentially abundant proteins in the KEGG database showed that metabolic pathways (ko01100) and glyoxylate and dicarboxylate metabolism (ko00630) were the pathways enriched for the high-abundance proteins in corn, while pathways in cancer (ko05200) and rap1 signaling pathway (ko04015) were enriched for the low-abundance proteins (Fig. 24).

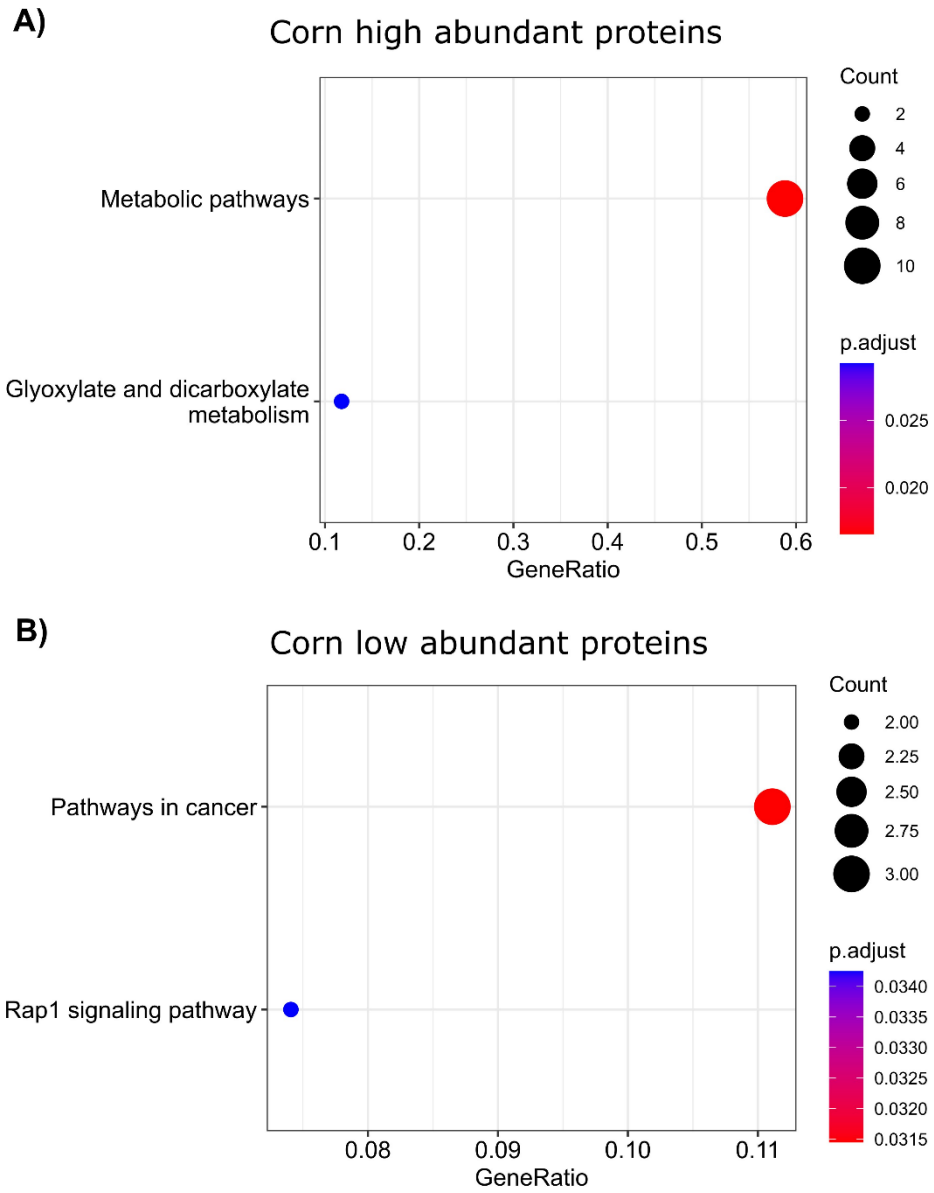

Fig. 24. The significant enriched KEGG pathways of the A) high-abundance and B) low-abundance proteins between the spinetoram-resistant and susceptible strains of *Spodoptera frugiperda* when feeding on corn plants.

In soybean plants, Toll and Imd signaling (ko04624) and tuberculosis (ko05152) were the significantly enriched pathways for the high-abundance proteins, for the low-abundance proteins AMPK signaling (ko04152), insulin signaling (ko04910), longevity regulating (ko04212), fatty acid metabolism (ko01212) and autophagy (ko04140) were the most significantly enriched pathways (Fig. 25).

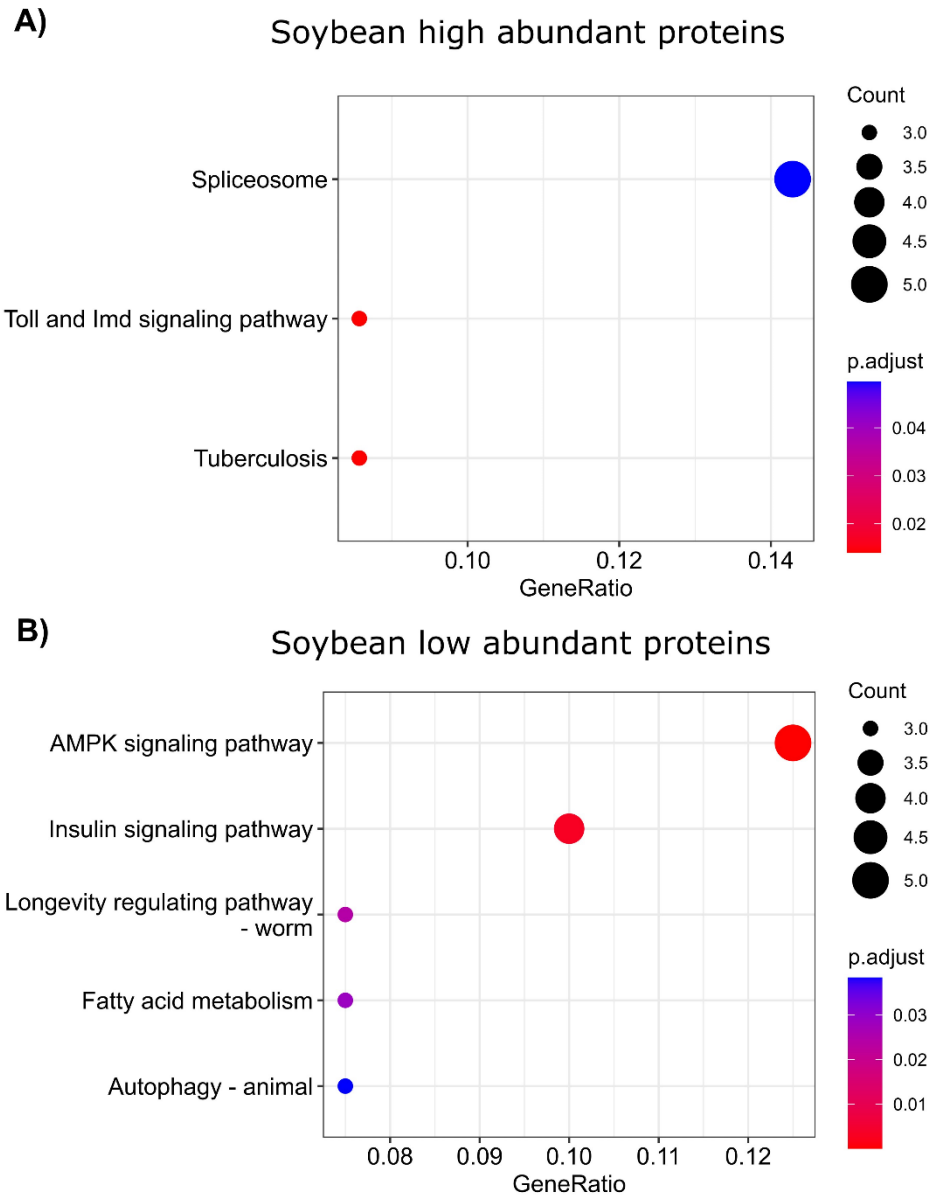

Fig. 25. The significant enriched KEGG pathways of the A) high-abundance and B) low-abundance proteins between the spinetoram-resistant and susceptible strains of *Spodoptera frugiperda* when feeding on soybean plants.

Five pathways were found in the enrichment analysis of the high-abundance proteins in cotton plants: Aminoacyl-tRNA biosynthesis (ko00970), metabolic pathways (ko01100), glutathione metabolism (ko00480), biosynthesis of nucleotide sugars (ko001250) and amino sugar and nucleotide sugar metabolism (ko00520). Ribosome biogenesis in eukaryotes (ko03008) was the only enriched pathway for the low-abundance proteins in cotton plants (Fig. 26).

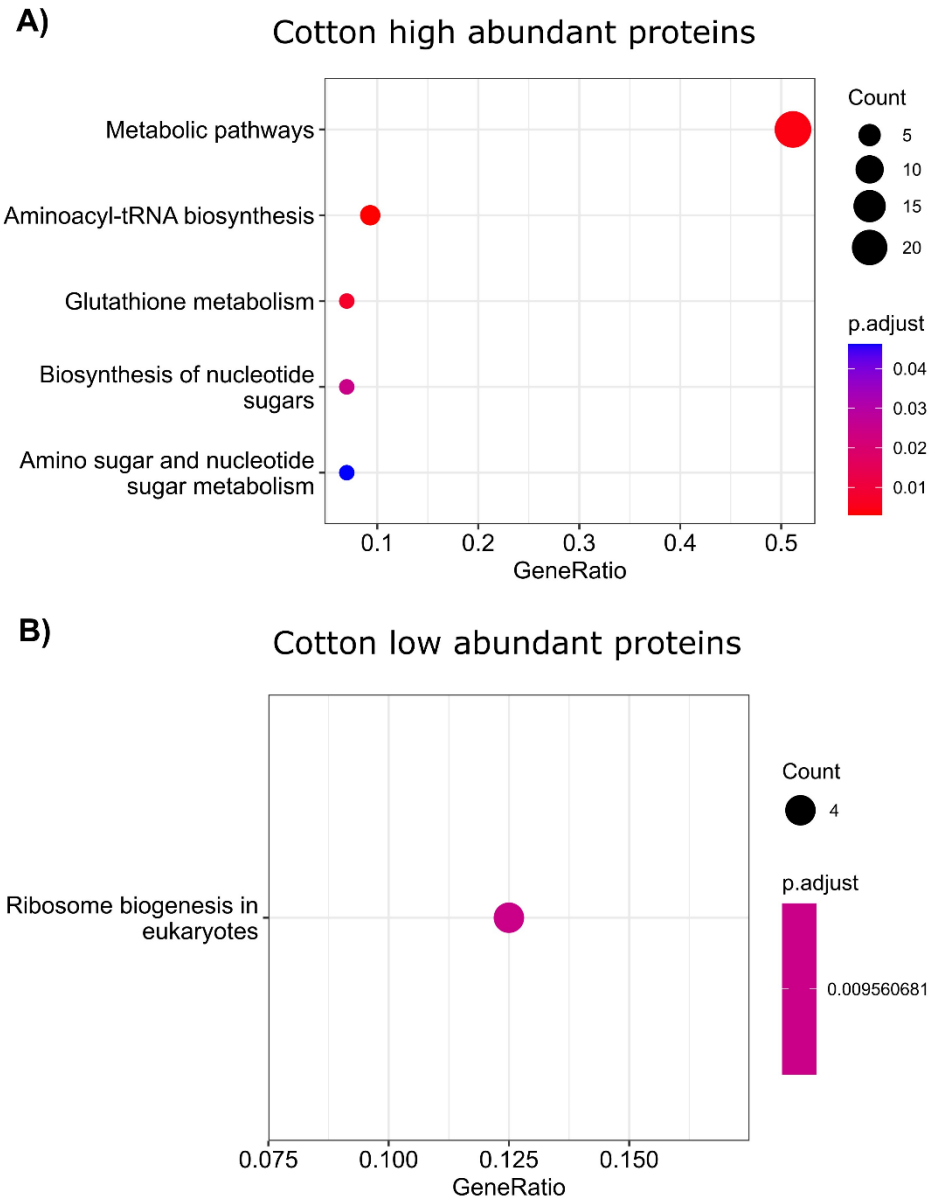

Fig. 26. The significant enriched KEGG pathways of the A) high-abundance and B) low-abundance proteins between the spinetoram-resistant and susceptible strains of *Spodoptera frugiperda* when feeding on cotton plants.

The 17 proteins that were common in the comparison of resistant and susceptible strain in the three host plants were enriched in pathways of microbial metabolism in diverse environments (ko01120), pentose phosphate pathway (ko00030), fructose and mannose metabolism (ko000510), methane metabolism (ko00680) and carbon fixation in photosynthetic organisms (ko00710) (Fig. 27).

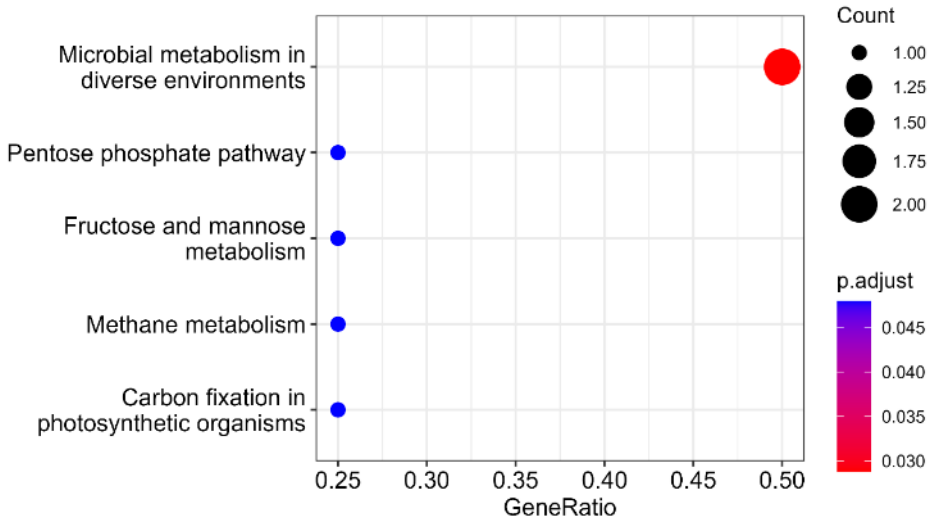

Fig. 27. The significant enriched KEGG pathways of proteins were common in the comparison of the spinetoram-resistant and susceptible strains of *Spodoptera frugiperda* in the three host plants.

4.3.4. Protein-protein interaction

The STRING database was used to predict the protein-protein interaction of the exclusive differential abundant proteins between the resistant and susceptible strains of *S. frugiperda* on corn, soybean, and cotton plants. Analyzing the interactions of 178 proteins that were exclusively found on corn plants, there were 30 proteins that presented some interaction among them with 23 edges (Fig. 28A). For the proteins found when the *S. frugiperda* strains fed on soybean plants, 76 of 254 proteins presented some interaction with 80 edges (Fig. 28B). 57 of 225 proteins that were found exclusively in cotton plants presented some interaction with 87 edges (Fig. 28C). There was no protein-protein interaction among the 17 differently abundant proteins between that were common in the three host plants.

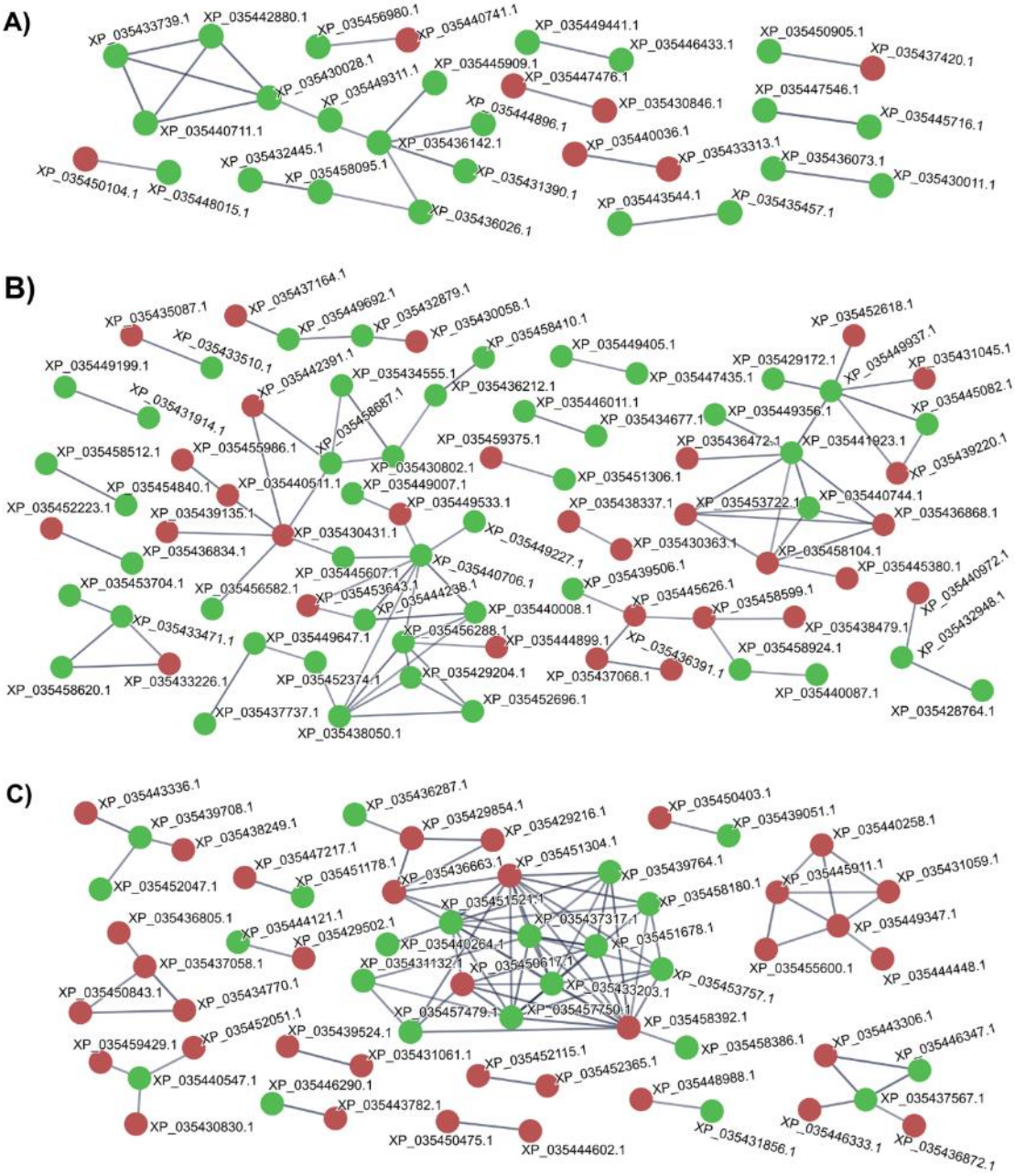

Fig. 28. Protein-protein interaction (PPI) network analysis of the exclusively proteins that were differentially abundant between the spinetoram-resistant and susceptible strains of *Spodoptera frugiperda* when feeding on A) corn, B) soybean and C) cotton plants. Red circles represent the high-abundance proteins and the green circles represents the low-abundance proteins.

Gene ontology enrichment analysis was also performed for the proteins that presented some interaction among them. The 10 most significant terms for biological process are shown in Fig. 29. The proteins of *S. frugiperda* that presented some interaction when the strains fed on plants of corn, soybean and cotton were almost enriched in the same biological process terms. Many of them are related to regulation of gene expression and epigenetic

process which includes the GO: 0016570 – Histone modification, GO: 0016569 – Covalent chromatin modification, GO: 0043414 – Macromolecule methylation, GO: 0010467 – Gene expression, GO: 0034660 – ncRNA metabolic process and GO: 0010628 – Positive regulation of gene expression.

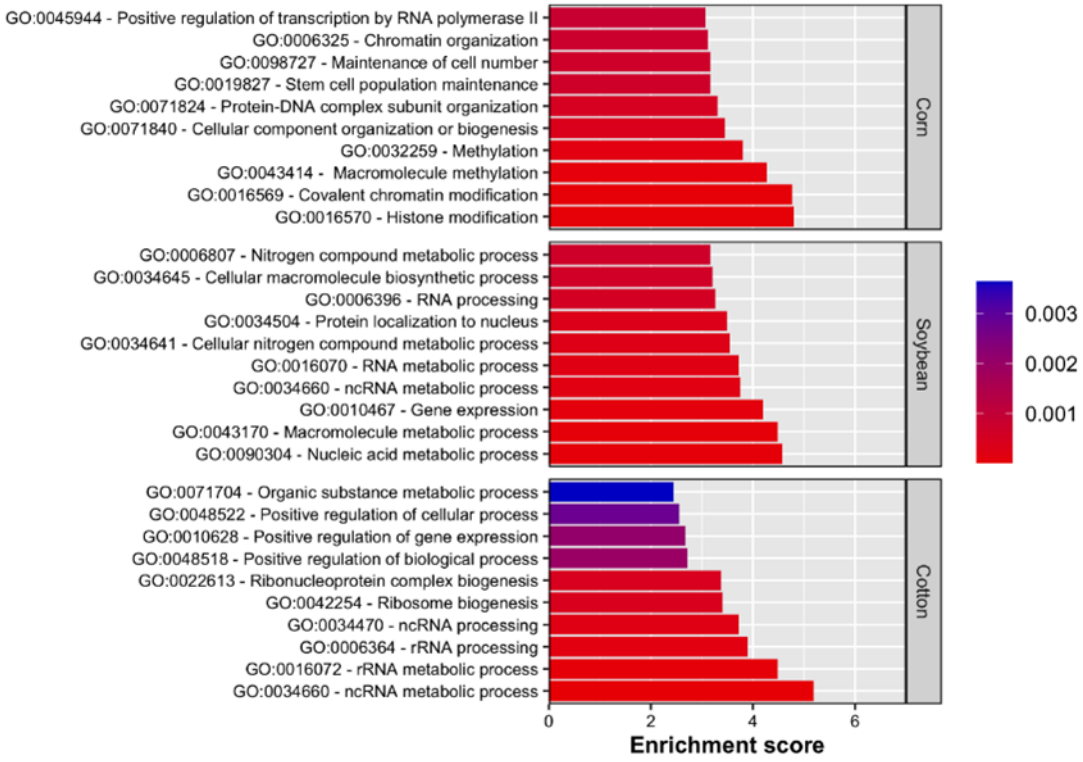

Fig. 29. Gene ontology enrichment analysis of the differentially abundant proteins that presented some interaction among them when the spinetoram-resistant and susceptible strains of *Spodoptera frugiperda* fed on plants of corn, soybean, and cotton.

4.4. Discussion

In this study, we conducted a comparative proteomic analysis to identify the changes at protein level between spinetoram-resistant and susceptible strains of *S. frugiperda* in plants of corn, soybean, and cotton. Host plant adaptation can led to different physiological changes in insects (Vogel et al., 2014). Being a polyphagous pest, *S. frugiperda* can fed on a large range of host plants (Montezano et al., 2018) and consequently leading to different molecular and physiological responses. Proteomics is a relevant approach to investigate and elucidate the molecular mechanisms of biological processes. Furthermore, the identification of molecular mechanisms using omics approaches can provide new insights into the metabolic

pathways driving the adaptation process of insect pests to host plants or xenobiotics such as chemical insecticides (Barah and Bones, 2015; Pittendrigh et al., 2014).

Our results showed that there was a significant number of proteins that were exclusively affected by the host plant compared to the number of proteins exclusively affected by strain or by the interaction of host plant and strain. This is consistent with previous studies showing that the host plant is a significant factor in shaping the protein abundance patterns in insect pests. Many studies have used differential expression analysis to identify the genes and proteins involved in adaptation of *S. frugiperda* on different host plant species. A transcriptome analysis study found differential expression of genes related to herbivory mechanisms, such as peptidases, when *S. frugiperda* was reared on corn, cotton and rice (Murad et al., 2021). In another study, Acevedo et al. (2017) found that fifteen salivary proteins of *S. frugiperda* changed when the larvae fed on plants of maize, Bermuda grass and tomato. This suggests that the environmental factors, such as the host plant on which the insect feeds, are an important driver of differences in protein abundance of *S. frugiperda*.

Another interesting aspect of the results is the identification of 660 proteins that were simultaneously affected by both host plants and strain, as well as their interaction. It appears that certain biological processes are essential for *S. frugiperda* survival and development, which is influenced by both genetic (resistant or susceptible genotype) and environmental factors (host plant). The analysis using volcano plot and Venn diagram demonstrated that the proteome profile of *S. frugiperda* strains changed according to the host plant that the insects fed on. Furthermore, almost all differentially abundant proteins between resistant and susceptible strains were found to be specific to each host plant.

The identification of enriched GO terms and KEGG pathways provided insights into the specific biological processes and metabolic pathways that are associated with the differential protein abundance between resistant and susceptible strains in each host plant. Based on our results, the resistant strain in corn plants appears to have a higher capability of small molecule degradation and energy production. Moreover, the enrichment of the high-abundance proteins in apoptotic signaling pathway might suggest that that programmed cell death may be involved in the response to stress. The response to plant defense mechanisms for example that can lead to the production of reactive oxygen species (ROS) within cells and these ROS can cause cellular damage and trigger apoptosis (Redza-Dutordoir and Averill-Bates, 2016). Programmed cell death and ROS accumulation were also associated with spinosad treatment in *S. frugiperda* cells (Yang et al., 2017b, 2017a). On the other hand, the low-abundance proteins indicate that corn plants may be limiting the growth and development

of the resistant strain by suppressing biological processes related to gene expression and development, although no apparent fitness cost was observed when the resistant strain was reared on corn plants (Kanno et al., 2023).

When the resistant strain feeds on soybeans plants, we observed that the high-abundance proteins were enriched in GO terms associated with transcription and chromatin organization. These processes are closely correlated with each other, once transcription by RNA polymerase II is regulated by different processes including changes in chromatin structure (Linzer et al., 2021) and possibly regulating the expression of other proteins. The observed low-abundance of proteins involved in cellular and metabolic processes, as well as response to stimulus, implies that the resistant strain have a limited capacity to cope with the secondary compounds of soybean plants. The soybean-induced defenses such as phenolic compounds impaired the development of *S. frugiperda* (Peruca et al., 2018). Additionally, the low-abundance proteins of the resistant strain also show enrichment in pathways related to energy metabolism, cellular homeostasis, and lifespan regulation. The decrease in the abundance of these proteins could potentially be associated with reduced fitness of the resistant individuals in soybean plants compared to the susceptible individuals (Kanno et al., 2023).

A reduced fitness of spinetoram-resistant strain were also observed when reared in cotton plants (Kanno et al., 2023). This could be related to the high-abundance proteins of the resistant strain were associated with metabolism of small molecules and response to xenobiotics, as identified in the enrichment analysis. The production of detoxification enzymes to overcome xenobiotics is a high energy demand processes in insects, which can result in a reduced fitness (Kliot and Ghanim, 2012). Furthermore, the upregulation of detoxification enzymes can also affect the resistance management of *S. frugiperda* to spinetoram, particularly in the use of insecticides with different mode of action in a rotation scheme. Since most of these enzymes can metabolize both plant secondary compounds and insecticides (Li et al., 2007), it can reduce the susceptibility of the resistant strain to other insecticides. Consequently, this could limit the effectiveness of insecticides used to control the spinetoram-resistant individuals in the field. The low-abundance proteins of the resistant strain were enriched in GO terms of biological regulation and development process involved in reproduction, which can also be associated with a lower net reproductive rate observed when this strain was reared in cotton plants.

Immune response processes were also an enriched GO and KEGG terms among the high-abundance proteins when the resistant strain fed on cotton and soybean plants. Toll and

IMD signaling pathways plays an important role in mediating the innate immune responses (Myllymäki et al., 2014; Tanji and Ip, 2005). Several studies have demonstrated that the immune responses in insects can be affected by the host plant species they feed on (Lampert, 2012; Vogelweith et al., 2011). This has an implication for example in the use of entomopathogenic agents to control the resistant individuals of *S. frugiperda* in soybean and cotton fields, since insect uses the innate immune defenses against the invading pathogens (Lu and St. Leger, 2016; Qu and Wang, 2018). Furthermore, differences in the susceptibility to a nuclear polyhedrosis virus was found when *S. frugiperda* larvae fed on different host plants (Richter et al., 1987).

Part of the differentially abundant proteins of *S. frugiperda* strains found in the plants of corn, soybean and cotton presented some interaction among them. Interestingly, almost all proteins that presented some interactions were enriched in the same biological process terms related to regulation of gene expression and epigenetic processes. Many of the proteins were enriched in terms associated with histone modification, chromatin organization, DNA methylation and non-coding RNA metabolic process, which are all considered epigenetic mechanisms (Skinner, 2014). These modifications can regulate the gene expression and led to phenotypic plasticity in insects. Differences in the insect response to insecticides can be affected by the host plant and could be mediated by these epigenetic modifications. The response of *S. frugiperda* larvae to spinetoram and other insecticides on plants of corn, soybean and cotton should be conducted in future studies, especially considering the potential influence of the epigenetic mechanisms when *S. frugiperda* larvae feed on different host plants.

The few proteins that were differential abudant between the resistant and susceptible strain regardless the host plant was related to energy production and cellular metabolism. It has been reported that insecticide resistance may affect energy production pathways in many insects. Acetyl CoA synthase and fatty acid synthase were overexpressed in pyrethroid resistant strain of A*nopheles gambiae* (Vontas et al., 2005). In study with insecticide resistant populations of *Sitophilus zeamais* showed an enhanced activity of carbohydrate and lipid metabolizing enzymes (Araújo et al., 2008). Sagri et al. (2014) suggested that the increased expression of energy metabolism genes observed in a spinosad-resistany strain of *Bractocera oleae* is to compensate for the costs of energy-consuming detoxification process. It is consistent with the fact that insecticide resistance usually carry fitness costs, demanding high resource and energy reallocation for the adaptation process of insecticide resistance (Kliot and

Ghanim, 2012), as observed for spinosyn resistance in *S. frugiperda* (Kanno et al., 2023; Okuma et al., 2018).

However, we expected to find some detoxification enzymes among the proteins that were differential abundant between the resistant and susceptible strain regardless the host plant, since these enzymes are one of the main mechanisms of insecticide resistance (ffrench-Constant et al., 2004; Li et al., 2007; Nauen et al., 2022). These results reinforce that the major mechanism for spinetoram resistance in *S. frugiperda* is a target site insensitivity. A modification in the nAChR α6 gene were found in this resistant strain through whole genome sequencing analysis and probably there is a minor role of detoxification enzymes in spinetoram resistance in *S. frugiperda.*

In summary, we showed that the proteomic profile of spinetoram-resistant and susceptible strains of *S. frugiperda* varied according to the host plant that larvae fed on. Different biological processes were identified between the differentially abundant proteins of resistant and susceptible strain in each host plant. Besides, proteins involved in the regulation of other proteins through epigenetic mechanisms could be associated with host plant adaptation in *S. frugiperda*. The proteins that were differentially abundant between the resistant and susceptible strain in all host plants are related to energy and cellular metabolism. The findings of this study highlight the importance of considering the role of the environment in insecticide resistance and thus to achieve an efficient management of this pest in different agricultural landscapes.

4.5. Conclusions

- A total of 3267 proteins were identified in the molecular and physiological responses of spinetoram-resistant and susceptible strain of *S. frugiperda* feeding on corn, soybean, and cotton plants;
- Most of differentially abundant proteins between the spinetoram-resistant and susceptible strains of *S. frugiperda* were specific to each host plant;
- The proteins that were differentially abundant between the spinetoram-resistant and susceptible strains of *S. frugiperda* regardless of the host plant were related to energy production and cellular metabolism.

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5. COMPARATIVE METABOLOMIC ANALYSIS OF SPINETORAM RESISTANT AND SUSCEPTIBLE STRAINS OF *Spodoptera frugiperda* (LEPIDOPTERA: NOCTUIDAE)

Abstract
Spinetoram resistance in *Spodoptera frugiperda* (J. E. Smith) has been characterized at genomic, transcriptomic, and proteomic levels. However, the impact of spinetoram resistance on metabolite profile of *S. frugiperda* is not clear. To address this knowledge gap, GC-MS metabolomic analysis were employed to investigate the metabolome profile of spinetoram-resistant and susceptible strains of *S. frugiperda*. A total of 86 metabolites were detected, of which 20 metabolites were differentially abundant between the spinetoram-resistant and susceptible strains. These differential metabolites were mainly amino acids, carbohydrates, dicarboxylic acids, and fatty acids. The enriched pathways of the differential metabolites were cysteine and methionine metabolism, linoleic acid metabolism and aminoacyl-tRNA biosynthesis. Our findings suggest that the identified metabolic pathways may be affected by spinetoram resistance in *S. frugiperda*, thereby providing a new perspective on potential metabolic pathways associated with insecticide resistance.

Keywords: fall armyworm, GC-MS; spinosyns; insecticide resistance

5.1. Introduction

Insecticide resistance is an ongoing challenge of increasing concern that threatens sustainable pest management programs. Currently, more than 600 species of arthropod pests have evolved resistance to at least one insecticide compound (Nauen et al., 2019). The rapid increase in the number of insecticide resistance cases impairs the effectiveness of these control methods, highlighting the need of resistance management strategies. In this context, understanding the molecular basis and how insect pests evolve resistance is critical for developing resistance management strategies to mitigate the threat of insecticide resistance.

Research using omics approaches has prompted a significant progress in several areas due to its cost-efficient and high-throughput analysis of biological molecules on a wide-scale level (Dai and Shen, 2022). The advancements in next generation DNA and RNA sequencing for genomic and transcriptome studies, as well as mass spectrometry-based proteomics and metabolomics, have opened new possibilities for a deeper analysis of complex biological systems (Misra et al., 2019). This has made it possible to address questions regarding the adaptation process of insect pests to insecticides at molecular level, especially in uncovering the main mechanisms underlying insecticide resistance (Pittendrigh et al., 2014).

Metabolites are small molecules that represent the final downstream products of metabolism (Fiehn, 2002). These small molecules include compounds such as lipids, sugars

and amino acids that can be used to find correlations and causal relationships of a determined phenotype (Jorge et al., 2016; Wang and Lei, 2018). Metabolomics is the large-scale study of metabolites in a given cell, tissue or organism, offering insights into the changes in biological processes at the metabolite level under the influence of intrinsic and extrinsic factors (Idle and Gonzalez, 2007; Tsoukalas et al., 2022). Thus, metabolomics approaches can provide a comprehensive overview of the metabolic changes associated to environmental stressors such as xenobiotics (Johnson et al., 2012; Lankadurai et al., 2013), and it can also be used to identify the metabolic pathways associated with insecticide resistance.

The fall armyworm, *Spodoptera frugiperda* (J. E. Smith) (Noctuidae), is a highly destructive pest of corn and many other economically cultivated crops (Montezano et al., 2018). The intensive use of synthetic insecticides against this pest has led to the evolution of resistance to many of the compounds used for its control (Bolzan et al., 2019; Carvalho et al., 2013; Diez-Rodríguez and Omoto, 2001; Garlet et al., 2021; Muraro et al., 2021; Nascimento et al., 2022, 2016). This includes the spinosyn insecticides, one of the main chemical groups of insecticides used to control *S. frugiperda* (Burtet et al., 2017), for which resistance cases have already been documented (Lira et al., 2020; Okuma et al., 2018). Spinosyn resistance in *S. frugiperda* has been characterized at genomic, transcriptomic, and proteomic level, and the resistance is associated with a modification in the subunit α6 of the nicotinic acetylcholine receptor gene (Chapter 2). Although these studies have enhanced our knowledge about the molecular basis of spinosyn resistance in *S. frugiperda*, insects can respond to xenobiotics in a multifaceted ways, which can include different biochemical and physiological pathways (ffrench-Constant et al., 2004; Hawkins et al., 2019). In this way, metabolomics analysis will complement the data derived from other omics approaches, providing a systematic approach to studying the molecular basis of spinetoram resistance in *S. frugiperda*. To address this knowledge gap, in this study, GC-MS metabolomic analysis were employed to investigate the metabolome profile of spinetoram-resistant and susceptible strains of *S. frugiperda*.

5.2. Material and Methods

5.2.1. Insect strains

The spinetoram resistant (RR) and susceptible (SS) strain of *S. frugiperda* were used in this study. These two strains were obtained from a field population collected in São Desidério, Bahia State, Brazil, in 2018 (Kanno et al., 2023). Both strains were reared in

artificial diet (Kasten Jr et al., 1978) under laboratory conditions of 25 ± 2 °C, 70% relative humidity and 14:10 h (L:D) photoperiod.

The RR and SS strains were reared in non-Bt plants of corn (3700 RR2). All plants were cultivated in 12-liter pots in a greenhouse. Leaves of corn were collected and placed into a gelled mixture of 2.5% agar-water in 16-well plastic trays (Advento do Brasil). Neonate larvae (<24h old) from RR and SS strains were infested in each well and reared until the fourth instar. Newly and fresh leaves were replaced every day. Six pools of five fourth-instar larvae from each strain were collected. The larvae were frozen in liquid nitrogen and then stored at -80ºC for the metabolite extraction.

5.2.2. Metabolite extraction and derivatization

Approximately 25 mg of tissue samples were crushed using a TissueLyser (Qiagen, Hilden, Germany). Then, 212.5 µl of the extraction solution containing chloroform, methanol and water (1:3:1) was added in each sample and sonicated (40 Hz x 15 min) in an ice bath. 62.5 µl of chloroform and 50 µl of water was added to each sample and centrifuged at 16,000 g for 5 minutes at 4ºC. The supernatant (100 µl) was transferred to amber glass vials. The samples were freeze-dried under vacuum. The derivatization of the samples was performed by adding a solution composed of 40 µL of pyridine containing methoxyamine hydrochloride (20 mg/mL). Then, 50 µl of MSTFA (N-methyl-N(trimethylsilyl)trifluoroacetamide) with 1% TMCS (trimethylchlorosilane) was added and kept for 1h at room temperature. The samples were analyzed on Pegasus 4D time-of-flight mass spectrometer (GC-MS) (LECO).

5.2.3. Data processing and analysis

The chromatograms generated by the GC-MS were analyzed using the ChromaTOF software (LECO), in which baseline correction, peak detection, retention time alignment and identification of metabolites were performed using the NIST library. A minimum similarity of 700 was used for the metabolite identification. Metabolites intensities were normalized by TIC (total ion chromatogram).

The following statistical analysis were performed using Metaboanalyst 5.0 (Pang et al., 2022). The data were log-transformed and pareto-scaled. Principal component analysis (PCA) was performed to show the similarity between the samples. Volcano plot was used to

identify the differences in the abundance of the metabolites in resistant and susceptible samples. This analysis combines fold change (FC ≥ |2.0|) and *t-test* analysis ($p < 0.05$) to determine the significant differences between the two samples. A supervised (orthogonal) partial least squares discriminate analysis (OPLS-DA) was performed to identify the most important metabolites in the differentiation of spinetoram-resistant and susceptible strains. The metabolites were ranked by variable importance in the projection (VIP) in the first principal component of the OPLS-DA model. VIP > 1 was considered statistically significant.

The identified metabolites were submitted to Kyoto Encyclopedia of Genes and Genomes (KEGG) database to obtain the KEGG compound ID. Only metabolites that were identified in the KEGG database were used for pathway analysis. The KEGG mapper tool was used to identify the pathways in which the metabolites were involved, using *S. litura* as the organism in the search mode. The metabolite set enrichment analysis (MSEA) of the differential metabolites was performed using Metaboanalyst 5.0 (Pang et al., 2022).

5.3. Results

5.3.1. Metabolite profile of spinetoram-resistant and susceptible strains of *Spodoptera frugiperda*

Using GC-MS analysis a total of 86 metabolites were detected in the spinetoram-resistant and susceptible strains of *S. frugiperda* (Appendix H). Different class of metabolites were identified. Most of the identified metabolites belongs to the following classes: amino acids, peptides, and analogues (29 metabolites), carbohydrates and carbohydrate conjugates (12 metabolites), fatty acids and conjugates (6 metabolites) and dicarboxylic acids and derivatives (4 metabolites). Metabolites from others classes such as alcohols and polyols, amines, benzenoids and nucleosides were also detected.

Hierarchical clustering analysis of spinetoram-resistant and susceptible samples showed three main clusters and the samples almost clustered according to the strain with exception of four samples (Fig. 30A). A principal component analysis (PCA) showed some separation between the metabolites of the spinetoram-resistant and susceptible samples, with 61.1% of the variation explained by the two first principal components (PC1 and PC2) (Fig. 30B).

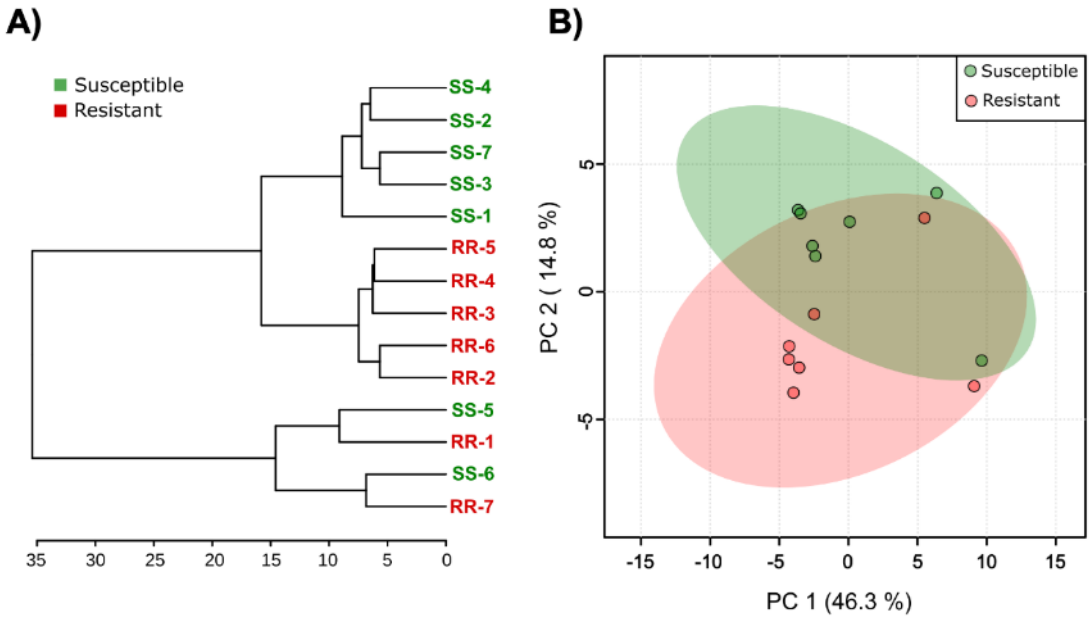

Fig. 30. A) Hierarchical cluster analysis; B) Principal Component Analysis (PCA) of spinetoram-resistant and susceptible strains of *Spodoptera frugiperda*

5.3.2. Pathways of the identified metabolites

The pathways in which the metabolites are involved were obtained from KEGG pathway database. 69 metabolites were identified in the database, of which, participate in 65 different pathways. The most representative pathways include metabolic pathways (58 metabolites), biosynthesis of amino acids (20 metabolites), ABC transporters (18 metabolites), D-Amino acid metabolism (15 metabolites) and aminoacyl-tRNA biosynthesis (14 metabolites) (Fig. 31).

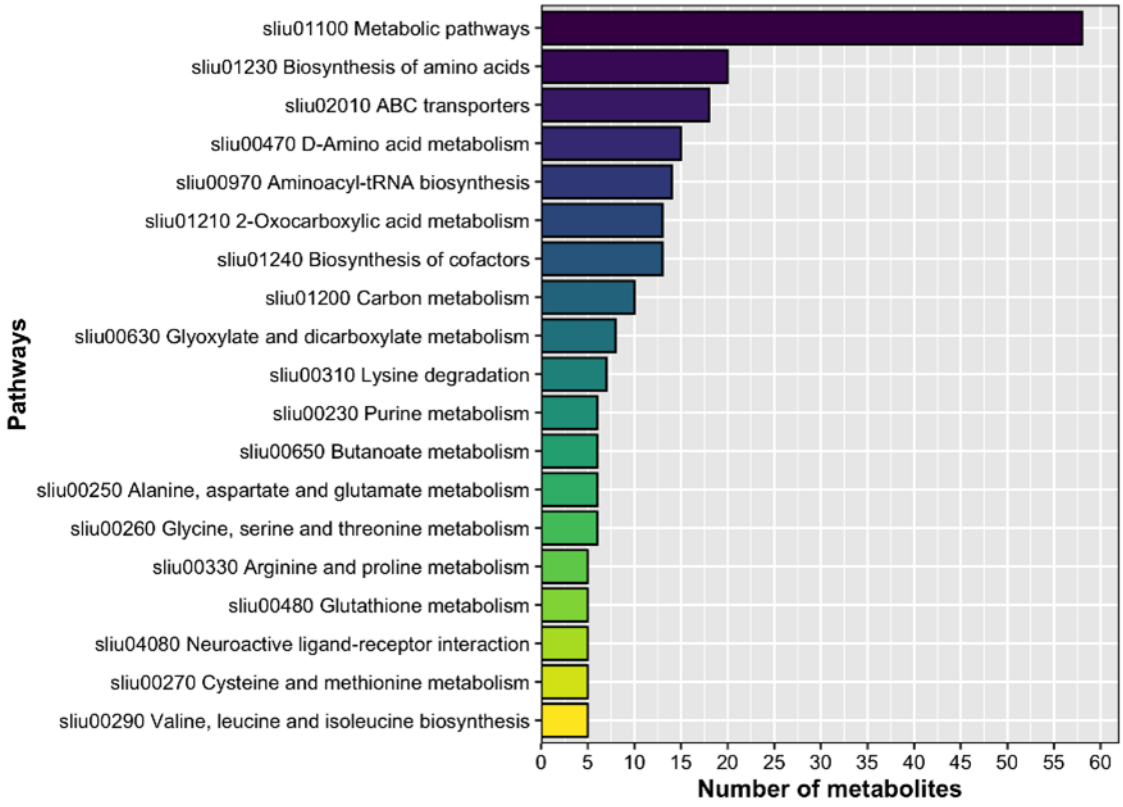

Fig. 31. Main metabolic pathways identified in the KEGG database of metabolites (metabolites number ≥ 5) from spinetoram-resistant and susceptible strains of *Spodoptera frugiperda*.

5.3.3. Differential analysis of metabolites

Differential analysis were performed to further assess the metabolic differences between resistant and susceptible samples. There were 20 metabolites with differential abundances between the resistant and susceptible strain. Among these metabolites, 11 metabolites were more abundant in the resistant strain and 9 metabolites were more abundant in the susceptible strain (Fig. 32).

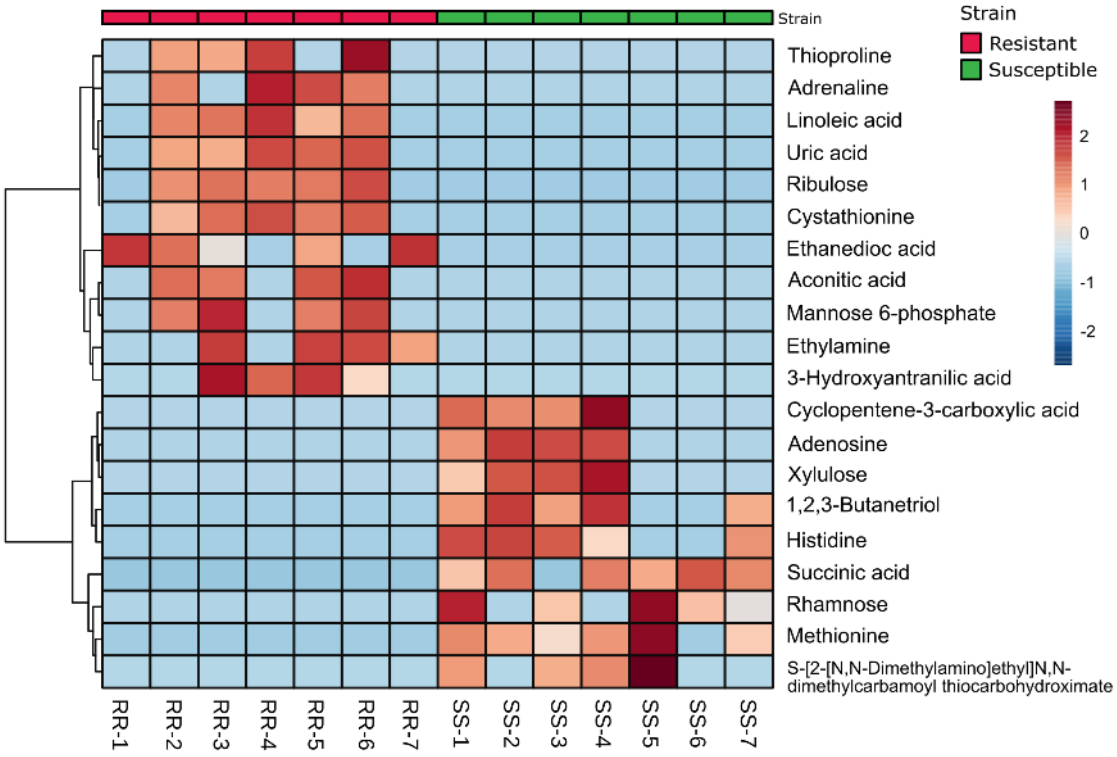

Fig. 32. Heatmap representing metabolites with differential abundance between spinetoram-resistant and susceptible strains of *Spodoptera frugiperda*.

The classes of the differential metabolites included amino acids, peptides, and analogues (histidine, cystathionine, thioproline and methionine), carbohydrates and carbohydrate conjugates (xylulose, rhamnose, mannose-6-phosphate and ribulose) and dicarboxylic and tricarboxylic acids and derivatives (succinic acid, ethane dioic acid and aconitic acid).

A supervised multivariate analysis (OPLS-DA) maximized the difference between the resistant and susceptible strain and a clear separation was observed in the score plot (Fig. 33A). The metabolites were ranked based on the VIP scores from the OPLS-DA model. A total of 26 metabolites presented a VIP score > 1, of which the top 20 metabolites are the same metabolites identified by fold change (FC ≥ |2.0|) and t-test ($p < 0.05$) analysis (Fig. 33B). The metabolites with highest VIP score include succinic acid, methionine, ribulose, cystathionine, and uric acid.

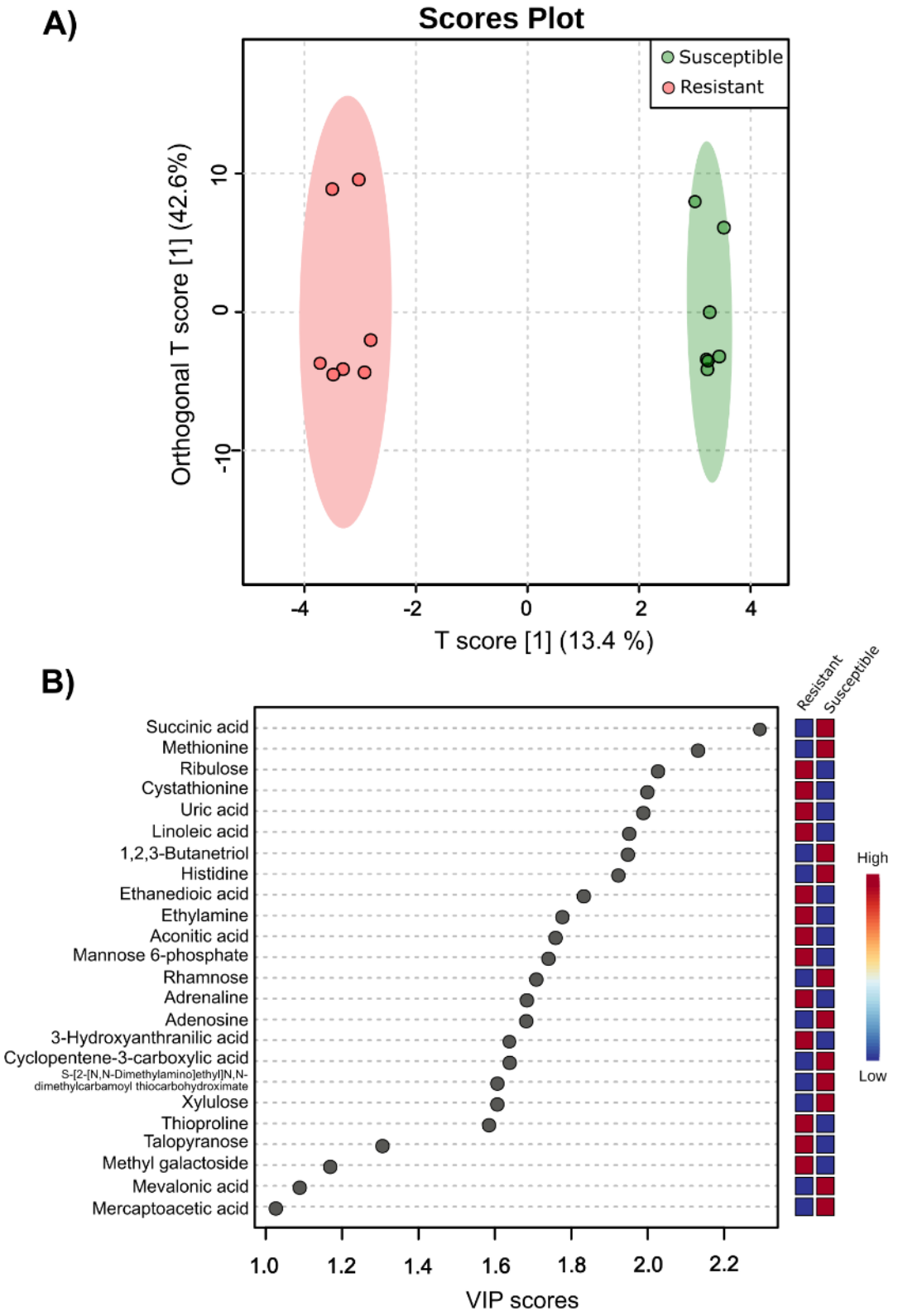

Fig. 33. A) Supervised multivariate analysis (OPLS-DA) and B) classification of metabolites of the spinetoram-resistant and susceptible strains of *Spodoptera frugiperda* according to the variable importance in projection (VIP) scores of the OPLS-DA model.

The results of the metabolite set enrichment analysis showed that the differential metabolites were enriched in 17 pathways. Among them, 3 pathways showed significant enrichment, which were cysteine and methionine metabolism, linoleic acid metabolism and aminoacyl-tRNA biosynthesis (Fig. 34).

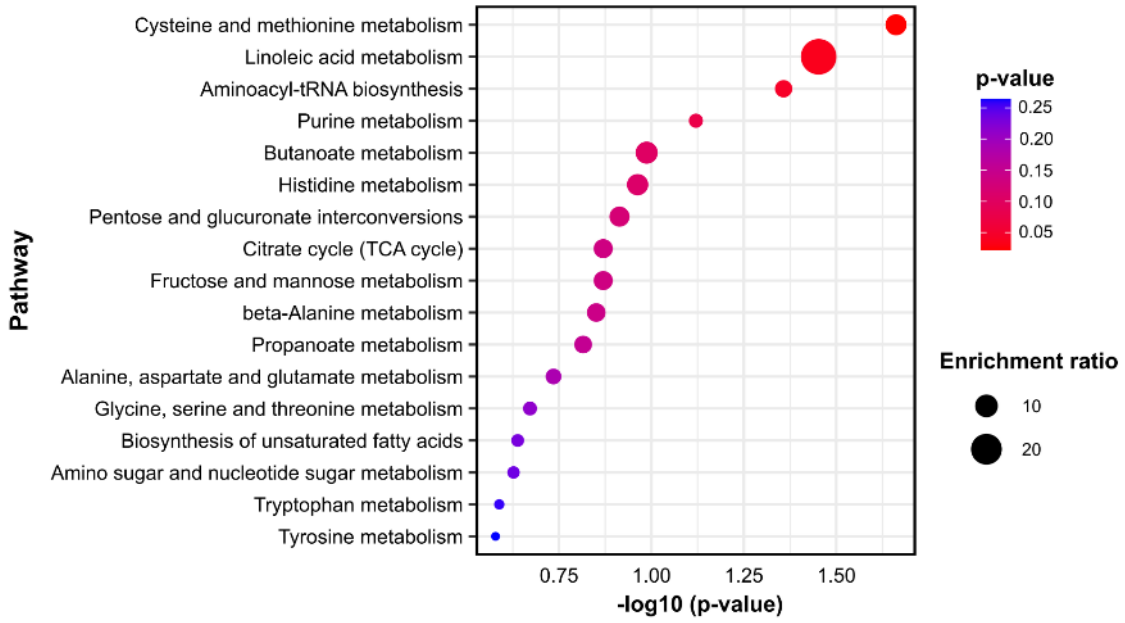

Fig. 34. Metabolite set enrichment analysis showing the enriched pathways of the differential metabolites of spinetoram-resistant and susceptible strains of *Spodoptera frugiperda*.

5.4. Discussion

Metabolomics approaches have significantly contributed to increasing our understanding of biological systems (Harrison, 2016). In this study, we investigated the metabolome profile of spinetoram-resistant and susceptible strain of *S. frugiperda* through GC-MS metabolomics analysis. Most of the metabolites identified in the spinetoram-resistant and susceptible samples are involved in the major biological pathways such as amino acid metabolism, carbohydrate metabolism, lipid metabolism and tri-carboxylic acid cycle. There were differences in the abundance of some metabolites between the spinetoram-resistant and susceptible strains, indicating that there are specific pathways affected by spinetoram resistance in *S. frugiperda*.

Differences in the abundance of metabolites from amino acids class were observed between the strains. For example, methionine and histidine, two amino acids used in the protein biosynthesis, were down-regulated in the resistant strain indicating protein

biosynthesis might be affected by spinetoram resistance. Furthermore, methionine is linked to reproduction and longevity, and studies conducted with *Drosophila melanogaster* have demonstrated that restriction of methionine has a significant impact on the lifespan and fecundity (Grandison et al., 2009; Lee et al., 2014; Troen et al., 2007). On the other hand, cystathione and thioproline were up-regulated metabolites in the resistant strain. Cystathione is an intermediate in the transsulfuration pathway of methionine and cysteine metabolism, converting homocysteine to cysteine (Banerjee et al., 2003). This is an important pathway because cysteine is a precursor of glutathione, which is an antioxidant to minimize the effects of oxidative stress (Kerksick and Willoughby, 2005). In a similar way, thioproline is also an antioxidant that protects cells from oxidation-induced damage (Ham et al., 2020). Oxidative stress can be caused in response to chemical stress such as insecticides and may be involved with insecticide resistance (Oliver and Brooke, 2016; Vontas et al., 2001). Some studies demonstrated that oxidative stress can trigger signaling pathways such as CncC and regulate xenobiotic detoxification genes (Amezian et al., 2021; Chen et al., 2018; Lu et al., 2020, 2019). Further studies are required to provide a more direct involvement of oxidative stress in spinetoram resistance in *S. frugiperda*.

Aminoacyl-tRNA biosynthesis is another pathway that were significantly enriched among the differential metabolites. This pathway is associated with amino acid metabolism since the identity of an amino acid inserted at a particular position during the protein synthesis is determined by aminoacyl-tRNA (Ibba and Söll, 2000). Imbalance in this pathway indicate a different utilization of amino acids between the spinetoram-resistant and susceptible strains. An altered amino acid metabolism was also reported for deltamethrin resistance in *Anopheles sinensis* (Li et al., 2022) and *Aedes albopictus* (Huang et al., 2021), demonstrating that amino acid metabolism is one of the pathways affected by insecticide resistance.

Enrichment analysis also showed the linoleic acid metabolism as a significant pathway of the differential metabolites. Linoleic acid serves an important constituent of phospholipids which is the main component of the cell membrane (Brownlee et al., 2016; Whelan and Fritsche, 2013). It confers the structure, fluidity and flexibility to the membrane (Green et al., 1980; Rawicz et al., 2000), and can also modulate the membrane protein function (Vásquez et al., 2014). Structural and functional changes in nAChR could be induced by lipids of the phospholipid membrane (Barrantes, 2004; Fabiani et al., 2022; Fernández-Carvajal et al., 2006; Sunshine and McNamee, 1994). Our results showed an up-regulation of linoleic acid in the spinetoram-resistant strain, and it could be preserving the nAChR α6 function, even with the presence of the deletion of tyrosine amino acid reported in RR strain.

In summary, this study identified different compounds and metabolic pathways affected by spinetoram resistance in *S. frugiperda*. The differential metabolites were mainly amino acids, carbohydrates, dicarboxylic acids, and fatty acids. Among the enriched pathways, cysteine and methionine metabolism, linoleic acid metabolism and aminoacyl-tRNA biosynthesis were significantly affected. Although target-site insensitivity has been considered the main mechanism for spinosyn resistance, this study indicated that the identified metabolic pathways might be involved in the physiological process such as synthesis, energy demand and maintenance of the target-site insensitivity mechanism as well as other functional mechanisms associated with spinetoram resistance as identified by transcriptomic and proteomic analysis. Furthermore, the finding of this study enhanced our understanding of the metabolic pathways affected by insecticide resistance, providing information to support the implementation of resistance management strategies and the development of novel insecticides for *S. frugiperda* control.

5.5. Conclusions

- A total of 86 metabolites were identified in the metabolome profile of spinetoram-resistant and susceptible strains of *S. frugiperda*;
- Eleven metabolites were more abundant in the spinetoram-resistant strain and nine metabolites were more abundant in the susceptible strain;
- The differentially abundant metabolites between spinetoram-resistant and susceptible strains of *S. frugiperda* were mainly amino acids, carbohydrates, dicarboxylic acids and fatty acids.

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6. FINAL CONSIDERATIONS

The combined genomic and transcriptomic approaches were effective in identifying the molecular mechanisms associated with spinetoram resistance in *S. frugiperda*. The results from DNA and RNA sequencing indicate that resistance of *S. frugiperda* to spinetoram is mainly characterized as insensitive target site-based resistance, although up-regulation of some genes related to metabolic resistance was detected in the transcriptome analysis. The deletion in the nAChR α6 gene is pottentially one of the main resistance mechanisms of spinetoram resistance in *S. frugiperda,* and we provide evidence of the causal role of this deletion by demonstrating that it cosegregates with spinetoram resistance in survival bioassays. Furthermore, this deletion can be used to develop molecular diagnostic tools to detect and monitor the frequency of this resistant allele in field populations for resistance monitoring studies.

Based on the fitness costs studies, our results demonstrated that magnitude of the fitness costs associated with spinetoram resistance in *S. frugiperda* may depend on the host plant. The lack of fitness costs associated with spinetoram resistance in corn plants suggests that removing the selection pressure of this insecticide from the environment will not reduce the frequency of spinetoram resistance alleles in *S. frugiperda* populations that feeding on corn. As a result, regions with two corn crop seasons will typically present higher frequencies of spinetoram resistance. On the other hand, in regions where soybean and cotton are prevalent, the frequency of resistant individuals tends to be lower due to the presence of significant fitness costs of spinetoram-resistant strain in these two host plants.

Proteomics approaches then allowed us to identify the possible biological processes associated with corn, soybean, and cotton adaptation and spinetoram resistance in *S. frugiperda*, revealing that most of the identified proteins were specific to each host plant. This highlights the importance to considering the host plant in which the *S. frugiperda* larvae are feeding on to design effective resistance management strategies, mainly because the different proteins expressed in each host plant can be one of the main determinants of the fitness and alter the insects response to a given resistance management strategy. The distinct protein profiles found in spinetoram-resistant and susceptible strains present a unique opportunity to improve control strategies for managing *S. frugiperda* in the field. Variation in the abundance of proteins associated with important biological processes, including immune response mechanisms, have been identified in spinetoram-resistant and susceptible strains in plants of corn, soybean and cotton. This difference can be harnessed, for example, to employ

entomopathogenic agents to effectively manage spinetoram-resistant indivuals of *S. frugiperda* in the field. The results of fitness costs and proteomics studies highlight the importance of considering the role of the environment in insecticide resistance to achive efficient management of insect pests in different agricultural landscapes.

While our results have shown that spinetoram resistance in *S. frugiperda* is associated with target site insensitivity, we cannot neglect the existence of other important metabolic pathways, as shown by the transcriptomics, proteomics, and metabolomics studies. In the last chapter, we found that different metabolic pathways are affected by spinetoram resistance, suggesting their potential influence on the spinetoram-resistant phenotype in *S. frugiperda*.

Overall, insecticide resistance, like any other adaptation process needs to be viewed in a holistic way, combining different approaches and integrating data from multiple sources. Using multi-omics approaches allowed us to investigate on large-scale the molecular mechanisms of spinetoram resistance in *S. frugiperda*, providing novel biological insights and expanding the existing knowledge about the mechanisms driving the evolution of insecticide resistance.

APPENDIX

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains.

Gene ID	log2FC	Description
LOC118266460	-5.74	(2R)-3-sulfolactate dehydrogenase (NADP(+))-like
LOC118271698	-2.32	1,4-alpha-glucan-branching enzyme-like
LOC118273853	3.35	15-hydroxyprostaglandin dehydrogenase [NAD(+)
LOC118264063	-5.80	15-hydroxyprostaglandin dehydrogenase [NAD(+)-like
LOC118264062	-5.21	15-hydroxyprostaglandin dehydrogenase [NAD(+)-like
LOC118264064	-4.17	15-hydroxyprostaglandin dehydrogenase [NAD(+)-like
LOC118263962	-3.59	15-hydroxyprostaglandin dehydrogenase [NAD(+)-like
LOC118264065	-2.01	15-hydroxyprostaglandin dehydrogenase [NAD(+)-like
LOC118269979	-2.55	17-beta-hydroxysteroid dehydrogenase 13-like isoform X1
LOC118269957	-2.39	17-beta-hydroxysteroid dehydrogenase 13-like isoform X1
LOC118268885	-4.32	17-beta-hydroxysteroid dehydrogenase 14-like
LOC118269452	-2.72	17-beta-hydroxysteroid dehydrogenase 14-like
LOC118269450	-2.71	17-beta-hydroxysteroid dehydrogenase 14-like
LOC118262433	-2.70	1-acyl-sn-glycerol-3-phosphate acyltransferase beta-like
LOC118262431	2.65	1-acyl-sn-glycerol-3-phosphate acyltransferase beta-like
LOC118267056	2.49	23 kDa integral membrane protein-like
LOC118276616	2.65	23 kDa integral membrane protein-like
LOC118279051	4.32	32 kDa beta-galactoside-binding lectin-like
LOC118278788	5.47	32 kDa beta-galactoside-binding lectin-like
LOC118278787	3.37	32 kDa beta-galactoside-binding lectin-like isoform X1
LOC118267426	-4.13	39S ribosomal protein L33, mitochondrial-like
LOC118279782	2.52	3-hydroxy-3-methylglutaryl-coenzyme A reductase
LOC118266304	-3.23	3-ketoacyl-CoA thiolase, mitochondrial-like
LOC118266245	-2.65	3-ketoacyl-CoA thiolase, mitochondrial-like
LOC118266444	-2.02	3-ketoacyl-CoA thiolase, mitochondrial-like
LOC118271177	-4.81	3-oxoacyl-[acyl-carrier-protein reductase FabG-like
LOC118267137	-4.31	3-oxoacyl-[acyl-carrier-protein reductase FabG-like
LOC118275088	-4.16	3-oxoacyl-[acyl-carrier-protein reductase FabG-like
LOC118275021	-3.81	3-oxoacyl-[acyl-carrier-protein reductase FabG-like
LOC118275066	-3.66	3-oxoacyl-[acyl-carrier-protein reductase FabG-like
LOC118275087	-3.14	3-oxoacyl-[acyl-carrier-protein reductase FabG-like
LOC118269451	-2.72	3-oxoacyl-[acyl-carrier-protein reductase FabG-like
LOC118268884	-2.34	3-oxoacyl-[acyl-carrier-protein reductase FabG-like
LOC118268882	-2.23	3-oxoacyl-[acyl-carrier-protein reductase FabG-like
LOC118269453	-2.03	3-oxoacyl-[acyl-carrier-protein reductase FabG-like
LOC118273846	2.35	3-phosphoinositide-dependent protein kinase 1-like isoform X1
LOC118278663	-2.70	4-coumarate--CoA ligase 1-like
LOC118267916	-2.30	4-coumarate--CoA ligase 1-like
LOC118269139	-6.70	4-hydroxyphenylpyruvate dioxygenase-like
LOC118268976	-6.52	4-hydroxyphenylpyruvate dioxygenase-like
LOC118277296	-2.24	6-pyruvoyl tetrahydrobiopterin synthase-like
LOC118266126	2.43	A disintegrin and metalloproteinase with thrombospondin motifs 16-like
LOC118266517	2.78	A disintegrin and metalloproteinase with thrombospondin motifs 16-like
LOC118270222	2.35	ABC transporter G family member 23-like
LOC118270767	2.56	ABC transporter G family member 23-like
LOC118278083	-5.37	acanthoscurrin-2-like
LOC118276153	-3.23	acetylcholinesterase-like
LOC118276152	-2.82	acetylcholinesterase-like
LOC118276155	-2.24	acetylcholinesterase-like
LOC118262776	2.15	acetylcholinesterase-like
LOC118280473	-2.11	acetyl-CoA carboxylase 1-like
LOC118264687	8.90	acidic repeat-containing protein-like
LOC118281870	8.90	acidic repeat-containing protein-like
LOC118275009	-3.85	acrosin-like
LOC118265670	-2.06	actin cytoskeleton-regulatory complex protein PAN1-like
LOC118270032	2.28	actin cytoskeleton-regulatory complex protein PAN1-like
LOC118270598	11.36	actin cytoskeleton-regulatory complex protein PAN1-like
LOC118279603	4.41	actin-like protein 6B
LOC118273023	3.52	activating signal cointegrator 1 complex subunit 1-like isoform X1
LOC118264933	-2.72	acyl-CoA Delta(11) desaturase-like
LOC118269215	10.34	acyl-CoA Delta(11) desaturase-like
LOC118269154	13.59	acyl-CoA Delta(11) desaturase-like
LOC118269923	5.88	acyl-CoA desaturase 1-like
LOC118269922	13.63	acyl-CoA desaturase 1-like
LOC118278116	-2.48	acyl-CoA synthetase short-chain family member 3, mitochondrial-like
LOC118275169	2.02	adenosine deaminase 2-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118275125	4.63	adenosine deaminase 2-like
LOC118264822	-2.23	adenylosuccinate lyase-like
LOC118264826	-2.16	adenylosuccinate lyase-like
LOC118270960	2.42	adiponectin receptor protein-like
LOC118281460	5.58	adult-specific cuticular protein ACP-20-like
LOC118261995	7.27	adult-specific cuticular protein ACP-20-like
LOC118262128	9.32	adult-specific cuticular protein ACP-20-like
LOC118275749	9.62	adult-specific cuticular protein ACP-20-like
LOC118264590	3.48	alcohol dehydrogenase [acceptor-like
LOC118264589	3.99	alcohol dehydrogenase [acceptor-like
LOC118264588	4.86	alcohol dehydrogenase [acceptor-like
LOC118263961	-3.89	alcohol dehydrogenase 1-like
LOC118272357	-4.40	alcohol dehydrogenase class-3 chain L-like
LOC118265216	-2.62	aldehyde dehydrogenase X, mitochondrial-like isoform X1
LOC118268489	-3.04	aldehyde dehydrogenase, cytosolic 1-like
LOC118265756	-2.14	aldehyde dehydrogenase, dimeric NADP-preferring-like isoform X1
LOC118273932	-3.07	aldehyde dehydrogenase, mitochondrial-like
LOC118267799	3.16	aldehyde oxidase 1-like
LOC118279519	-6.49	aldo-keto reductase AKR2E4-like
LOC118279607	-5.11	aldo-keto reductase AKR2E4-like
LOC118274962	-4.04	aldo-keto reductase AKR2E4-like
LOC118274940	-3.93	aldo-keto reductase AKR2E4-like
LOC118280048	-2.42	aldo-keto reductase AKR2E4-like
LOC118279988	-2.40	aldo-keto reductase AKR2E4-like isoform X1
LOC118279733	-2.36	aldo-keto reductase AKR2E4-like isoform X1
LOC118264688	-6.07	aldo-keto reductase family 1 member B1-like
LOC118269437	4.27	alkaline phosphatase, tissue-nonspecific isozyme-like
LOC118267498	-3.60	alkaline phosphatase-like isoform X1
LOC118264112	4.13	alkyldihydroxyacetonephosphate synthase-like
LOC118268332	-2.35	alkylglycerol monooxygenase-like
LOC118268627	-2.94	allantoicase-like
LOC118266455	-4.62	allergen Tha p 1-like
LOC118265699	-4.50	allergen Tha p 1-like
LOC118265697	-2.14	allergen Tha p 1-like
LOC118265698	-2.30	allergen Tha p 1-like isoform X1
LOC118265695	4.33	allergen Tha p 1-like isoform X1
LOC118266098	4.58	allergen Tha p 1-like isoform X1
LOC118265620	2.15	alpha-aminoadipic semialdehyde synthase, mitochondrial-like
LOC118268996	-2.04	alpha-amylase 2-like
LOC118266145	-3.59	alpha-amylase 4N-like
LOC118266156	-3.40	alpha-amylase 4N-like
LOC118277109	4.20	alpha-crystallin A chain-like
LOC118276752	4.47	alpha-crystallin A chain-like
LOC118267030	-2.32	alpha-mannosidase 2-like
LOC118266499	5.02	alpha-N-acetylgalactosaminidase-like
LOC118266307	5.23	alpha-N-acetylgalactosaminidase-like
LOC118271281	-3.52	alpha-N-acetylglucosaminidase-like
LOC118271305	-2.89	alpha-N-acetylglucosaminidase-like
LOC118274753	-4.48	alpha-tocopherol transfer protein-like
LOC118274760	-3.72	alpha-tocopherol transfer protein-like
LOC118274755	-3.63	alpha-tocopherol transfer protein-like
LOC118274737	-2.29	alpha-tocopherol transfer protein-like
LOC118274796	-2.01	alpha-tocopherol transfer protein-like
LOC118274766	2.40	alpha-tocopherol transfer protein-like
LOC118274072	2.44	alpha-tocopherol transfer protein-like
LOC118274015	2.76	alpha-tocopherol transfer protein-like
LOC118274939	3.24	alpha-tocopherol transfer protein-like
LOC118263738	3.24	alpha-tocopherol transfer protein-like
LOC118275108	3.76	alpha-tocopherol transfer protein-like
LOC118274961	3.99	alpha-tocopherol transfer protein-like
LOC118263381	4.19	alpha-tocopherol transfer protein-like
LOC118275225	4.46	alpha-tocopherol transfer protein-like
LOC118273527	2.58	alpha-tocopherol transfer protein-like isoform X1
LOC118273546	3.13	alpha-tocopherol transfer protein-like isoform X1
LOC118273542	3.76	alpha-tocopherol transfer protein-like isoform X1
LOC118273544	4.85	alpha-tocopherol transfer protein-like isoform X1
LOC118275177	5.59	alpha-tocopherol transfer protein-like isoform X1
LOC118275090	5.83	alpha-tocopherol transfer protein-like isoform X1
LOC118265489	6.04	altered inheritance of mitochondria protein 3-like
LOC118264312	-2.62	amino acid transporter AVT1A-like
LOC118265511	-3.59	aminoacylase-1-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118261808	-3.57	aminoacylase-1-like
LOC118265252	-2.07	aminoacylase-1-like
LOC118278202	-3.09	aminomethyltransferase, mitochondrial-like
LOC118269054	2.01	amyloid protein-binding protein 2-like isoform X1
LOC118279894	-3.34	androgen-dependent TFPI-regulating protein-like
LOC118279866	-3.34	androgen-dependent TFPI-regulating protein-like
LOC118273698	-2.69	androgen-dependent TFPI-regulating protein-like
LOC118279898	-2.61	androgen-dependent TFPI-regulating protein-like
LOC118281823	-2.33	androgen-induced gene 1 protein-like
LOC118267158	3.04	angiopoietin-related protein 2-like
LOC118270470	2.51	ankyrin repeat and MYND domain-containing protein 1-like
LOC118280221	-2.16	anoctamin-4-like isoform X1
LOC118265780	-3.64	antichymotrypsin-1-like isoform X1
LOC118265781	-3.12	antichymotrypsin-1-like isoform X1
LOC118274630	-3.13	apolipophorin-3
LOC118280748	-5.12	apolipophorins-like isoform X1
LOC118276696	4.26	apolipoprotein D-like
LOC118266695	2.48	armadillo repeat-containing protein gudu-like
LOC118265551	-2.30	arrestin domain-containing protein 5-like
LOC118265003	2.45	arrestin domain-containing protein 5-like
LOC118268296	2.39	arylsulfatase B-like
LOC118268635	2.68	arylsulfatase B-like
LOC118268302	3.15	arylsulfatase J-like
LOC118268295	3.26	arylsulfatase J-like
LOC118263189	-2.57	aspartate aminotransferase, cytoplasmic-like isoform X1
LOC118262037	2.40	aspartate--tRNA ligase, mitochondrial-like
LOC118278708	4.13	ATP synthase subunit beta, mitochondrial-like
LOC118278986	5.37	ATP synthase subunit beta, mitochondrial-like
LOC118265165	2.16	ATP-binding cassette sub-family G member 1-like
LOC118265120	2.28	ATP-binding cassette sub-family G member 1-like
LOC118272465	2.36	ATP-binding cassette sub-family G member 1-like
LOC118278502	-2.02	ATP-citrate synthase-like
LOC118270306	-2.67	ATP-dependent 6-phosphofructokinase-like isoform X1
LOC118276278	7.27	ATP-dependent RNA helicase glh-1-like
LOC118279379	-3.06	ATP-sensitive inward rectifier potassium channel 15-like isoform X1
LOC118279386	2.72	ATP-sensitive inward rectifier potassium channel 1-like
LOC118267152	3.07	atrial natriuretic peptide-converting enzyme-like
LOC118264419	2.18	autophagy protein 12-like
LOC118280363	4.12	axonemal 84 kDa protein-like
LOC118281825	4.34	azurocidin-like
LOC118275658	2.01	b(0,+)-type amino acid transporter 1-like
LOC118264512	3.17	B9 domain-containing protein 1-like
LOC118266597	2.20	band 7 protein AGAP004871
LOC118261904	3.41	band 7 protein AGAP004871-like isoform X1
LOC118261942	7.31	band 7 protein AGAP004871-like isoform X1
LOC118282051	-3.62	B-cell CLL/lymphoma 6 member B protein-like
LOC118281636	-2.98	beta-1,3-glucan-binding protein-like
LOC118272701	-2.78	beta-1,3-glucan-binding protein-like
LOC118263845	-2.16	beta-1,4-glucuronyltransferase 1-like
LOC118274075	-6.03	beta-ureidopropionase-like
LOC118273984	-3.15	beta-ureidopropionase-like
LOC118262803	-8.65	bile salt-activated lipase-like
LOC118282211	-3.22	bile salt-activated lipase-like
LOC118275840	-2.31	bile salt-activated lipase-like
LOC118275724	2.28	bile salt-activated lipase-like
LOC118267724	-2.74	brachyurin-like
LOC118280118	5.50	brain-specific serine protease 4-like isoform X1
LOC118266456	8.64	bromodomain-containing protein 4-like
LOC118275625	-3.84	C-1-tetrahydrofolate synthase, cytoplasmic isoform X1
LOC118281677	-2.08	cadherin-related tumor suppressor-like
LOC118272071	-2.12	calexcitin-2-like
LOC118274847	-3.07	calmodulin-like isoform X1
LOC118274334	-3.13	calphotin-like
LOC118265672	-2.82	calphotin-like
LOC118266204	-2.25	calphotin-like
LOC118265665	-2.14	calphotin-like
LOC118263689	-2.49	capon-like protein isoform X1
LOC118270569	-2.08	carbonic anhydrase 1-like
LOC118268288	-3.16	carbonic anhydrase 1-like isoform X1
LOC118268251	-3.41	carbonic anhydrase 7-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118276151	-3.78	carboxylesterase 1C-like
LOC118272141	-4.66	carboxylesterase 1E-like
LOC118272142	-4.49	carboxylesterase 5A-like
LOC118279505	-2.93	carboxylesterase 5A-like
LOC118271425	-4.94	carboxypeptidase B-like
LOC118271478	-4.04	carboxypeptidase B-like
LOC118271477	-3.45	carboxypeptidase B-like
LOC118271474	-2.72	carboxypeptidase B-like
LOC118275622	-2.48	carboxypeptidase B-like
LOC118271473	-2.40	carboxypeptidase B-like
LOC118266420	5.12	carboxypeptidase B-like
LOC118271974	6.35	carboxypeptidase B-like
LOC118271913	6.49	carboxypeptidase B-like
LOC118271475	-3.07	carboxypeptidase B-like isoform X1
LOC118269492	2.37	carboxypeptidase M-like
LOC118267946	-4.91	carcinine transporter-like
LOC118280466	-3.16	carcinine transporter-like
LOC118280478	-2.54	carcinine transporter-like
LOC118268571	-2.19	carcinine transporter-like
LOC118261782	4.12	cardioacceleratory peptide receptor-like isoform X1
LOC118282333	4.13	cardioacceleratory peptide receptor-like isoform X1
LOC118277523	2.77	caspase-1-like
LOC118267266	3.07	caspase-1-like
LOC118276022	-3.66	catalase-like
LOC118262513	-2.31	catalase-like
LOC118261836	4.20	catalase-like
LOC118261852	4.22	catalase-like
LOC118262151	4.37	catalase-like
LOC118282418	4.61	catalase-like
LOC118262153	4.84	catalase-like
LOC118261835	4.84	catalase-like
LOC118261834	6.02	catalase-like
LOC118262150	6.51	catalase-like
LOC118282430	9.11	catalase-like
LOC118276442	2.40	cathepsin L1-like
LOC118271292	-3.16	cathepsin O-like
LOC118271264	-2.56	cathepsin O-like
LOC118271291	-2.26	cathepsin O-like
LOC118269235	2.14	cationic amino acid transporter 2-like isoform X1
LOC118277463	6.91	CCAAT/enhancer-binding protein-like
LOC118266494	-3.51	CD109 antigen-like
LOC118279053	2.29	cell surface glycoprotein 1-like
LOC118269430	2.32	cell surface glycoprotein 1-like isoform X1
LOC118280675	2.73	cell wall protein DAN4-like
LOC118267654	7.63	cell wall protein DAN4-like
LOC118275077	-2.94	ceramide synthase 6-like
LOC118275180	-2.32	ceramide synthase 6-like
LOC118268439	2.69	chaoptin-like
LOC118269637	2.44	chaoptin-like isoform X1
LOC118269698	2.72	chaoptin-like isoform X1
LOC118273193	2.44	chitin deacetylase 1
LOC118272095	7.30	chitin deacetylase 1-like
LOC118273685	2.21	chitin deacetylase 1-like isoform X1
LOC118279269	3.50	chitin deacetylase 8-like
LOC118282002	4.69	chitinase A-like
LOC118277800	5.11	chitinase A-like
LOC118281031	2.11	cholesterol 7-desaturase-like
LOC118281054	2.86	cholesterol 7-desaturase-like
LOC118263178	-4.01	cholinesterase 1-like
LOC118272377	-3.30	cholinesterase 1-like
LOC118274190	2.34	chondroitin proteoglycan 2-like
LOC118276246	-3.19	chorion peroxidase-like
LOC118264035	3.40	chorion peroxidase-like
LOC118264969	-2.05	chromatin assembly factor 1 subunit B-like
LOC118276450	5.49	chromatin modification-related protein eaf-1-like
LOC118267662	-3.48	chymotrypsin-1-like
LOC118267584	-3.19	chymotrypsin-1-like
LOC118267770	-2.98	chymotrypsin-1-like
LOC118267815	-2.80	chymotrypsin-1-like
LOC118267797	-2.57	chymotrypsin-1-like
LOC118267822	-2.24	chymotrypsin-1-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118267759	-4.11	chymotrypsin-2-like
LOC118267586	-3.99	chymotrypsin-2-like
LOC118267771	-3.50	chymotrypsin-2-like
LOC118267597	-3.31	chymotrypsin-2-like
LOC118267607	-2.85	chymotrypsin-2-like
LOC118267760	-2.84	chymotrypsin-2-like
LOC118267593	-2.67	chymotrypsin-2-like
LOC118276154	2.50	cilia- and flagella-associated protein 161-like
LOC118264636	-3.67	cilia- and flagella-associated protein 251-like
LOC118282047	-3.88	cilia- and flagella-associated protein 36-like
LOC118276492	-5.38	circadian clock-controlled protein daywake-like
LOC118276100	-4.26	circadian clock-controlled protein daywake-like
LOC118276282	-3.08	circadian clock-controlled protein daywake-like
LOC118275991	-2.99	circadian clock-controlled protein daywake-like
LOC118276477	-2.80	circadian clock-controlled protein daywake-like
LOC118276479	-2.63	circadian clock-controlled protein daywake-like
LOC118263879	-2.38	circadian clock-controlled protein daywake-like
LOC118276116	2.11	circadian clock-controlled protein daywake-like
LOC118263001	5.01	circadian clock-controlled protein daywake-like
LOC118276328	7.12	circadian clock-controlled protein daywake-like
LOC118264172	2.17	class A basic helix-loop-helix protein 15-like
LOC118274964	-2.26	clavesin-1-like
LOC118265087	2.80	clavesin-1-like
LOC118273241	-3.43	clavesin-2-like
LOC118267845	-2.35	CLIP domain-containing serine protease 14D-like
LOC118272697	2.03	C-Maf-inducing protein-like
LOC118280568	-4.65	coagulation factor IX-like
LOC118280680	-2.74	coagulation factor IX-like
LOC118262957	2.69	collagen alpha-1(I) chain-like
LOC118266475	2.94	collagen alpha-1(I) chain-like
LOC118265974	3.10	collagen alpha-1(I) chain-like
LOC118262955	2.29	collagen alpha-1(I) chain-like isoform X1
LOC118274984	-3.03	collagenase-like
LOC118267612	-2.31	collagenase-like
LOC118280955	-2.01	copper chaperone for superoxide dismutase-like
LOC118281831	2.54	COX assembly mitochondrial protein homolog
LOC118272895	8.80	craniofacial development protein 2-like
LOC118267606	2.54	ctenidin-3-like
LOC118270464	2.61	C-type lectin domain family 4 member E-like
LOC118264375	-2.04	C-type mannose receptor 2-like
LOC118267044	-3.93	C-type mannose receptor 2-like isoform X1
LOC118265693	6.22	CUB and sushi domain-containing protein 3-like isoform X1
LOC118272903	2.26	cuticle protein 16.5-like
LOC118272366	2.33	cuticle protein 16.5-like
LOC118279659	2.37	cuticle protein 16.5-like
LOC118279658	2.88	cuticle protein 16.5-like
LOC118276092	4.93	cuticle protein 16.5-like
LOC118276281	6.03	cuticle protein 16.5-like
LOC118277907	6.58	cuticle protein 16.5-like
LOC118272646	9.78	cuticle protein 16.5-like
LOC118273867	10.69	cuticle protein 16.5-like
LOC118272879	10.92	cuticle protein 16.5-like
LOC118273866	12.82	cuticle protein 16.5-like
LOC118261734	5.53	cuticle protein 18.6-like
LOC118261733	6.24	cuticle protein 18.6-like
LOC118261732	9.48	cuticle protein 18.6-like
LOC118274137	9.83	cuticle protein 18.6-like
LOC118274138	11.81	cuticle protein 18.6-like
LOC118277977	10.15	cuticle protein 19.8-like
LOC118277978	11.02	cuticle protein 19.8-like
LOC118282419	4.87	cuticle protein 19-like
LOC118261962	5.39	cuticle protein 19-like
LOC118266418	5.53	cuticle protein 19-like
LOC118261786	6.29	cuticle protein 19-like
LOC118261992	6.29	cuticle protein 19-like
LOC118261804	7.64	cuticle protein 19-like
LOC118281467	8.79	cuticle protein 19-like
LOC118262072	9.55	cuticle protein 19-like
LOC118262025	10.59	cuticle protein 19-like
LOC118281454	11.19	cuticle protein 19-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118272371	-3.56	cuticle protein 21-like
LOC118272373	-3.45	cuticle protein 21-like
LOC118265978	7.20	cuticle protein 3-like
LOC118265851	7.46	cuticle protein 3-like
LOC118266512	8.10	cuticle protein 3-like
LOC118265980	9.20	cuticle protein 3-like
LOC118265844	9.84	cuticle protein 3-like
LOC118265845	10.04	cuticle protein 3-like
LOC118265979	8.00	cuticle protein 3-like isoform X1
LOC118272743	12.09	cuticle protein 63-like
LOC118273869	12.09	cuticle protein 63-like
LOC118273856	-5.38	cuticle protein 65-like
LOC118262030	4.49	cuticle protein 7-like
LOC118262028	5.11	cuticle protein 7-like
LOC118281445	5.67	cuticle protein 7-like
LOC118264710	6.80	cuticle protein 7-like
LOC118281381	7.50	cuticle protein 7-like
LOC118281406	7.71	cuticle protein 7-like
LOC118261774	7.94	cuticle protein 7-like
LOC118262024	8.84	cuticle protein 7-like
LOC118262023	8.85	cuticle protein 7-like
LOC118277981	9.14	cuticle protein 7-like
LOC118262033	9.31	cuticle protein 7-like
LOC118262026	10.66	cuticle protein 7-like
LOC118281416	11.80	cuticle protein 7-like
LOC118281423	10.53	cuticle protein 7-like isoform X1
LOC118282350	4.37	cuticle protein 8-like
LOC118262022	4.46	cuticle protein 8-like
LOC118281367	4.54	cuticle protein 8-like
LOC118281401	6.32	cuticle protein 8-like
LOC118261907	9.09	cuticle protein 8-like
LOC118281375	9.51	cuticle protein 8-like
LOC118281439	9.75	cuticle protein 8-like
LOC118261945	9.92	cuticle protein 8-like
LOC118274135	9.93	cuticle protein 8-like
LOC118262027	10.81	cuticle protein 8-like
LOC118262019	11.33	cuticle protein 8-like
LOC118281391	12.52	cuticle protein 8-like
LOC118262020	12.90	cuticle protein 8-like
LOC118282313	8.00	cuticle protein 8-like isoform X1
LOC118262125	8.76	cuticle protein 8-like isoform X1
LOC118274134	9.71	cuticle protein 8-like isoform X1
LOC118272369	-4.05	cuticle protein LPCP-23-like
LOC118261759	6.00	cuticle protein-like
LOC118261775	7.24	cuticle protein-like
LOC118274403	7.68	cuticle protein-like
LOC118261779	8.17	cuticle protein-like
LOC118278046	8.48	cuticle protein-like
LOC118261737	8.68	cuticle protein-like
LOC118261780	9.34	cuticle protein-like
LOC118274136	11.74	cuticle protein-like
LOC118278885	2.02	cyclin-dependent kinase 9-like
LOC118275589	2.71	cyclin-dependent kinase-like 1 isoform X1
LOC118272798	3.64	cysteine sulfinic acid decarboxylase-like
LOC118276791	2.69	cysteine-rich PDZ-binding protein-like
LOC118276723	3.10	cysteine-rich PDZ-binding protein-like
LOC118281691	5.50	cytadherence high molecular weight protein 3-like
LOC118265393	5.53	cytadherence high molecular weight protein 3-like
LOC118267804	-2.07	cytochrome b561 domain-containing protein 1-like
LOC118271394	-2.53	cytochrome b5-like
LOC118268104	-3.63	cytochrome b5-related protein-like
LOC118268452	-3.21	cytochrome b5-related protein-like
LOC118268438	-2.48	cytochrome b5-related protein-like
LOC118268424	-2.37	cytochrome b5-related protein-like
LOC118268419	-2.31	cytochrome b5-related protein-like
LOC118268105	2.04	cytochrome b5-related protein-like
LOC118268449	2.05	cytochrome b5-related protein-like
LOC118268107	-2.33	cytochrome b5-related protein-like isoform X1
LOC118269113	-4.16	cytochrome P450 315a1, mitochondrial-like
LOC118270459	-11.00	cytochrome P450 4C1-like
LOC118270313	-8.90	cytochrome P450 4C1-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118270823	-6.27	cytochrome P450 4C1-like
LOC118270314	-5.67	cytochrome P450 4C1-like
LOC118270860	-4.04	cytochrome P450 4C1-like
LOC118270689	-3.95	cytochrome P450 4C1-like
LOC118270695	-3.45	cytochrome P450 4C1-like
LOC118270758	-3.15	cytochrome P450 4C1-like
LOC118270312	-3.08	cytochrome P450 4C1-like
LOC118282305	-2.92	cytochrome P450 4C1-like
LOC118282379	-2.88	cytochrome P450 4C1-like
LOC118273959	-2.33	cytochrome P450 4C1-like
LOC118270307	2.42	cytochrome P450 4C1-like
LOC118281716	2.46	cytochrome P450 4C1-like
LOC118281717	2.98	cytochrome P450 4C1-like
LOC118275081	3.26	cytochrome P450 4C1-like
LOC118270578	3.98	cytochrome P450 4C1-like
LOC118270461	7.94	cytochrome P450 4C1-like
LOC118270719	-7.02	cytochrome P450 4C1-like isoform X1
LOC118270718	-2.98	cytochrome P450 4C1-like isoform X1
LOC118270458	3.22	cytochrome P450 4c21-like
LOC118270308	3.90	cytochrome P450 4c21-like
LOC118270750	-5.93	cytochrome P450 4c3-like
LOC118272240	-4.44	cytochrome P450 4c3-like
LOC118281843	-2.49	cytochrome P450 4c3-like
LOC118270728	2.19	cytochrome P450 4c3-like
LOC118270311	-3.48	cytochrome P450 4d1-like isoform X1
LOC118261999	-4.68	cytochrome P450 4d2-like
LOC118282337	-4.05	cytochrome P450 4d2-like
LOC118263710	-2.71	cytochrome P450 4d2-like
LOC118263397	-2.12	cytochrome P450 4d2-like
LOC118263448	-3.91	cytochrome P450 4g15-like
LOC118263457	-2.04	cytochrome P450 4g15-like
LOC118262004	-5.05	cytochrome P450 4V2-like
LOC118282334	-5.01	cytochrome P450 4V2-like
LOC118270854	-4.26	cytochrome P450 4V2-like
LOC118282338	-3.81	cytochrome P450 4V2-like
LOC118281824	-3.81	cytochrome P450 4V2-like
LOC118271683	-3.73	cytochrome P450 4V2-like
LOC118270575	-3.32	cytochrome P450 4V2-like
LOC118270460	-9.85	cytochrome P450 4V2-like isoform X1
LOC118270694	-4.95	cytochrome P450 4V2-like isoform X1
LOC118274185	-4.23	cytochrome P450 6a9-like
LOC118274106	6.06	cytochrome P450 6B1-like
LOC118272349	-3.23	cytochrome P450 6B2-like
LOC118273914	-2.86	cytochrome P450 6B2-like
LOC118273915	-2.08	cytochrome P450 6B2-like
LOC118281490	-3.38	cytochrome P450 6B5-like
LOC118274503	-3.15	cytochrome P450 6B5-like
LOC118282199	-2.99	cytochrome P450 6B5-like
LOC118274506	-2.46	cytochrome P450 6B5-like
LOC118262947	-8.77	cytochrome P450 6B6-like
LOC118263005	-7.14	cytochrome P450 6B6-like
LOC118262642	-6.20	cytochrome P450 6B6-like
LOC118263048	-5.76	cytochrome P450 6B6-like
LOC118273912	-2.72	cytochrome P450 6B6-like
LOC118274094	-2.06	cytochrome P450 6B6-like
LOC118265346	2.10	cytochrome P450 6j1-like
LOC118265371	2.89	cytochrome P450 6j1-like
LOC118263083	-5.43	cytochrome P450 6k1-like
LOC118263077	-5.11	cytochrome P450 6k1-like
LOC118274285	-3.38	cytochrome P450 6k1-like
LOC118264058	-2.95	cytochrome P450 9e2-like
LOC118264410	-2.89	cytochrome P450 9e2-like
LOC118264788	5.03	cytochrome P450 9e2-like
LOC118264068	-2.05	cytochrome P450 9e2-like
LOC118263547	-2.96	cytochrome P450 CYP12A2-like
LOC118263546	-2.23	cytochrome P450 CYP12A2-like
LOC118264200	-2.23	cytoglobin-1-like isoform X1
LOC118281643	-2.29	D-2-hydroxyglutarate dehydrogenase, mitochondrial-like
LOC118280252	-6.43	D-arabinitol dehydrogenase 1-like
LOC118280432	-5.00	D-arabinitol dehydrogenase 1-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118265945	-2.71	D-aspartate oxidase-like
LOC118268135	3.01	decaprenyl-diphosphate synthase subunit 1-like
LOC118279850	4.27	decaprenyl-diphosphate synthase subunit 2-like
LOC118279842	4.92	decaprenyl-diphosphate synthase subunit 2-like
LOC118267307	-2.18	dehydrogenase/reductase SDR family protein 7-like
LOC118276294	-4.78	dehydrogenase-like
LOC118280239	-2.18	dehydrogenase-like
LOC118266266	2.90	dehydrogenase-like
LOC118280738	-4.20	delta(24)-sterol reductase-like
LOC118265731	-3.23	delta(24)-sterol reductase-like
LOC118265730	-3.02	delta(24)-sterol reductase-like
LOC118268457	-3.93	delta(7)-sterol 5(6)-desaturase erg32-like
LOC118276214	-3.10	delta-1-pyrroline-5-carboxylate synthase-like isoform X1
LOC118264591	4.27	dentin sialophosphoprotein-like isoform X1
LOC118264400	-5.29	D-erythronate dehydrogenase-like
LOC118264622	-5.11	D-erythronate dehydrogenase-like
LOC118262730	2.02	diacylglycerol kinase eta-like
LOC118267631	2.19	disheveled-associated activator of morphogenesis 1-like isoform X1
LOC118267630	2.78	disheveled-associated activator of morphogenesis 1-like isoform X1
LOC118273376	-2.14	DNA primase large subunit-like
LOC118267086	-2.11	DNA primase small subunit-like isoform X1
LOC118265573	2.66	DNA translocase FtsK-like isoform X1
LOC118267715	2.07	drebrin-like protein
LOC118265067	5.75	drebrin-like protein
LOC118269141	2.41	dual oxidase-like isoform X1
LOC118264986	5.67	dynein heavy chain 2, axonemal-like
LOC118264984	7.57	dynein heavy chain 2, axonemal-like
LOC118273262	3.71	dynein intermediate chain 3, ciliary-like
LOC118278254	-2.80	dynein light chain Tctex-type 1-like
LOC118263091	3.76	dynein regulatory complex subunit 5-like
LOC118262808	4.64	dynein regulatory complex subunit 5-like
LOC118265527	-4.88	early nodulin-75-like
LOC118265127	3.45	early nodulin-75-like
LOC118267732	2.32	ecdysteroid-regulated 16 kDa protein-like
LOC118269902	6.50	eclosion hormone
LOC118274613	-2.12	ectonucleoside triphosphate diphosphohydrolase 5-like isoform X1
LOC118265694	-4.40	ejaculatory bulb-specific protein 3-like
LOC118266097	-4.02	ejaculatory bulb-specific protein 3-like
LOC118265701	-3.52	ejaculatory bulb-specific protein 3-like
LOC118266106	-3.52	ejaculatory bulb-specific protein 3-like
LOC118266099	-2.25	ejaculatory bulb-specific protein 3-like
LOC118266101	-2.08	ejaculatory bulb-specific protein 3-like
LOC118274267	3.61	ejaculatory bulb-specific protein 3-like
LOC118265700	5.47	ejaculatory bulb-specific protein 3-like
LOC118272394	10.24	elongation of very long chain fatty acids protein 1-like
LOC118272832	10.28	elongation of very long chain fatty acids protein 1-like
LOC118263756	2.59	elongation of very long chain fatty acids protein 4-like
LOC118263487	2.71	elongation of very long chain fatty acids protein 4-like
LOC118261977	2.06	elongation of very long chain fatty acids protein 7-like
LOC118262043	2.60	elongation of very long chain fatty acids protein 7-like
LOC118261956	3.07	elongation of very long chain fatty acids protein 7-like
LOC118282375	6.78	elongation of very long chain fatty acids protein 7-like
LOC118282383	7.37	elongation of very long chain fatty acids protein 7-like
LOC118261979	5.05	elongation of very long chain fatty acids protein 7-like isoform X1
LOC118261900	5.21	elongation of very long chain fatty acids protein 7-like isoform X1
LOC118262109	-4.36	elongation of very long chain fatty acids protein AAEL008004-like
LOC118282252	-4.04	elongation of very long chain fatty acids protein AAEL008004-like
LOC118262014	-3.42	elongation of very long chain fatty acids protein AAEL008004-like
LOC118262083	-3.17	elongation of very long chain fatty acids protein AAEL008004-like
LOC118282220	-2.79	elongation of very long chain fatty acids protein AAEL008004-like
LOC118261849	2.07	elongation of very long chain fatty acids protein AAEL008004-like
LOC118261948	2.56	elongation of very long chain fatty acids protein AAEL008004-like isoform X1
LOC118275867	-4.26	elongation of very long chain fatty acids protein-like
LOC118275898	7.31	endochitinase A-like isoform X1
LOC118278006	4.94	endochitinase-like
LOC118278803	2.38	endocuticle structural glycoprotein ABD-4-like
LOC118278717	3.41	endocuticle structural glycoprotein ABD-4-like
LOC118282348	4.26	endocuticle structural glycoprotein ABD-4-like
LOC118282374	5.66	endocuticle structural glycoprotein ABD-5-like
LOC118275283	13.25	endocuticle structural glycoprotein ABD-5-like
LOC118261896	5.92	endocuticle structural glycoprotein SgAbd-2-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118282356	-2.53	endocuticle structural glycoprotein SgAbd-5-like
LOC118282407	6.36	endocuticle structural glycoprotein SgAbd-5-like
LOC118261870	8.69	endocuticle structural glycoprotein SgAbd-5-like
LOC118261868	9.70	endocuticle structural glycoprotein SgAbd-5-like
LOC118261848	-4.02	endocuticle structural glycoprotein SgAbd-5-like isoform X1
LOC118282354	-2.05	endocuticle structural glycoprotein SgAbd-5-like isoform X1
LOC118282349	5.99	endocuticle structural glycoprotein SgAbd-8-like
LOC118282304	6.89	endocuticle structural glycoprotein SgAbd-8-like
LOC118282343	8.03	endocuticle structural glycoprotein SgAbd-8-like
LOC118261898	-3.21	endocuticle structural protein SgAbd-6-like
LOC118276055	2.00	endoribonuclease Dicer-like
LOC118268804	-2.03	enolase-like
LOC118269470	-2.23	enolase-like isoform X1
LOC118279735	-2.15	ephrin-B2a-like
LOC118269538	-2.28	epidermal retinol dehydrogenase 2-like isoform X1
LOC118271971	3.10	epidermal retinol dehydrogenase 2-like isoform X1
LOC118271766	6.87	espin-like isoform X1
LOC118267335	-4.25	ester hydrolase C11orf54 homolog
LOC118277582	-3.15	esterase B1-like
LOC118276148	-2.11	esterase B1-like
LOC118265499	-2.05	esterase B1-like isoform X1
LOC118276232	-8.39	esterase FE4-like
LOC118276233	-7.87	esterase FE4-like
LOC118276149	-4.93	esterase FE4-like
LOC118262722	-3.70	esterase FE4-like
LOC118273652	-3.58	esterase FE4-like
LOC118276230	-2.81	esterase FE4-like
LOC118265387	-2.42	esterase FE4-like
LOC118275861	-2.21	esterase FE4-like
LOC118276227	-2.08	esterase FE4-like
LOC118276150	-3.86	esterase FE4-like isoform X1
LOC118271630	2.23	estradiol 17-beta-dehydrogenase 11-like
LOC118277327	2.74	ethanolaminephosphotransferase 1-like
LOC118282394	-3.08	eukaryotic peptide chain release factor GTP-binding subunit ERF3A-like
LOC118262073	2.69	eukaryotic translation initiation factor 4E1-like
LOC118265547	-2.07	excitatory amino acid transporter-like isoform X1
LOC118269090	2.60	exonuclease GOR-like
LOC118267658	4.99	extensin-like
LOC118263017	10.02	extensin-like
LOC118277657	-6.01	facilitated trehalose transporter Tret1-2 homolog
LOC118277673	-4.92	facilitated trehalose transporter Tret1-2 homolog
LOC118270022	-7.68	facilitated trehalose transporter Tret1-like
LOC118277593	-6.18	facilitated trehalose transporter Tret1-like
LOC118277596	-4.90	facilitated trehalose transporter Tret1-like
LOC118277644	-4.90	facilitated trehalose transporter Tret1-like
LOC118270686	-4.86	facilitated trehalose transporter Tret1-like
LOC118279125	-4.25	facilitated trehalose transporter Tret1-like
LOC118277661	-4.22	facilitated trehalose transporter Tret1-like
LOC118277392	-4.10	facilitated trehalose transporter Tret1-like
LOC118277648	-4.09	facilitated trehalose transporter Tret1-like
LOC118270205	-3.86	facilitated trehalose transporter Tret1-like
LOC118264956	-3.56	facilitated trehalose transporter Tret1-like
LOC118270389	-3.19	facilitated trehalose transporter Tret1-like
LOC118277640	-3.08	facilitated trehalose transporter Tret1-like
LOC118277658	-2.61	facilitated trehalose transporter Tret1-like
LOC118278124	-2.58	facilitated trehalose transporter Tret1-like
LOC118265246	-2.48	facilitated trehalose transporter Tret1-like
LOC118265245	-2.47	facilitated trehalose transporter Tret1-like
LOC118280742	-2.45	facilitated trehalose transporter Tret1-like
LOC118263818	-2.00	facilitated trehalose transporter Tret1-like
LOC118279231	2.14	facilitated trehalose transporter Tret1-like
LOC118272123	3.88	facilitated trehalose transporter Tret1-like
LOC118270388	3.99	facilitated trehalose transporter Tret1-like
LOC118277887	4.43	facilitated trehalose transporter Tret1-like
LOC118270601	5.75	facilitated trehalose transporter Tret1-like
LOC118270392	6.03	facilitated trehalose transporter Tret1-like
LOC118277850	7.01	facilitated trehalose transporter Tret1-like
LOC118269337	-3.81	farnesol dehydrogenase-like
LOC118266039	2.11	farnesyl pyrophosphate synthase-like
LOC118268284	-3.19	fasciclin-1-like isoform X1

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118268287	-2.66	fasciclin-1-like isoform X1
LOC118275042	-4.00	fatty acid synthase-like
LOC118274779	-3.39	fatty acid synthase-like
LOC118275041	-3.32	fatty acid synthase-like
LOC118274970	-3.18	fatty acid synthase-like
LOC118274634	-2.94	fatty acid synthase-like
LOC118274778	-2.87	fatty acid synthase-like
LOC118274969	-2.84	fatty acid synthase-like
LOC118274609	-2.84	fatty acid synthase-like
LOC118274998	-2.75	fatty acid synthase-like
LOC118274989	-2.48	fatty acid synthase-like
LOC118274999	-2.09	fatty acid synthase-like
LOC118274972	5.18	fatty acid synthase-like
LOC118275043	5.34	fatty acid synthase-like
LOC118267601	8.50	fatty acid synthase-like
LOC118274557	-3.89	fatty acid synthase-like isoform X1
LOC118274601	-3.40	fatty acid synthase-like isoform X1
LOC118275186	2.06	fatty acid-binding protein 1-like
LOC118275711	6.63	fatty acid-binding protein-like
LOC118265399	-3.88	fatty acyl-CoA reductase 1-like
LOC118265386	-3.54	fatty acyl-CoA reductase 1-like
LOC118265401	-3.21	fatty acyl-CoA reductase 1-like
LOC118280282	2.20	fatty acyl-CoA reductase 1-like
LOC118267780	-7.05	fatty acyl-CoA reductase wat-like
LOC118280298	-5.41	fatty acyl-CoA reductase wat-like
LOC118280456	-4.77	fatty acyl-CoA reductase wat-like
LOC118280458	3.24	fatty acyl-CoA reductase wat-like
LOC118280319	5.13	fatty acyl-CoA reductase wat-like
LOC118280321	5.35	fatty acyl-CoA reductase wat-like
LOC118280723	8.21	fatty acyl-CoA reductase wat-like
LOC118272338	3.34	F-box only protein 32-like isoform X1
LOC118269908	2.81	fibril-forming collagen alpha chain-like
LOC118275600	2.73	fibroin heavy chain-like
LOC118270722	4.25	fibroin heavy chain-like
LOC118270804	4.47	fibroin heavy chain-like
LOC118274569	4.51	fibroin heavy chain-like
LOC118275411	4.59	fibroin heavy chain-like
LOC118270733	4.13	fibroin heavy chain-like isoform X1
LOC118268277	2.02	flexible cuticle protein 12-like
LOC118268278	2.34	flexible cuticle protein 12-like
LOC118267000	-2.01	flightin-like isoform X1
LOC118262265	3.53	flocculation protein FLO11-like isoform X1
LOC118274056	2.91	forkhead box protein C1-like
LOC118275119	-3.29	fructose-bisphosphate aldolase-like
LOC118275099	-3.21	fructose-bisphosphate aldolase-like
LOC118274664	-2.34	fructose-bisphosphate aldolase-like isoform X1
LOC118274716	-2.21	fructose-bisphosphate aldolase-like isoform X1
LOC118272026	-3.14	fumarylacetoacetase-like
LOC118271599	-3.08	fumarylacetoacetate hydrolase domain-containing protein 2-like
LOC118272227	-2.70	fumarylacetoacetate hydrolase domain-containing protein 2-like
LOC118267111	-2.37	fungal protease inhibitor-1-like
LOC118274380	3.52	furin-like protease 2
LOC118264704	-3.64	galactokinase-like
LOC118278868	-2.19	galectin-4-like
LOC118265550	3.84	gamma-aminobutyric acid type B receptor subunit 2-like
LOC118278769	-3.72	gamma-gliadin-like
LOC118272840	-2.44	gamma-glutamyl hydrolase A-like isoform X1
LOC118270884	2.08	GAS2-like protein 3
LOC118280880	-2.78	gastrula zinc finger protein XlCGF49.1-like
LOC118265973	5.76	GATA zinc finger domain-containing protein 7-like
LOC118267984	-5.25	general odorant-binding protein 28a-like
LOC118279913	-3.60	general odorant-binding protein 69a-like
LOC118267782	-2.52	general odorant-binding protein 69a-like isoform X1
LOC118261908	3.59	general odorant-binding protein 70-like
LOC118267992	-5.65	general odorant-binding protein 72-like
LOC118270815	-2.13	general odorant-binding protein 83a-like
LOC118278869	2.24	GILT-like protein 1 isoform X1
LOC118272261	-2.11	GILT-like protein 2 isoform X1
LOC118268426	-4.73	girdin-like isoform X1
LOC118269449	-2.43	glucose 1-dehydrogenase-like
LOC118276420	-7.89	glucose dehydrogenase [FAD, quinone

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118274655	-7.30	glucose dehydrogenase [FAD, quinone
LOC118276416	-6.40	glucose dehydrogenase [FAD, quinone
LOC118265894	-6.20	glucose dehydrogenase [FAD, quinone
LOC118265750	-4.67	glucose dehydrogenase [FAD, quinone
LOC118274656	-3.86	glucose dehydrogenase [FAD, quinone
LOC118279078	-3.77	glucose dehydrogenase [FAD, quinone
LOC118276929	-3.65	glucose dehydrogenase [FAD, quinone
LOC118266265	-2.87	glucose dehydrogenase [FAD, quinone
LOC118266253	-2.61	glucose dehydrogenase [FAD, quinone
LOC118274648	2.44	glucose dehydrogenase [FAD, quinone
LOC118279376	2.97	glucose dehydrogenase [FAD, quinone
LOC118279366	3.31	glucose dehydrogenase [FAD, quinone
LOC118271174	3.84	glucose dehydrogenase [FAD, quinone
LOC118271447	4.36	glucose dehydrogenase [FAD, quinone
LOC118274802	4.63	glucose dehydrogenase [FAD, quinone
LOC118279377	5.22	glucose dehydrogenase [FAD, quinone
LOC118274823	5.91	glucose dehydrogenase [FAD, quinone
LOC118274660	6.15	glucose dehydrogenase [FAD, quinone
LOC118271457	6.39	glucose dehydrogenase [FAD, quinone
LOC118274658	7.43	glucose dehydrogenase [FAD, quinone
LOC118271446	8.08	glucose dehydrogenase [FAD, quinone
LOC118274651	8.28	glucose dehydrogenase [FAD, quinone
LOC118274653	8.95	glucose dehydrogenase [FAD, quinone
LOC118265598	-7.22	glucose dehydrogenase [FAD, quinone-like
LOC118265594	-7.09	glucose dehydrogenase [FAD, quinone-like
LOC118264728	-4.04	glucose dehydrogenase [FAD, quinone-like
LOC118265591	-2.86	glucose dehydrogenase [FAD, quinone-like
LOC118265561	-2.23	glucose dehydrogenase [FAD, quinone-like
LOC118264299	-2.06	glucose dehydrogenase [FAD, quinone-like
LOC118264370	2.64	glucose dehydrogenase [FAD, quinone-like
LOC118264389	2.82	glucose dehydrogenase [FAD, quinone-like
LOC118264860	3.37	glucose dehydrogenase [FAD, quinone-like
LOC118264388	3.55	glucose dehydrogenase [FAD, quinone-like
LOC118263014	4.92	glucose dehydrogenase [FAD, quinone-like
LOC118263006	5.30	glucose dehydrogenase [FAD, quinone-like
LOC118265446	5.98	glucose dehydrogenase [FAD, quinone-like
LOC118264453	6.50	glucose dehydrogenase [FAD, quinone-like
LOC118280537	2.24	glucose-1-phosphatase-like
LOC118277306	-2.88	glucose-6-phosphate isomerase-like
LOC118269835	-3.99	glutamate dehydrogenase, mitochondrial-like
LOC118266855	-4.74	glutamate receptor ionotropic, delta-2-like
LOC118276073	2.01	glutamate receptor ionotropic, kainate 2-like
LOC118277778	-5.66	glutathione S-transferase 1-like
LOC118277779	-5.10	glutathione S-transferase 1-like
LOC118282243	-4.40	glutathione S-transferase 1-like
LOC118261932	-3.14	glutathione S-transferase 1-like
LOC118261929	-3.04	glutathione S-transferase 1-like
LOC118282244	-2.43	glutathione S-transferase 1-like
LOC118269546	-2.28	glutathione S-transferase 1-like
LOC118261931	-2.05	glutathione S-transferase 1-like
LOC118269545	-2.01	glutathione S-transferase 1-like
LOC118270502	3.40	glutathione S-transferase 1-like
LOC118266709	-2.98	glutathione S-transferase 1-like isoform X1
LOC118271639	-2.72	glutathione S-transferase 2-like
LOC118272015	-2.71	glutathione S-transferase 2-like
LOC118272232	2.18	glutathione S-transferase 2-like
LOC118271636	2.76	glutathione S-transferase 2-like
LOC118270053	-2.78	glutathione S-transferase S1-like
LOC118270030	-4.72	glutathione S-transferase-like
LOC118278454	-3.69	glutenin, low molecular weight subunit-like
LOC118278457	2.46	glutenin, low molecular weight subunit-like
LOC118271716	-2.17	glyceraldehyde-3-phosphate dehydrogenase
LOC118268196	-2.17	glycerol-3-phosphate dehydrogenase [NAD(+), cytoplasmic-like isoform X1
LOC118263297	-2.67	glycine N-methyltransferase-like
LOC118263254	-2.55	glycine N-methyltransferase-like
LOC118281892	3.64	glycine receptor subunit alpha-2-like
LOC118278076	3.90	glycine, alanine and asparagine-rich protein-like
LOC118279384	8.54	glycine-rich cell wall structural protein 1.0-like
LOC118274210	-5.00	glycine-rich cell wall structural protein 1.8-like
LOC118278606	2.22	glycine-rich cell wall structural protein 1.8-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118278016	8.55	glycine-rich cell wall structural protein 1.8-like
LOC118273737	-4.84	glycine-rich cell wall structural protein 1.8-like isoform X1
LOC118265961	2.39	glycine-rich cell wall structural protein-like
LOC118267835	3.30	glycine-rich cell wall structural protein-like
LOC118268964	8.25	glycine-rich cell wall structural protein-like
LOC118269040	11.45	glycine-rich cell wall structural protein-like
LOC118275779	-4.82	glycine-rich protein DOT1-like
LOC118276030	-4.80	glycine-rich protein DOT1-like
LOC118267709	7.81	glycine-rich protein-like
LOC118277916	-2.94	glycine-rich RNA-binding protein 2-like
LOC118265847	-2.21	glycine-rich RNA-binding protein 3, mitochondrial-like
LOC118280330	-4.08	glycogen [starch synthase-like
LOC118280302	-3.13	glycogen [starch synthase-like isoform X1
LOC118280331	-2.62	glycogen [starch synthase-like isoform X1
LOC118265183	-2.13	glycogen phosphorylase-like
LOC118266715	2.19	glycolipid transfer protein-like
LOC118266636	-2.42	glyoxalase domain-containing protein 4-like
LOC118266627	-2.26	glyoxalase domain-containing protein 4-like
LOC118271727	-2.44	glyoxylate reductase/hydroxypyruvate reductase-like
LOC118271984	-2.99	glyoxylate reductase/hydroxypyruvate reductase-like isoform X1
LOC118270698	-4.74	G-protein coupled receptor Mth2-like isoform X1
LOC118270547	-4.24	G-protein coupled receptor Mth2-like isoform X1
LOC118280678	-3.98	granzyme-like protein 1
LOC118266836	3.11	granzyme-like protein 1
LOC118272831	2.57	GTP-binding protein REM 1-like
LOC118281868	2.23	heme peroxidase 2-like
LOC118271465	-2.56	hemicentin-1-like
LOC118271466	-2.13	hemicentin-2-like
LOC118271417	2.00	hemicentin-2-like isoform X1
LOC118271416	2.49	hemicentin-2-like isoform X1
LOC118272929	3.68	heparan sulfate 2-O-sulfotransferase pipe-like
LOC118263480	2.20	heparan-alpha-glucosaminide N-acetyltransferase-like isoform X1
LOC118268703	2.38	hepatic leukemia factor-like isoform X1
LOC118265352	6.90	hepatic triacylglycerol lipase-like
LOC118278739	5.36	hepatocyte growth factor-regulated tyrosine kinase substrate-like
LOC118276284	5.73	heterogeneous nuclear ribonucleoprotein A2 homolog 1-like
LOC118262485	-2.54	HIG1 domain family member 1A, mitochondrial-like
LOC118261746	4.94	histidine-rich glycoprotein-like
LOC118281584	6.23	histidine-rich glycoprotein-like
LOC118261742	7.14	histidine-rich glycoprotein-like
LOC118261791	7.18	histidine-rich glycoprotein-like
LOC118261800	7.20	histidine-rich glycoprotein-like
LOC118261788	7.82	histidine-rich glycoprotein-like
LOC118281476	8.39	histidine-rich glycoprotein-like
LOC118261795	8.95	histidine-rich glycoprotein-like
LOC118261751	9.41	histidine-rich glycoprotein-like
LOC118261793	9.42	histidine-rich glycoprotein-like
LOC118261752	9.73	histidine-rich glycoprotein-like
LOC118265442	10.61	histidine-rich glycoprotein-like
LOC118265488	11.59	histidine-rich glycoprotein-like
LOC118281596	11.69	histidine-rich glycoprotein-like
LOC118265472	11.73	histidine-rich glycoprotein-like
LOC118281568	11.74	histidine-rich glycoprotein-like
LOC118265441	12.33	histidine-rich glycoprotein-like
LOC118281597	12.49	histidine-rich glycoprotein-like
LOC118265473	12.65	histidine-rich glycoprotein-like
LOC118281572	12.82	histidine-rich glycoprotein-like
LOC118261991	9.98	histidine-rich protein PFHRP-II-like
LOC118262126	10.05	histidine-rich protein PFHRP-II-like
LOC118280946	6.76	histone-lysine N-methyltransferase 2D-like
LOC118272764	2.98	histone-lysine N-methyltransferase, H3 lysine-79 specific-like isoform X1
LOC118277569	-3.86	holotricin-3-like
LOC118268309	4.27	homeobox protein engrailed-2-B-like
LOC118279865	2.36	homeobox protein Hox-A1-like
LOC118273125	2.33	homeobox protein Mohawk-like
LOC118273254	-2.64	homocysteine S-methyltransferase-like
LOC118272070	-3.14	homogentisate 1,2-dioxygenase-like
LOC118262489	7.44	hormone receptor 4-like isoform X1
LOC118279116	4.73	hyaluronidase-like
LOC118265848	-2.06	hyphally-regulated protein-like isoform X1
LOC118276002	5.16	ice-structuring glycoprotein-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118262918	9.35	ichor-like
LOC118270327	-2.52	ileal sodium/bile acid cotransporter-like isoform X1
LOC118273522	2.07	inactive hydroxysteroid dehydrogenase-like protein 1
LOC118280921	-2.04	inactive peptidyl-prolyl cis-trans isomerase shutdown-like
LOC118267674	-2.10	indole-3-acetaldehyde oxidase-like
LOC118267675	-2.06	indole-3-acetaldehyde oxidase-like
LOC118261862	-5.21	inducible metalloproteinase inhibitor protein-like
LOC118282206	-3.33	inducible metalloproteinase inhibitor protein-like
LOC118282208	-2.28	inducible metalloproteinase inhibitor protein-like
LOC118282478	4.14	inducible metalloproteinase inhibitor protein-like
LOC118261951	4.44	inducible metalloproteinase inhibitor protein-like
LOC118262604	2.18	innexin inx7-like
LOC118262995	2.29	innexin inx7-like
LOC118262557	-2.06	inosine-uridine preferring nucleoside hydrolase-like
LOC118275434	-2.23	insecticyanin-B-like
LOC118263873	2.17	insulin-like growth factor-binding protein complex acid labile subunit
LOC118276404	2.24	insulin-like growth factor-binding protein complex acid labile subunit
LOC118275904	2.69	insulin-like growth factor-binding protein complex acid labile subunit
LOC118280820	4.80	integrator complex subunit 3 homolog
LOC118262522	-2.40	inter-alpha-trypsin inhibitor heavy chain H4-like isoform X1
LOC118264697	4.19	interaptin-like isoform X1
LOC118264699	4.25	interaptin-like isoform X1
LOC118269814	2.71	iodotyrosine deiodinase 1-like
LOC118268534	4.99	IQ and AAA domain-containing protein 1-like
LOC118276822	-2.02	irregular chiasm C-roughest protein-like isoform X1
LOC118272200	3.77	IST1-like protein
LOC118263778	-4.56	junctional adhesion molecule A-like
LOC118279322	-3.97	juvenile hormone epoxide hydrolase-like
LOC118279351	-3.39	juvenile hormone epoxide hydrolase-like
LOC118279248	3.18	juvenile hormone epoxide hydrolase-like
LOC118276234	-4.98	juvenile hormone esterase-like
LOC118276231	-4.22	juvenile hormone esterase-like
LOC118281026	4.17	juvenile hormone esterase-like
LOC118266127	3.11	juvenile hormone esterase-like isoform X1
LOC118275326	-2.81	kelch repeat and BTB domain-containing protein 2-like
LOC118272812	-3.55	kelch-like protein 2
LOC118272760	-3.19	kelch-like protein 2
LOC118274496	-5.83	keratin, type I cytoskeletal 10-like
LOC118275334	-4.91	keratin, type I cytoskeletal 10-like
LOC118268908	10.60	keratin, type I cytoskeletal 10-like
LOC118278260	-6.04	keratin, type I cytoskeletal 9-like
LOC118266481	-2.14	keratin, type I cytoskeletal 9-like
LOC118266476	-3.71	keratin, type II cytoskeletal 2 epidermal-like
LOC118281713	2.97	keratin, type II cytoskeletal I-like
LOC118266488	-5.68	keratin-3, type I cytoskeletal 51 kDa-like
LOC118267839	2.50	keratin-associated protein 19-2-like
LOC118267836	2.53	keratin-associated protein 19-2-like
LOC118274293	3.23	keratin-associated protein 19-2-like
LOC118274402	4.18	keratin-associated protein 19-2-like
LOC118276093	6.59	keratin-associated protein 19-2-like
LOC118276094	2.36	keratin-associated protein 6-2-like
LOC118275761	5.23	kinesin-like protein KIF18A
LOC118274147	-4.82	kynureninase-like
LOC118267147	-4.95	kynurenine 3-monooxygenase-like
LOC118279380	-2.86	kynurenine/alpha-aminoadipate aminotransferase, mitochondrial-like
LOC118267107	2.31	laccase-2-like
LOC118266894	5.65	laccase-5-like isoform X1
LOC118280431	-2.05	lachesin-like
LOC118277045	-2.89	lachesin-like isoform X1
LOC118277083	-2.34	lachesin-like isoform X1
LOC118282275	-2.55	lambda-crystallin homolog
LOC118279156	5.27	la-related protein 6-like
LOC118273122	-2.05	large neutral amino acids transporter small subunit 2-like
LOC118282151	-4.21	larval cuticle protein 16/17-like
LOC118282159	-9.05	larval cuticle protein 1-like
LOC118261853	-3.63	larval cuticle protein 1-like
LOC118282167	-3.17	larval cuticle protein 1-like
LOC118282178	-2.08	larval cuticle protein 1-like isoform X1
LOC118277988	7.31	larval cuticle protein A1A-like
LOC118277984	3.87	larval cuticle protein A2B-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118277985	13.34	larval cuticle protein A2B-like
LOC118277982	14.16	larval cuticle protein A2B-like
LOC118277980	7.28	larval cuticle protein A3A-like
LOC118277983	7.93	larval cuticle protein A3A-like
LOC118279159	8.43	larval cuticle protein A3A-like
LOC118269434	-4.14	larval cuticle protein LCP-14-like
LOC118269179	-4.06	larval cuticle protein LCP-14-like
LOC118282344	-7.30	larval cuticle protein LCP-17-like
LOC118282346	2.97	larval cuticle protein LCP-22-like
LOC118282347	4.19	larval cuticle protein LCP-22-like isoform X1
LOC118273864	-3.56	larval/pupal cuticle protein H1C-like
LOC118272499	-3.17	larval/pupal cuticle protein H1C-like
LOC118269802	3.69	larval/pupal cuticle protein H1C-like
LOC118276091	5.40	larval/pupal cuticle protein H1C-like
LOC118273370	-4.80	larval/pupal rigid cuticle protein 66-like
LOC118273336	-3.40	larval/pupal rigid cuticle protein 66-like
LOC118273654	-2.60	larval/pupal rigid cuticle protein 66-like
LOC118273319	-2.57	larval/pupal rigid cuticle protein 66-like
LOC118273639	-2.18	larval/pupal rigid cuticle protein 66-like
LOC118275158	-2.24	L-asparaginase-like
LOC118268498	-3.99	lathosterol oxidase-like isoform X1
LOC118280999	-2.45	L-dopachrome tautomerase yellow-f2-like
LOC118281155	-2.35	L-dopachrome tautomerase yellow-f2-like
LOC118281154	-2.09	L-dopachrome tautomerase yellow-f2-like
LOC118282274	2.94	L-dopachrome tautomerase yellow-f2-like
LOC118280606	2.28	lebocin-4-like
LOC118280911	2.45	leishmanolysin-like peptidase isoform X1
LOC118269675	2.99	leucine-rich repeat transmembrane protein FLRT3-like
LOC118271352	3.83	leucine-rich repeat-containing protein 24-like
LOC118269404	2.46	leucine-rich repeat-containing protein 39-like
LOC118265769	3.80	leucine-rich repeat-containing protein 49-like
LOC118263065	3.47	leucine-rich repeat-containing protein 57-like isoform X1
LOC118278050	-2.63	leukocyte elastase inhibitor-like
LOC118277884	-2.14	leukocyte elastase inhibitor-like
LOC118267564	2.41	leukocyte surface antigen CD53-like
LOC118264583	-4.39	lipase 1-like
LOC118264586	-4.29	lipase 1-like
LOC118277642	-3.70	lipase 1-like
LOC118271511	-3.68	lipase 1-like
LOC118264830	-3.10	lipase 1-like
LOC118272791	-5.35	lipase 3-like
LOC118272788	-4.32	lipase 3-like
LOC118272789	-4.19	lipase 3-like
LOC118272790	-2.97	lipase 3-like
LOC118275653	-2.71	lipase 3-like
LOC118275483	-2.35	lipase 3-like
LOC118268348	4.10	lipase 3-like
LOC118268083	4.47	lipase 3-like
LOC118262771	4.89	lipase 3-like
LOC118273710	2.86	lipase 3-like isoform X1
LOC118265419	7.02	lipase member H-A-like isoform X1
LOC118273140	-3.64	lipase member H-like
LOC118273242	-3.60	lipase member H-like
LOC118273155	-3.32	lipase member H-like
LOC118273252	-2.96	lipase member H-like
LOC118273148	-2.82	lipase member H-like
LOC118273165	-2.36	lipase member H-like
LOC118265609	7.64	lipase member H-like
LOC118275811	5.51	lipase member I-like
LOC118272575	4.93	lipase member I-like isoform X1
LOC118272619	5.69	lipase member I-like isoform X1
LOC118281624	-2.62	lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial-like
LOC118263908	2.69	lipopolysaccharide-induced tumor necrosis factor-alpha factor homolog
LOC118277908	-5.05	loricrin-like
LOC118265619	5.43	loricrin-like
LOC118272241	7.03	low density lipoprotein receptor adapter protein 1-B-like
LOC118266454	2.04	LOW QUALITY PROTEIN: acetylcholinesterase-like
LOC118276125	-4.69	LOW QUALITY PROTEIN: acyl-CoA Delta(11) desaturase-like
LOC118271573	-2.98	LOW QUALITY PROTEIN: adenosine kinase-like
LOC118279947	-2.38	LOW QUALITY PROTEIN: aldo-keto reductase AKR2E4-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118274159	-2.75	LOW QUALITY PROTEIN: arrestin domain-containing protein 17-like
LOC118269941	9.15	LOW QUALITY PROTEIN: cadherin-89D-like
LOC118264954	-2.17	LOW QUALITY PROTEIN: cadherin-related tumor suppressor-like
LOC118273450	-2.71	LOW QUALITY PROTEIN: carbonyl reductase [NADPH 3-like
LOC118271482	-4.38	LOW QUALITY PROTEIN: carboxypeptidase B-like
LOC118274156	-3.54	LOW QUALITY PROTEIN: cell surface glycoprotein 1-like
LOC118265222	6.68	LOW QUALITY PROTEIN: circadian clock-controlled protein daywake-like
LOC118269093	2.49	LOW QUALITY PROTEIN: coiled-coil-helix-coiled-coil-helix domain-containing protein 10, mitochondrial-like
LOC118268156	-2.85	LOW QUALITY PROTEIN: contactin-like
LOC118267194	2.02	LOW QUALITY PROTEIN: cytochrome P450 18a1-like
LOC118263350	-2.39	LOW QUALITY PROTEIN: cytochrome P450 4g15-like
LOC118261903	5.10	LOW QUALITY PROTEIN: decaprenyl-diphosphate synthase subunit 2-like
LOC118277633	6.96	LOW QUALITY PROTEIN: E3 ubiquitin-protein ligase RNF123-like
LOC118266191	5.33	LOW QUALITY PROTEIN: esterase E4-like
LOC118264707	-3.23	LOW QUALITY PROTEIN: galactokinase-like
LOC118276784	3.29	LOW QUALITY PROTEIN: glucose dehydrogenase [FAD, quinone
LOC118273179	-2.18	LOW QUALITY PROTEIN: glucose-6-phosphate 1-dehydrogenase-like
LOC118269821	-3.30	LOW QUALITY PROTEIN: glutamate dehydrogenase, mitochondrial-like
LOC118267113	-6.14	LOW QUALITY PROTEIN: glutathione S-transferase 1-like
LOC118267525	2.75	LOW QUALITY PROTEIN: heme transporter hrg1-B-like
LOC118272663	3.17	LOW QUALITY PROTEIN: histamine H2 receptor-like
LOC118261744	8.75	LOW QUALITY PROTEIN: histidine-rich glycoprotein-like
LOC118268000	9.00	LOW QUALITY PROTEIN: histone acetyltransferase p300-like
LOC118270109	2.53	LOW QUALITY PROTEIN: kinesin-like protein KIF21B
LOC118276760	3.25	LOW QUALITY PROTEIN: low-density lipoprotein receptor-like
LOC118275005	-3.48	LOW QUALITY PROTEIN: luciferin 4-monooxygenase-like
LOC118281883	-2.08	LOW QUALITY PROTEIN: methylenetetrahydrofolate reductase 2-like
LOC118273878	4.34	LOW QUALITY PROTEIN: mucin-3A-like
LOC118280674	2.03	LOW QUALITY PROTEIN: mucin-5AC-like
LOC118268973	3.13	LOW QUALITY PROTEIN: mutS protein homolog 4-like
LOC118263793	3.13	LOW QUALITY PROTEIN: N-acetylglucosamine-6-phosphate deacetylase-like
LOC118268159	-2.23	LOW QUALITY PROTEIN: neurexin-4-like
LOC118267427	4.33	LOW QUALITY PROTEIN: nuclear hormone receptor FTZ-F1-like
LOC118273318	2.39	LOW QUALITY PROTEIN: probable G-protein coupled receptor Mth-like 4
LOC118275786	-2.08	LOW QUALITY PROTEIN: probable maleylacetoacetate isomerase 2
LOC118280038	2.22	LOW QUALITY PROTEIN: protein FAM214A-like
LOC118280936	2.27	LOW QUALITY PROTEIN: protein javelin-like
LOC118263458	-2.91	LOW QUALITY PROTEIN: protein UBASH3A homolog
LOC118269800	8.45	LOW QUALITY PROTEIN: pupal cuticle protein C1B-like
LOC118261789	9.71	LOW QUALITY PROTEIN: pupal cuticle protein Edg-84A-like
LOC118281339	6.92	LOW QUALITY PROTEIN: putative GPI-anchored protein pfl2
LOC118273838	-3.24	LOW QUALITY PROTEIN: regulating synaptic membrane exocytosis protein 2-like
LOC118266607	-3.32	LOW QUALITY PROTEIN: sulfotransferase 1E1-like
LOC118274780	-2.09	LOW QUALITY PROTEIN: tetratricopeptide repeat protein 28-like
LOC118265105	2.36	LOW QUALITY PROTEIN: thyrostimulin beta-5 subunit-like
LOC118279414	2.31	LOW QUALITY PROTEIN: transcription factor Ken-like
LOC118279630	2.69	LOW QUALITY PROTEIN: transcription factor SPT20 homolog
LOC118269739	5.75	LOW QUALITY PROTEIN: trypsin-like
LOC118263791	-3.15	LOW QUALITY PROTEIN: uncharacterized oxidoreductase YrbE-like
LOC118262222	8.41	LOW QUALITY PROTEIN: uncharacterized protein LOC118262222
LOC118263418	-3.82	LOW QUALITY PROTEIN: uncharacterized protein LOC118263418
LOC118263558	-3.18	LOW QUALITY PROTEIN: uncharacterized protein LOC118263558
LOC118264824	2.93	LOW QUALITY PROTEIN: uncharacterized protein LOC118264824
LOC118264827	2.54	LOW QUALITY PROTEIN: uncharacterized protein LOC118264827
LOC118265044	7.90	LOW QUALITY PROTEIN: uncharacterized protein LOC118265044
LOC118265094	5.78	LOW QUALITY PROTEIN: uncharacterized protein LOC118265094
LOC118267020	2.46	LOW QUALITY PROTEIN: uncharacterized protein LOC118267020
LOC118267615	6.34	LOW QUALITY PROTEIN: uncharacterized protein LOC118267615
LOC118267755	6.18	LOW QUALITY PROTEIN: uncharacterized protein LOC118267755
LOC118267871	-2.20	LOW QUALITY PROTEIN: uncharacterized protein LOC118267871
LOC118269609	3.29	LOW QUALITY PROTEIN: uncharacterized protein LOC118269609
LOC118270144	-2.79	LOW QUALITY PROTEIN: uncharacterized protein LOC118270144
LOC118270667	2.19	LOW QUALITY PROTEIN: uncharacterized protein LOC118270667
LOC118270982	3.15	LOW QUALITY PROTEIN: uncharacterized protein LOC118270982
LOC118271043	8.76	LOW QUALITY PROTEIN: uncharacterized protein LOC118271043
LOC118273359	8.71	LOW QUALITY PROTEIN: uncharacterized protein LOC118273359
LOC118276079	8.41	LOW QUALITY PROTEIN: uncharacterized protein LOC118276079
LOC118276623	2.66	LOW QUALITY PROTEIN: uncharacterized protein LOC118276623
LOC118277148	-2.33	LOW QUALITY PROTEIN: uncharacterized protein LOC118277148

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118280777	3.22	LOW QUALITY PROTEIN: uncharacterized protein LOC118280777
LOC118281364	3.55	LOW QUALITY PROTEIN: uncharacterized protein LOC118281364
LOC118282020	5.86	LOW QUALITY PROTEIN: uncharacterized protein LOC118282020
LOC118273156	-2.99	LOW QUALITY PROTEIN: venom serine carboxypeptidase-like
LOC118274931	-2.04	LOW QUALITY PROTEIN: venom serine carboxypeptidase-like
LOC118273705	2.33	LOW QUALITY PROTEIN: villin-like protein quail
LOC118274873	-9.71	luciferin 4-monooxygenase-like
LOC118274572	-5.09	luciferin 4-monooxygenase-like
LOC118281710	-4.68	luciferin 4-monooxygenase-like
LOC118274486	-4.62	luciferin 4-monooxygenase-like
LOC118274574	-3.38	luciferin 4-monooxygenase-like
LOC118274571	-3.22	luciferin 4-monooxygenase-like
LOC118280070	-2.38	luciferin 4-monooxygenase-like
LOC118274573	-4.58	luciferin 4-monooxygenase-like isoform X1
LOC118266603	-6.27	luciferin sulfotransferase-like
LOC118266605	-5.97	luciferin sulfotransferase-like
LOC118266604	-2.80	luciferin sulfotransferase-like
LOC118281846	-3.05	lymphocyte antigen 75-like
LOC118272562	2.23	lysophosphatidylcholine acyltransferase-like
LOC118271261	3.23	lysoplasmalogenase-like
LOC118271619	-4.64	lysozyme-like
LOC118270004	-2.35	lysozyme-like
LOC118265277	2.86	lysozyme-like
LOC118265132	5.98	lysozyme-like
LOC118274702	2.86	major facilitator-type transporter sorT-like
LOC118265350	-2.29	malate dehydrogenase, cytoplasmic-like
LOC118265523	-2.14	malate dehydrogenase, cytoplasmic-like
LOC118274552	-2.18	malate dehydrogenase, mitochondrial-like isoform X1
LOC118269324	4.71	malate dehydrogenase, mitochondrial-like isoform X1
LOC118273030	-2.62	maltase A1-like
LOC118267648	5.71	mantle protein-like
LOC118276238	3.69	MAPK-interacting and spindle-stabilizing protein-like
LOC118280764	-3.66	mast cell protease 1A-like
LOC118280570	-3.34	mast cell protease 1A-like
LOC118280681	-3.34	mast cell protease 1A-like
LOC118280567	-5.53	mast cell protease 3-like
LOC118280760	-2.47	mast cell protease 3-like
LOC118270949	2.63	MATH and LRR domain-containing protein PFE0570w-like
LOC118264236	2.98	MATH and LRR domain-containing protein PFE0570w-like
LOC118261986	5.08	MATH and LRR domain-containing protein PFE0570w-like
LOC118276931	10.30	mediator of RNA polymerase II transcription subunit 15-like
LOC118276902	10.37	mediator of RNA polymerase II transcription subunit 15-like isoform X1
LOC118265532	-2.96	medium-chain acyl-CoA ligase ACSF2, mitochondrial-like
LOC118270791	-3.15	melanotransferrin-like
LOC118268948	3.86	melatonin-related receptor-like isoform X1
LOC118271569	-3.40	membrane-bound alkaline phosphatase-like
LOC118271570	-2.81	membrane-bound alkaline phosphatase-like isoform X1
LOC118272627	-2.51	methanethiol oxidase-like
LOC118262355	-2.30	microsomal glutathione S-transferase 1-like
LOC118281239	-2.84	microvitellogenin-like
LOC118265038	8.23	midnolin homolog
LOC118264784	-2.36	MIF-like protein mif-2
LOC118271740	-2.32	mitochondrial 2-oxoglutarate/malate carrier protein-like
LOC118276975	-2.84	mitochondrial enolase superfamily member 1-like
LOC118270416	-2.36	mitochondrial enolase superfamily member 1-like
LOC118278295	6.00	mitochondrial glutamate carrier 1-like
LOC118269683	-2.27	mitochondrial pyruvate carrier 1-like
LOC118269613	-2.03	mitochondrial pyruvate carrier 1-like
LOC118278440	-3.92	modular serine protease-like
LOC118274611	-5.90	monocarboxylate transporter 1-like
LOC118271952	3.00	monocarboxylate transporter 4-like isoform X1
LOC118272007	3.35	monocarboxylate transporter 4-like isoform X1
LOC118263449	-4.20	monocarboxylate transporter 9-like
LOC118272336	3.15	mpv17-like protein
LOC118279179	5.39	mucin-17-like isoform X1
LOC118266000	-4.67	mucin-19-like isoform X1
LOC118265872	-4.42	mucin-19-like isoform X1
LOC118280089	-2.76	mucin-22-like isoform X1
LOC118276098	-2.42	mucin-2-like
LOC118265097	2.98	mucin-2-like
LOC118278048	4.34	mucin-2-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118278119	5.85	mucin-3A-like
LOC118279275	3.13	mucin-5AC-like
LOC118276086	3.53	mucin-5AC-like
LOC118273996	4.68	mucin-5AC-like
LOC118268441	8.21	mucin-5AC-like isoform X1
LOC118269877	-2.51	mucin-5B-like
LOC118271848	3.04	mucin-6-like isoform X1
LOC118262367	-2.31	multifunctional protein ADE2-like
LOC118262526	-2.24	multifunctional protein ADE2-like
LOC118268599	2.71	multiple epidermal growth factor-like domains protein 10
LOC118269393	-2.00	multiple inositol polyphosphate phosphatase 1-like
LOC118261984	2.46	multiple inositol polyphosphate phosphatase 1-like
LOC118279279	2.88	muscle M-line assembly protein unc-89-like
LOC118280714	-3.93	myb/SANT-like DNA-binding domain-containing protein 3
LOC118261983	8.75	myb-like protein F isoform X1
LOC118270257	4.77	mycosubtilin synthase subunit C-like
LOC118270248	5.85	mycosubtilin synthase subunit C-like
LOC118264510	-2.19	myoglobin-like
LOC118263540	4.45	myosin-3-like isoform X1
LOC118263542	3.22	myosin-4-like isoform X1
LOC118270226	-3.52	myrosinase 1-like
LOC118277638	2.85	myrosinase 1-like
LOC118277675	3.42	myrosinase 1-like
LOC118270227	-2.73	myrosinase 1-like isoform X1
LOC118270798	3.13	myrosinase 1-like isoform X1
LOC118270752	3.37	myrosinase 1-like isoform X1
LOC118276964	2.12	N-acetylgalactosamine kinase-like
LOC118275853	-5.15	N-acetylneuraminate lyase-like isoform X1
LOC118279333	2.78	NADPH oxidase 5-like
LOC118280864	4.44	nascent polypeptide-associated complex subunit alpha, muscle-specific form-like
LOC118262896	2.61	neprilysin-2-like isoform X1
LOC118263251	3.59	neprilysin-4-like
LOC118263294	4.49	neprilysin-4-like
LOC118264023	2.20	neprilysin-4-like isoform X1
LOC118276446	3.15	neurofilament medium polypeptide-like
LOC118274628	-4.54	neurogenic locus notch homolog protein 3-like isoform X1
LOC118267572	8.89	neurogenic locus protein delta-like isoform X1
LOC118273655	2.03	neurogenic protein big brain-like
LOC118262827	4.33	neuroligin-4, X-linked-like isoform X1
LOC118277877	2.06	neuronal PAS domain-containing protein 4B-like
LOC118275923	-6.05	neuropeptide-like protein 31
LOC118262123	6.31	neurotrophin 1-like
LOC118276613	-2.30	neutral alpha-glucosidase AB-like isoform X1
LOC118265043	2.61	neutral ceramidase-like
LOC118265404	2.63	neutral ceramidase-like
LOC118265117	-2.60	nidogen-like
LOC118266177	2.60	ninjurin-1-like isoform X1
LOC118266978	-2.82	nitric oxide synthase-like
LOC118278472	5.10	non-classical arabinogalactan protein 31-like
LOC118276608	-4.52	nose resistant to fluoxetine protein 6-like
LOC118266467	-4.01	nose resistant to fluoxetine protein 6-like
LOC118266134	-3.65	nose resistant to fluoxetine protein 6-like
LOC118279120	-3.32	nose resistant to fluoxetine protein 6-like
LOC118266008	-3.26	nose resistant to fluoxetine protein 6-like
LOC118266053	-3.14	nose resistant to fluoxetine protein 6-like
LOC118263678	3.21	nose resistant to fluoxetine protein 6-like
LOC118263671	3.51	nose resistant to fluoxetine protein 6-like
LOC118274733	4.92	nose resistant to fluoxetine protein 6-like
LOC118262496	6.44	nose resistant to fluoxetine protein 6-like
LOC118266468	6.49	nose resistant to fluoxetine protein 6-like
LOC118262975	7.07	nose resistant to fluoxetine protein 6-like
LOC118266462	8.40	nose resistant to fluoxetine protein 6-like
LOC118275143	-2.23	NPC intracellular cholesterol transporter 2-like
LOC118275380	7.13	nucleoside diphosphate kinase 7-like
LOC118265078	-4.35	O-acyltransferase like protein-like
LOC118265308	-3.21	O-acyltransferase like protein-like
LOC118279400	-2.83	O-acyltransferase like protein-like
LOC118265077	-2.48	O-acyltransferase like protein-like
LOC118276609	2.11	O-acyltransferase like protein-like
LOC118270548	3.66	octopamine receptor beta-1R-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118270587	3.97	octopamine receptor beta-1R-like
LOC118266412	-5.30	odorant-binding protein 59a-like
LOC118272567	-3.53	ommochrome-binding protein-like
LOC118277314	2.73	orexin receptor type 1-like
LOC118276478	-2.19	organic cation transporter protein-like
LOC118282149	2.74	organic cation transporter protein-like
LOC118263733	3.84	organic cation transporter protein-like
LOC118280511	5.94	organic cation transporter protein-like
LOC118280301	6.18	organic cation transporter protein-like
LOC118282153	-2.30	organic cation transporter protein-like isoform X1
LOC118276256	2.62	organic cation transporter-like protein
LOC118277783	2.72	organic cation transporter-like protein
LOC118269968	-6.25	organic cation/carnitine transporter 7-like
LOC118270037	2.67	organic cation/carnitine transporter 7-like
LOC118269771	-2.50	organic cation/carnitine transporter 7-like isoform X1
LOC118279308	-3.35	ovalbumin-related protein X-like
LOC118271176	2.27	paired box protein Pax-6-like isoform X1
LOC118263701	-2.76	paired mesoderm homeobox protein 2A-like isoform X1
LOC118265237	2.25	palmitoyltransferase ZDHHC23-like
LOC118273267	-7.35	pancreatic lipase-related protein 2-like
LOC118273275	-6.85	pancreatic lipase-related protein 2-like
LOC118274199	-5.10	pancreatic lipase-related protein 2-like
LOC118274201	-2.99	pancreatic lipase-related protein 2-like
LOC118265369	-2.32	pancreatic lipase-related protein 2-like
LOC118264914	-2.28	pancreatic lipase-related protein 2-like
LOC118278929	2.02	pancreatic lipase-related protein 2-like
LOC118265265	5.82	pancreatic lipase-related protein 2-like
LOC118274200	-6.84	pancreatic triacylglycerol lipase-like
LOC118273885	-6.70	pancreatic triacylglycerol lipase-like
LOC118277406	-5.91	pancreatic triacylglycerol lipase-like
LOC118273258	-5.02	pancreatic triacylglycerol lipase-like
LOC118273259	-4.64	pancreatic triacylglycerol lipase-like
LOC118277405	-4.54	pancreatic triacylglycerol lipase-like
LOC118273205	-4.44	pancreatic triacylglycerol lipase-like
LOC118273225	-4.36	pancreatic triacylglycerol lipase-like
LOC118273213	-3.42	pancreatic triacylglycerol lipase-like
LOC118273181	-3.01	pancreatic triacylglycerol lipase-like
LOC118274292	-2.81	pancreatic triacylglycerol lipase-like
LOC118273173	-2.79	pancreatic triacylglycerol lipase-like
LOC118273884	-2.70	pancreatic triacylglycerol lipase-like
LOC118281263	-2.69	pancreatic triacylglycerol lipase-like
LOC118281256	-2.18	pancreatic triacylglycerol lipase-like
LOC118273883	-5.19	pancreatic triacylglycerol lipase-like isoform X1
LOC118273882	-4.07	pancreatic triacylglycerol lipase-like isoform X1
LOC118277404	-3.20	pancreatic triacylglycerol lipase-like isoform X1
LOC118262060	3.83	pancreatic triacylglycerol lipase-like isoform X1
LOC118263044	-4.01	para-nitrobenzyl esterase-like
LOC118262756	-3.22	para-nitrobenzyl esterase-like
LOC118262239	-2.61	para-nitrobenzyl esterase-like
LOC118266649	3.22	patched domain-containing protein 3-like
LOC118266705	3.25	patched domain-containing protein 3-like
LOC118262097	6.64	paternally-expressed gene 3 protein-like
LOC118261899	-2.61	paxillin-like isoform X1
LOC118281639	-2.13	PDZ and LIM domain protein Zasp-like isoform X1
LOC118266470	8.78	PE-PGRS family protein PE_PGRS16-like
LOC118268059	2.20	peptide transporter family 1-like isoform X1
LOC118274475	-2.49	peptidoglycan-recognition protein LB-like
LOC118268825	-2.02	perilipin-4-like isoform X1
LOC118262077	-4.57	peroxidase-like
LOC118282279	-4.06	peroxidase-like
LOC118282278	-2.77	peroxidase-like
LOC118280597	-2.45	peroxidase-like
LOC118280613	-2.07	peroxidase-like
LOC118269917	3.86	peroxidase-like isoform X1
LOC118269931	5.18	peroxidase-like isoform X1
LOC118269806	-2.84	peroxisomal membrane protein 11C-like
LOC118279229	-3.66	phenoloxidase-activating factor 2-like
LOC118274872	-7.58	phosphatidylethanolamine-binding protein homolog F40A3.3-like
LOC118277526	-2.05	phosphoenolpyruvate carboxykinase [GTP
LOC118271607	-2.21	phosphoglucomutase-like
LOC118262502	-2.45	phosphoglycerate kinase-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118264978	6.46	phospholipase A1 member A-like
LOC118265142	2.60	phospholipase A1-like
LOC118276475	3.73	phospholipase A1-like
LOC118277646	4.24	phospholipase A1-like
LOC118274943	6.25	phospholipase A2-like
LOC118268474	6.30	phospholipase B1, membrane-associated-like
LOC118268476	6.56	phospholipase B1, membrane-associated-like
LOC118281765	-3.02	phosphoribosylformylglycinamidine synthase-like
LOC118279126	3.53	photoreceptor-specific nuclear receptor-like
LOC118275868	-5.58	phytanoyl-CoA dioxygenase, peroxisomal-like
LOC118281922	-5.14	phytanoyl-CoA dioxygenase, peroxisomal-like
LOC118274725	4.02	pickpocket protein 28-like isoform X1
LOC118274977	2.00	piggyBac transposable element-derived protein 2-like
LOC118270917	-2.99	piggyBac transposable element-derived protein 3-like
LOC118280179	2.98	piggyBac transposable element-derived protein 3-like
LOC118265584	3.55	piggyBac transposable element-derived protein 3-like isoform X1
LOC118265775	-3.00	piggyBac transposable element-derived protein 4-like
LOC118267393	2.93	piggyBac transposable element-derived protein 4-like
LOC118275718	4.41	piggyBac transposable element-derived protein 4-like
LOC118266692	11.38	pollen-specific leucine-rich repeat extensin-like protein 4
LOC118276552	-4.24	poly(A) polymerase type 3-like
LOC118263865	2.12	polyprenol reductase-like
LOC118281996	2.68	polyprenol reductase-like
LOC118281632	2.26	popeye domain-containing protein 3-like isoform X1
LOC118276891	-2.49	porphobilinogen deaminase-like
LOC118263573	3.33	potassium channel subfamily K member 18-like isoform X1
LOC118276158	-2.30	potassium channel subfamily K member 1-like isoform X1
LOC118276159	-2.07	potassium channel subfamily K member 1-like isoform X1
LOC118274833	3.14	poxin-like isoform X1
LOC118263665	11.67	pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16-like
LOC118266944	9.89	prisilkin-39-like
LOC118264573	-2.97	probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial
LOC118267917	-2.09	probable 4-coumarate--CoA ligase 3
LOC118271250	7.21	probable cytochrome P450 301a1, mitochondrial
LOC118268212	3.01	probable cytochrome P450 304a1
LOC118268370	3.30	probable cytochrome P450 304a1
LOC118266520	3.49	probable cytochrome P450 305a1 isoform X1
LOC118266312	5.55	probable cytochrome P450 49a1
LOC118265707	6.90	probable cytochrome P450 49a1
LOC118268527	-4.70	probable cytochrome P450 6a13
LOC118268605	-3.81	probable cytochrome P450 6a13
LOC118268604	-3.55	probable cytochrome P450 6a13
LOC118268618	-3.53	probable cytochrome P450 6a13
LOC118275709	9.94	probable cytochrome P450 6a14
LOC118274407	6.20	probable cytochrome P450 6a17
LOC118281706	-2.28	probable DNA mismatch repair protein Msh6 isoform X1
LOC118266977	2.04	probable G-protein coupled receptor Mth-like 1
LOC118275819	2.61	probable G-protein coupled receptor Mth-like 3
LOC118276040	-6.12	probable H/ACA ribonucleoprotein complex subunit 1
LOC118275557	-2.26	probable maleylacetoacetate isomerase 2 isoform X1
LOC118277655	-4.07	probable metabolite transport protein CsbC
LOC118277652	-3.47	probable metabolite transport protein CsbC
LOC118266428	-2.05	probable methylcrotonoyl-CoA carboxylase beta chain, mitochondrial
LOC118267546	-2.81	probable methylmalonate-semialdehyde dehydrogenase [acylating, mitochondrial
LOC118267560	-2.37	probable methylmalonate-semialdehyde dehydrogenase [acylating, mitochondrial
LOC118279845	5.72	probable nuclear hormone receptor HR3 isoform X1
LOC118279815	6.02	probable nuclear hormone receptor HR3 isoform X1
LOC118273391	2.14	probable nuclear hormone receptor HR38 isoform X1
LOC118270681	-2.77	probable peroxisomal acyl-coenzyme A oxidase 1
LOC118270783	-2.46	probable peroxisomal acyl-coenzyme A oxidase 1
LOC118270794	-2.43	probable peroxisomal acyl-coenzyme A oxidase 1
LOC118279187	-2.03	probable phytanoyl-CoA dioxygenase
LOC118277157	6.44	probable salivary secreted peptide
LOC118277155	6.56	probable salivary secreted peptide
LOC118277156	6.62	probable salivary secreted peptide
LOC118265976	6.08	probable serine/threonine-protein kinase clkA
LOC118282388	6.16	probable serine/threonine-protein kinase kinX isoform X1
LOC118282406	6.68	probable serine/threonine-protein kinase kinX isoform X1
LOC118266359	7.79	probable serine/threonine-protein kinase nek3
LOC118277175	-3.46	probable serine/threonine-protein kinase tsuA

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118263320	-2.07	probable transaldolase
LOC118267639	4.12	probable tubulin polyglutamylase ttll-15
LOC118267638	2.68	probable tubulin polyglutamylase ttll-15 isoform X1
LOC118282369	-2.05	probable tubulin polyglutamylase TTLL2 isoform X1
LOC118269929	7.46	proclotting enzyme-like
LOC118278272	7.74	proclotting enzyme-like isoform X1
LOC118280634	2.48	proline-, glutamic acid- and leucine-rich protein 1-like
LOC118272664	6.83	proline-rich protein 27-like
LOC118273865	7.36	proline-rich protein 27-like
LOC118268649	6.38	proline-rich protein 4-like
LOC118268648	9.86	proline-rich protein 4-like
LOC118275417	10.04	proline-rich protein 4-like
LOC118279931	4.47	pro-neuropeptide Y-like
LOC118276937	2.89	pro-resilin-like
LOC118276983	3.00	pro-resilin-like
LOC118276575	4.05	pro-resilin-like
LOC118276778	4.63	pro-resilin-like
LOC118276590	4.95	pro-resilin-like
LOC118276873	5.68	pro-resilin-like
LOC118276697	6.22	pro-resilin-like
LOC118269958	6.43	pro-resilin-like
LOC118276732	6.78	pro-resilin-like
LOC118276729	8.02	pro-resilin-like
LOC118274217	9.50	pro-resilin-like
LOC118267795	10.58	pro-resilin-like
LOC118276841	5.33	pro-resilin-like isoform X1
LOC118264792	-3.79	prostaglandin reductase 1-like
LOC118264101	-2.29	prostaglandin reductase 1-like
LOC118271356	-2.38	prostatic acid phosphatase-like
LOC118281121	-2.23	protein anon-37Cs-like isoform X1
LOC118264936	11.40	protein apnoia-like
LOC118269582	2.27	protein artichoke-like
LOC118269723	-2.59	protein CREG1-like isoform X1
LOC118265053	2.06	protein croquemort-like
LOC118275195	-7.66	protein D3-like
LOC118274870	-2.26	protein D3-like
LOC118265859	2.03	protein dead ringer-like
LOC118280343	-2.02	protein dj-1beta-like
LOC118276076	-2.17	protein enabled homolog
LOC118272824	2.95	protein FAM166B-like
LOC118280037	2.27	protein FAM214A-like
LOC118280035	2.26	protein FAM214A-like isoform X1
LOC118273899	2.05	protein fem-1 homolog CG6966-like isoform X1
LOC118274024	2.14	protein fem-1 homolog CG6966-like isoform X1
LOC118265418	-4.08	protein fuzzy homolog
LOC118269074	-2.15	protein IMPACT-A-like isoform X1
LOC118272087	3.08	protein KIAA0556-like
LOC118280743	-2.73	protein lethal(2)essential for life-like
LOC118276394	-2.62	protein lethal(2)essential for life-like
LOC118282420	-2.72	protein lethal(3)malignant blood neoplasm 1-like isoform X1
LOC118282238	2.07	protein lin-28 homolog isoform X1
LOC118277943	4.05	protein masquerade-like isoform X1
LOC118271033	2.63	protein mesh isoform X1
LOC118279541	-7.32	protein mono-ADP-ribosyltransferase PARP16-like
LOC118265375	2.28	protein nubbin-like
LOC118274195	-2.39	protein obstructor-E-like
LOC118263126	2.82	protein obstructor-E-like
LOC118262892	2.92	protein obstructor-E-like
LOC118263124	6.14	protein obstructor-E-like
LOC118263123	3.49	protein obstructor-E-like isoform X1
LOC118263754	3.45	protein O-mannosyl-transferase TMTC1-like
LOC118276104	6.47	protein piccolo-like
LOC118271418	3.19	protein rolling stone-like
LOC118278806	2.47	protein rolling stone-like isoform X1
LOC118277996	-3.82	protein scarlet-like
LOC118276911	-3.62	protein scarlet-like
LOC118267201	-3.26	protein scarlet-like
LOC118267200	-2.67	protein scarlet-like isoform X1
LOC118267228	4.51	protein singles bar-like
LOC118270780	3.28	protein Skeletor, isoforms D/E-like isoform X1
LOC118272064	2.91	protein spaetzle 3-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118272073	5.88	protein spaetzle 4-like isoform X1
LOC118281631	2.34	protein spaetzle 5-like
LOC118262012	2.37	protein spaetzle 5-like
LOC118276515	-4.59	protein takeout-like
LOC118263049	3.73	protein takeout-like
LOC118262192	3.86	protein takeout-like
LOC118262220	4.87	protein takeout-like
LOC118263038	5.06	protein takeout-like
LOC118275183	8.37	protein takeout-like
LOC118276042	2.67	protein TANC2-like isoform X1
LOC118278759	-2.20	protein TEX261-like
LOC118262046	-2.03	protein THEM6-like
LOC118277290	-2.38	protein tyrosine phosphatase domain-containing protein 1-like
LOC118278074	-2.19	protein unc-79 homolog
LOC118267199	-3.62	protein white-like
LOC118267197	-3.80	protein white-like isoform X1
LOC118264029	3.25	protein yellow-like
LOC118264592	5.40	protein yellow-like
LOC118263854	9.10	protein yellow-like
LOC118264674	4.63	protein yellow-like isoform X1
LOC118268714	2.63	protein yippee-like 2 isoform X1
LOC118268388	2.86	proteoglycan 4-like
LOC118267805	6.76	proteoglycan 4-like isoform X1
LOC118263852	2.50	proton-coupled amino acid transporter-like protein CG1139
LOC118263727	3.02	proton-coupled amino acid transporter-like protein CG1139 isoform X1
LOC118263387	3.41	proton-coupled amino acid transporter-like protein CG1139 isoform X2
LOC118263666	2.90	proton-coupled amino acid transporter-like protein pathetic
LOC118263719	3.28	proton-coupled amino acid transporter-like protein pathetic
LOC118266474	-3.74	proton-coupled folate transporter-like
LOC118262041	-3.22	proton-coupled folate transporter-like
LOC118265959	-2.78	proton-coupled folate transporter-like
LOC118282461	-2.26	proton-coupled folate transporter-like
LOC118265965	3.30	proton-coupled folate transporter-like
LOC118266345	3.87	proton-coupled folate transporter-like
LOC118262804	-2.43	proton-coupled folate transporter-like isoform X1
LOC118263987	3.11	pupal cuticle protein 20-like
LOC118263985	3.69	pupal cuticle protein 20-like
LOC118263980	6.63	pupal cuticle protein 20-like
LOC118263981	7.20	pupal cuticle protein 20-like
LOC118263986	4.01	pupal cuticle protein 20-like isoform X1
LOC118265850	-5.91	pupal cuticle protein 27-like
LOC118266107	-4.20	pupal cuticle protein 27-like
LOC118265977	5.19	pupal cuticle protein 36a-like
LOC118265842	6.63	pupal cuticle protein 36a-like isoform X1
LOC118266482	-4.56	pupal cuticle protein 36-like
LOC118265849	-3.90	pupal cuticle protein 36-like
LOC118266051	-2.56	pupal cuticle protein 36-like
LOC118265846	3.20	pupal cuticle protein 36-like
LOC118266013	3.29	pupal cuticle protein 36-like
LOC118272786	4.51	pupal cuticle protein C1B-like
LOC118272785	7.50	pupal cuticle protein C1B-like
LOC118272876	8.59	pupal cuticle protein C1B-like
LOC118272659	8.96	pupal cuticle protein C1B-like
LOC118279656	-7.44	pupal cuticle protein PCP52-like
LOC118279657	-5.51	pupal cuticle protein PCP52-like
LOC118274730	2.37	pupal cuticle protein-like
LOC118281116	-2.24	putative aminopeptidase W07G4.4
LOC118279876	2.56	putative ammonium transporter 2
LOC118269972	-3.40	putative carbonic anhydrase 5
LOC118275034	-2.44	putative cystathionine gamma-lyase 2
LOC118268608	4.67	putative defense protein 3
LOC118268170	6.06	putative defense protein 3
LOC118273606	2.35	putative defense protein Hdd11
LOC118280404	-5.98	putative fatty acyl-CoA reductase CG5065
LOC118265377	-3.08	putative fatty acyl-CoA reductase CG5065
LOC118265535	-2.70	putative fatty acyl-CoA reductase CG5065
LOC118280549	-2.34	putative fatty acyl-CoA reductase CG5065
LOC118280222	2.02	putative fatty acyl-CoA reductase CG5065
LOC118265593	3.53	putative fatty acyl-CoA reductase CG5065
LOC118280297	3.72	putative fatty acyl-CoA reductase CG5065

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118280261	4.10	putative fatty acyl-CoA reductase CG5065
LOC118280439	4.34	putative fatty acyl-CoA reductase CG5065
LOC118280293	4.63	putative fatty acyl-CoA reductase CG5065
LOC118280550	5.19	putative fatty acyl-CoA reductase CG5065
LOC118280263	-4.74	putative fatty acyl-CoA reductase CG5065 isoform X1
LOC118265382	-3.46	putative fatty acyl-CoA reductase CG5065 isoform X1
LOC118281711	4.51	putative glycine-rich cell wall structural protein 1
LOC118265028	8.69	putative glycine-rich cell wall structural protein 1
LOC118275766	3.03	putative helicase mov-10-B.1
LOC118275634	3.03	putative helicase mov-10-B.2
LOC118272630	-3.03	putative inactive cysteine synthase 2
LOC118268994	-5.03	putative inorganic phosphate cotransporter
LOC118269246	-2.38	putative inorganic phosphate cotransporter
LOC118266059	6.02	putative mediator of RNA polymerase II transcription subunit 29 isoform X1
LOC118277192	-3.43	putative nuclease HARBI1
LOC118264274	-2.96	putative nuclease HARBI1
LOC118280688	-2.26	putative nuclease HARBI1
LOC118269756	-2.55	putative transporter svop-1
LOC118269969	-2.39	putative transporter svop-1
LOC118275372	-2.05	putative tyrosine-protein kinase Wsck
LOC118274621	2.19	putative uncharacterized protein DDB_G0277255
LOC118281100	-2.10	putative uncharacterized protein DDB_G0286901
LOC118280754	-2.12	pyrroline-5-carboxylate reductase-like isoform X1
LOC118268451	5.02	ras-related and estrogen-regulated growth inhibitor-like protein
LOC118268315	3.92	ras-related and estrogen-regulated growth inhibitor-like protein isoform X1
LOC118281046	2.25	ras-related protein Rab-24-like
LOC118268789	-2.84	ras-related protein Rab-28-like
LOC118276390	-3.80	regucalcin-like
LOC118276488	-2.68	regucalcin-like isoform X1
LOC118272352	-3.57	regulating synaptic membrane exocytosis protein 2-like isoform X1
LOC118279228	3.56	regulator of hypoxia-inducible factor 1-like
LOC118268491	-3.85	retinal dehydrogenase 1-like
LOC118268490	-4.73	retinal dehydrogenase 1-like isoform X1
LOC118277209	2.60	retinaldehyde-binding protein 1-like
LOC118277338	-5.74	retinol dehydrogenase 11-like
LOC118262510	-5.41	retinol dehydrogenase 11-like
LOC118262117	-4.76	retinol dehydrogenase 11-like
LOC118282253	-4.08	retinol dehydrogenase 11-like
LOC118261967	-3.33	retinol dehydrogenase 11-like
LOC118261968	-2.33	retinol dehydrogenase 11-like
LOC118272390	2.52	retinol dehydrogenase 11-like
LOC118282233	3.44	retinol dehydrogenase 11-like
LOC118282026	5.55	retinol dehydrogenase 11-like
LOC118277341	-5.27	retinol dehydrogenase 12-like
LOC118277340	-2.65	retinol dehydrogenase 12-like
LOC118274079	5.13	retinol dehydrogenase 12-like
LOC118274286	-4.97	retinol dehydrogenase 13-like
LOC118262082	-4.15	retinol dehydrogenase 13-like
LOC118282234	-3.81	retinol dehydrogenase 13-like
LOC118270713	5.32	retinol dehydrogenase 14-like
LOC118274074	-4.37	ribose-phosphate pyrophosphokinase 2-like
LOC118270885	9.36	RNA polymerase II degradation factor 1-like
LOC118274336	12.62	RNA-binding protein 33-like
LOC118272878	13.22	RNA-binding protein 33-like
LOC118268638	2.33	RYamide receptor-like
LOC118269870	-2.95	saccharopine dehydrogenase-like oxidoreductase
LOC118269868	-2.36	saccharopine dehydrogenase-like oxidoreductase
LOC118262257	-2.05	saccharopine dehydrogenase-like oxidoreductase
LOC118282479	2.72	salivary glue protein Sgs-3-like
LOC118271756	-3.39	sarcoplasmic calcium-binding protein 1-like isoform X1
LOC118272231	-3.02	sarcoplasmic calcium-binding protein 1-like isoform X1
LOC118271854	-5.55	sarcoplasmic calcium-binding proteins I, III, and IV-like
LOC118278096	7.30	sarcoplasmic reticulum histidine-rich calcium-binding protein-like
LOC118269815	-2.99	scavenger receptor class B member 1-like
LOC118270036	2.12	scavenger receptor class B member 1-like
LOC118280352	2.47	scavenger receptor class B member 1-like
LOC118263056	-2.23	seminal metalloprotease 1-like
LOC118262634	3.34	seminal metalloprotease 1-like
LOC118262711	4.09	seminal metalloprotease 1-like
LOC118281999	-2.53	sensory neuron membrane protein 2
LOC118263803	-2.47	sensory neuron membrane protein 2-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118273082	2.03	sequestosome-1-like isoform X1
LOC118271701	-2.35	serendipity locus protein alpha-like
LOC118279688	8.97	serine protease filzig-like
LOC118280078	9.63	serine protease filzig-like
LOC118275138	-3.49	serine protease gd-like isoform X1
LOC118274841	-3.41	serine protease gd-like isoform X1
LOC118262736	3.43	serine protease inhibitor 88Ea-like
LOC118277572	5.11	serine protease inhibitor dipetalogastin-like
LOC118277508	4.81	serine protease inhibitor dipetalogastin-like isoform X1
LOC118271928	4.58	serine protease inhibitor swm-1-like
LOC118279329	2.03	serine protease inhibitor-like
LOC118274057	-3.84	serine protease snake-like
LOC118278673	-3.58	serine protease snake-like
LOC118280676	-3.31	serine protease snake-like
LOC118278559	-3.25	serine protease snake-like
LOC118278721	-2.52	serine protease snake-like
LOC118278810	-2.37	serine protease snake-like
LOC118280677	-2.36	serine protease snake-like
LOC118278662	-2.16	serine protease snake-like
LOC118280569	-3.35	serine protease snake-like isoform X1
LOC118279751	5.50	serine proteinase stubble-like
LOC118279917	6.08	serine proteinase stubble-like
LOC118279890	6.86	serine proteinase stubble-like
LOC118282258	2.13	serine/threonine-protein kinase STE20-like
LOC118282259	2.42	serine/threonine-protein kinase STE20-like
LOC118269184	-2.03	serine--pyruvate aminotransferase, mitochondrial-like
LOC118269185	2.52	serine--pyruvate aminotransferase, mitochondrial-like
LOC118263302	-3.83	serine-rich adhesin for platelets-like
LOC118281918	2.42	serine-rich adhesin for platelets-like
LOC118277885	4.06	serpin B12-like
LOC118279148	-8.77	serpin E3-like
LOC118279088	-7.48	serpin I2-like
LOC118276297	-2.08	short/branched chain specific acyl-CoA dehydrogenase, mitochondrial-like
LOC118267710	6.18	sialidase-like
LOC118271691	3.40	sialin-like isoform X1
LOC118268651	8.57	skin secretory protein xP2-like
LOC118266543	3.69	small nucleolar RNA U3
LOC118269286	-2.57	sodium channel protein Nach-like isoform X1
LOC118279643	3.27	sodium/nucleoside cotransporter 2-like
LOC118279642	2.92	sodium/nucleoside cotransporter 2-like isoform X1
LOC118266274	3.49	sodium/potassium/calcium exchanger Nckx30C-like
LOC118273245	-2.87	sodium/potassium-transporting ATPase subunit beta-2-like
LOC118270430	6.02	sodium-coupled monocarboxylate transporter 1-like
LOC118269386	2.28	sodium-dependent serotonin transporter-like isoform X1
LOC118264614	-2.54	sodium-independent sulfate anion transporter-like
LOC118264613	-2.05	sodium-independent sulfate anion transporter-like isoform X1
LOC118269584	3.03	soluble guanylate cyclase 89Db-like
LOC118274099	-2.32	soluble scavenger receptor cysteine-rich domain-containing protein SSC5D-like
LOC118277595	-3.45	solute carrier family 2, facilitated glucose transporter member 6-like
LOC118277592	-2.84	solute carrier family 2, facilitated glucose transporter member 6-like
LOC118265729	-2.35	solute carrier family 22 member 1-like
LOC118282147	4.63	solute carrier family 22 member 1-like
LOC118261875	2.73	solute carrier family 46 member 3-like
LOC118275137	3.88	somatomedin-B and thrombospondin type-1 domain-containing protein-like
LOC118275147	3.89	somatomedin-B and thrombospondin type-1 domain-containing protein-like
LOC118274164	-3.67	sorbitol dehydrogenase-like
LOC118277476	4.26	sperm mitochondrial-associated cysteine-rich protein-like
LOC118273828	-4.20	sperm-associated antigen 6-like
LOC118272944	-3.29	sperm-associated antigen 6-like isoform X1
LOC118276734	-2.57	spherulin-2A-like
LOC118276989	-2.15	spherulin-2A-like
LOC118281045	5.92	spherulin-2A-like
LOC118270137	3.05	sphingomyelin phosphodiesterase-like isoform X1
LOC118272367	-5.51	spidroin-1-like
LOC118277836	8.10	spidroin-2-like
LOC118265529	2.42	spore coat protein T-like
LOC118265518	2.88	spore coat protein T-like
LOC118265517	2.96	spore coat protein T-like isoform X1
LOC118279342	5.43	stabilizer of axonemal microtubules 1-like
LOC118265133	2.16	START domain-containing protein 10-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118265276	3.50	START domain-containing protein 10-like
LOC118264926	2.86	stearoyl-CoA desaturase 5-like
LOC118262242	2.22	stromelysin-3-like isoform X1
LOC118274488	3.19	structure-specific endonuclease subunit SLX1 homolog
LOC118265416	-4.04	succinate dehydrogenase cytochrome b560 subunit, mitochondrial-like
LOC118266608	-3.50	sulfotransferase 1C4-like
LOC118266602	-2.91	sulfotransferase 1C4-like
LOC118270564	-2.45	sulfotransferase 1C4-like
LOC118270544	-2.71	sulfotransferase family cytosolic 1B member 1-like
LOC118263505	-3.87	synaptic vesicle 2-related protein-like isoform X1
LOC118269963	5.41	synaptic vesicle glycoprotein 2B-like isoform X1
LOC118270044	-5.57	synaptic vesicle glycoprotein 2C-like
LOC118263868	-4.21	synaptic vesicle glycoprotein 2C-like
LOC118263902	-2.56	synaptic vesicle glycoprotein 2C-like
LOC118269942	-2.55	synaptic vesicle glycoprotein 2C-like isoform X1
LOC118279149	3.78	tektin-4-like
LOC118263714	2.02	tenascin-X-like
LOC118268517	-2.34	tensin-1-like isoform X1
LOC118267956	4.13	tetra-peptide repeat homeobox protein 1-like
LOC118267666	13.63	tetra-peptide repeat homeobox protein 1-like
LOC118266350	-3.35	tetraspanin-1-like
LOC118263709	2.67	tetraspanin-2A-like
LOC118277974	5.19	tetratricopeptide repeat protein 25-like
LOC118271480	2.87	three prime repair exonuclease 2-like
LOC118262723	3.17	three prime repair exonuclease 2-like
LOC118275696	2.58	thyroid transcription factor 1-like
LOC118268680	2.08	titin-like
LOC118279372	10.06	titin-like
LOC118269398	10.89	titin-like
LOC118264980	4.30	TLC domain-containing protein 5-like
LOC118272158	-4.07	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase-like
LOC118271922	2.72	transcription factor hamlet-like
LOC118279404	2.33	transcription factor Ken-like
LOC118268460	7.90	transcription factor SPT20 homolog
LOC118278221	8.49	transcription factor SPT20 homolog
LOC118273521	7.83	transcription factor SPT20 homolog isoform X1
LOC118277989	5.55	transcription factor stalky-like
LOC118280719	6.26	transcriptional activator GLI3-like
LOC118278458	3.00	transcriptional regulatory protein AlgP-like
LOC118277790	-3.03	transketolase-like protein 2
LOC118269970	4.99	transmembrane protease serine 12-like
LOC118267882	3.08	transmembrane protease serine 9-like
LOC118270083	5.15	transmembrane protease serine 9-like
LOC118269693	9.73	transmembrane protease serine 9-like
LOC118270532	3.66	transmembrane protein 216-like
LOC118264706	-2.82	trehalase-like
LOC118280551	-2.39	trehalase-like
LOC118264150	-2.65	trehalase-like isoform X1
LOC118268981	3.27	trichohyalin-like
LOC118263239	-3.83	trimethyllysine dioxygenase, mitochondrial-like
LOC118263267	-3.55	trimethyllysine dioxygenase, mitochondrial-like
LOC118265546	-3.47	triokinase/FMN cyclase-like
LOC118265049	-3.32	triokinase/FMN cyclase-like
LOC118273353	2.81	tripartite motif-containing protein 45-like
AOB78_gt10	2.39	tRNA-Gly
AOB78_gt08	2.07	tRNA-Lys
LOC118274264	2.33	tRNA-uridine aminocarboxypropyltransferase 2-like
LOC118263890	2.13	trypsin 3A1-like
LOC118263590	3.46	trypsin 3A1-like
LOC118274837	-2.84	trypsin CFT-1-like
LOC118274665	2.52	trypsin CFT-1-like
LOC118277917	2.73	trypsin CFT-1-like isoform X1
LOC118280050	3.92	trypsin inhibitor-like
LOC118280797	-4.22	trypsin, alkaline B-like
LOC118274829	2.12	trypsin, alkaline B-like
LOC118274764	4.16	trypsin, alkaline B-like
LOC118274659	6.65	trypsin, alkaline B-like
LOC118265193	-2.88	trypsin, alkaline C-like
LOC118265203	-2.17	trypsin, alkaline C-like
LOC118274623	5.85	trypsin, alkaline C-like
LOC118269924	9.96	trypsin-1-like isoform X1

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118263562	5.29	trypsin-3-like
LOC118280401	4.10	trypsin-like
LOC118280409	4.70	trypsin-like
LOC118273149	3.31	tubulin polyglutamylase complex subunit 2-like
LOC118281743	-2.18	tubulin polymerization-promoting protein homolog
LOC118263443	2.89	tyrosine 3-monooxygenase-like
LOC118277381	4.21	tyrosine-protein phosphatase cdc-14-like isoform X1
LOC118263196	4.01	U1 spliceosomal RNA
LOC118275940	-7.77	UDP-glucuronosyltransferase 1-2-like
LOC118279191	-5.50	UDP-glucuronosyltransferase 1-7-like
LOC118279190	-3.75	UDP-glucuronosyltransferase 1-7-like
LOC118269227	-4.06	UDP-glucuronosyltransferase 2B10-like
LOC118269255	-3.58	UDP-glucuronosyltransferase 2B10-like
LOC118277898	-2.04	UDP-glucuronosyltransferase 2B10-like isoform X1
LOC118266879	2.09	UDP-glucuronosyltransferase 2B13-like
LOC118277904	-4.20	UDP-glucuronosyltransferase 2B15-like
LOC118277906	-3.61	UDP-glucuronosyltransferase 2B15-like
LOC118277899	-3.08	UDP-glucuronosyltransferase 2B15-like
LOC118277768	-3.06	UDP-glucuronosyltransferase 2B15-like
LOC118268440	-2.82	UDP-glucuronosyltransferase 2B15-like
LOC118277903	-3.88	UDP-glucuronosyltransferase 2B19-like
LOC118279155	-3.81	UDP-glucuronosyltransferase 2B19-like
LOC118279416	-3.08	UDP-glucuronosyltransferase 2B19-like
LOC118265011	-3.72	UDP-glucuronosyltransferase 2B1-like
LOC118265297	2.63	UDP-glucuronosyltransferase 2B1-like
LOC118279415	-3.56	UDP-glucuronosyltransferase 2B20-like
LOC118265039	-4.71	UDP-glucuronosyltransferase 2B31-like
LOC118277901	-4.21	UDP-glucuronosyltransferase 2B31-like
LOC118279418	-2.25	UDP-glucuronosyltransferase 2B31-like
LOC118279189	-3.76	UDP-glucuronosyltransferase 2B33-like isoform X1
LOC118279153	-3.40	UDP-glucuronosyltransferase 2B4-like
LOC118277900	-4.14	UDP-glucuronosyltransferase 2C1-like
LOC118277905	-3.05	UDP-glucuronosyltransferase 2C1-like
LOC118267687	4.32	UDP-glucuronosyltransferase 2C1-like
LOC118267688	4.66	UDP-glucuronosyltransferase 2C1-like
LOC118264242	3.07	UNC93-like protein MFSD11
LOC118264165	3.23	UNC93-like protein MFSD11
LOC118263715	3.33	uncharacterized 30.3 kDa protein-like
LOC118263489	3.60	uncharacterized 30.3 kDa protein-like
LOC118263527	4.07	uncharacterized 30.3 kDa protein-like
LOC118278228	9.90	uncharacterized abhydrolase domain-containing protein DDB_G0269086-like isoform X1
LOC118276754	-3.68	uncharacterized GMC-type oxidoreductase Mb1310-like
LOC118261731	5.85	uncharacterized LOC118261731
LOC118261736	2.80	uncharacterized LOC118261736
LOC118261770	-3.81	uncharacterized LOC118261770
LOC118261933	-2.98	uncharacterized LOC118261933
LOC118262103	2.39	uncharacterized LOC118262103
LOC118262107	4.34	uncharacterized LOC118262107
LOC118262341	7.48	uncharacterized LOC118262341
LOC118262543	-2.39	uncharacterized LOC118262543
LOC118262817	5.58	uncharacterized LOC118262817
LOC118262908	3.41	uncharacterized LOC118262908
LOC118263526	5.91	uncharacterized LOC118263526
LOC118264010	4.27	uncharacterized LOC118264010
LOC118264504	-2.49	uncharacterized LOC118264504
LOC118264505	-2.56	uncharacterized LOC118264505
LOC118264515	4.72	uncharacterized LOC118264515
LOC118264665	-6.26	uncharacterized LOC118264665
LOC118264739	4.81	uncharacterized LOC118264739
LOC118264765	3.46	uncharacterized LOC118264765
LOC118264766	-5.66	uncharacterized LOC118264766
LOC118264767	3.44	uncharacterized LOC118264767
LOC118265451	2.40	uncharacterized LOC118265451
LOC118265924	3.87	uncharacterized LOC118265924
LOC118266072	4.20	uncharacterized LOC118266072
LOC118266079	-5.81	uncharacterized LOC118266079
LOC118266108	-3.48	uncharacterized LOC118266108
LOC118266116	-5.46	uncharacterized LOC118266116
LOC118266117	-3.14	uncharacterized LOC118266117
LOC118266120	-5.88	uncharacterized LOC118266120

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118266138	-6.30	uncharacterized LOC118266138
LOC118266215	-5.22	uncharacterized LOC118266215
LOC118266362	-5.04	uncharacterized LOC118266362
LOC118266387	-6.17	uncharacterized LOC118266387
LOC118266436	5.91	uncharacterized LOC118266436
LOC118266503	-4.89	uncharacterized LOC118266503
LOC118266518	2.78	uncharacterized LOC118266518
LOC118266519	5.10	uncharacterized LOC118266519
LOC118266521	2.68	uncharacterized LOC118266521
LOC118266537	-8.01	uncharacterized LOC118266537
LOC118266614	-3.53	uncharacterized LOC118266614
LOC118266631	-2.48	uncharacterized LOC118266631
LOC118266641	2.29	uncharacterized LOC118266641
LOC118266642	2.01	uncharacterized LOC118266642
LOC118266825	3.54	uncharacterized LOC118266825
LOC118266933	3.11	uncharacterized LOC118266933
LOC118267027	4.19	uncharacterized LOC118267027
LOC118267219	4.03	uncharacterized LOC118267219
LOC118267535	-5.41	uncharacterized LOC118267535
LOC118267659	3.70	uncharacterized LOC118267659
LOC118267663	-5.02	uncharacterized LOC118267663
LOC118267667	3.70	uncharacterized LOC118267667
LOC118268735	3.05	uncharacterized LOC118268735
LOC118268920	2.24	uncharacterized LOC118268920
LOC118269353	2.72	uncharacterized LOC118269353
LOC118269402	5.07	uncharacterized LOC118269402
LOC118269562	3.85	uncharacterized LOC118269562
LOC118269667	3.29	uncharacterized LOC118269667
LOC118269767	4.05	uncharacterized LOC118269767
LOC118270017	2.82	uncharacterized LOC118270017
LOC118270018	2.22	uncharacterized LOC118270018
LOC118270019	2.44	uncharacterized LOC118270019
LOC118270118	2.52	uncharacterized LOC118270118
LOC118270597	-2.32	uncharacterized LOC118270597
LOC118271238	4.54	uncharacterized LOC118271238
LOC118271251	2.09	uncharacterized LOC118271251
LOC118271921	5.28	uncharacterized LOC118271921
LOC118271949	5.68	uncharacterized LOC118271949
LOC118272487	4.05	uncharacterized LOC118272487
LOC118272526	2.20	uncharacterized LOC118272526
LOC118272741	3.88	uncharacterized LOC118272741
LOC118272775	-4.36	uncharacterized LOC118272775
LOC118272787	3.11	uncharacterized LOC118272787
LOC118272808	-6.94	uncharacterized LOC118272808
LOC118273916	-4.91	uncharacterized LOC118273916
LOC118274093	2.84	uncharacterized LOC118274093
LOC118274493	4.60	uncharacterized LOC118274493
LOC118274499	4.04	uncharacterized LOC118274499
LOC118274536	7.88	uncharacterized LOC118274536
LOC118274620	-2.70	uncharacterized LOC118274620
LOC118274882	3.11	uncharacterized LOC118274882
LOC118275091	-2.50	uncharacterized LOC118275091
LOC118275148	2.62	uncharacterized LOC118275148
LOC118275202	-4.78	uncharacterized LOC118275202
LOC118275891	3.00	uncharacterized LOC118275891
LOC118275895	6.15	uncharacterized LOC118275895
LOC118276137	-3.67	uncharacterized LOC118276137
LOC118276387	6.49	uncharacterized LOC118276387
LOC118276410	3.43	uncharacterized LOC118276410
LOC118276638	6.58	uncharacterized LOC118276638
LOC118276921	4.86	uncharacterized LOC118276921
LOC118276928	5.23	uncharacterized LOC118276928
LOC118277147	7.39	uncharacterized LOC118277147
LOC118277168	-3.94	uncharacterized LOC118277168
LOC118277425	8.38	uncharacterized LOC118277425
LOC118277842	-3.37	uncharacterized LOC118277842
LOC118277933	-2.79	uncharacterized LOC118277933
LOC118278523	4.10	uncharacterized LOC118278523
LOC118278597	2.40	uncharacterized LOC118278597
LOC118278921	-3.66	uncharacterized LOC118278921
LOC118279684	-3.78	uncharacterized LOC118279684

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118279812	-2.08	uncharacterized LOC118279812
LOC118280032	-2.21	uncharacterized LOC118280032
LOC118280496	4.31	uncharacterized LOC118280496
LOC118280658	-2.16	uncharacterized LOC118280658
LOC118280798	4.06	uncharacterized LOC118280798
LOC118281109	-5.38	uncharacterized LOC118281109
LOC118281386	7.14	uncharacterized LOC118281386
LOC118281395	7.03	uncharacterized LOC118281395
LOC118281468	3.86	uncharacterized LOC118281468
LOC118281510	3.46	uncharacterized LOC118281510
LOC118281866	-6.35	uncharacterized LOC118281866
LOC118282013	3.55	uncharacterized LOC118282013
LOC118282260	4.18	uncharacterized LOC118282260
LOC118282273	2.42	uncharacterized LOC118282273
LOC118275124	-3.00	uncharacterized oxidoreductase MexAM1_META1p0182-like
LOC118269454	-4.71	uncharacterized oxidoreductase TM_0325-like
LOC118275122	-4.54	uncharacterized oxidoreductase TM_0325-like
LOC118268887	-3.17	uncharacterized oxidoreductase TM_0325-like
LOC118276485	-2.72	uncharacterized oxidoreductase TM_0325-like
LOC118266443	-3.73	uncharacterized oxidoreductase YjmC-like
LOC118264328	-4.56	uncharacterized oxidoreductase YoxD-like
LOC118278316	-4.83	uncharacterized PE-PGRS family protein PE_PGRS36-like
LOC118274010	-4.69	uncharacterized PE-PGRS family protein PE_PGRS36-like
LOC118281712	4.94	uncharacterized PE-PGRS family protein PE_PGRS46-like
LOC118268380	-3.80	uncharacterized protein C15orf61-like isoform X1
LOC118273067	9.96	uncharacterized protein DDB_G0290587-like
LOC118262221	5.95	uncharacterized protein DDB_G0290685-like
LOC118278038	-8.98	uncharacterized protein K02A2.6-like
LOC118282007	-4.34	uncharacterized protein K02A2.6-like
LOC118272595	-3.04	uncharacterized protein K02A2.6-like
LOC118281254	-2.59	uncharacterized protein K02A2.6-like
LOC118261723	-2.35	uncharacterized protein LOC118261723
LOC118261738	8.57	uncharacterized protein LOC118261738
LOC118261776	9.88	uncharacterized protein LOC118261776
LOC118261777	8.85	uncharacterized protein LOC118261777
LOC118261794	8.49	uncharacterized protein LOC118261794
LOC118261809	4.52	uncharacterized protein LOC118261809
LOC118261817	2.85	uncharacterized protein LOC118261817 isoform X1
LOC118261820	-4.22	uncharacterized protein LOC118261820
LOC118261894	2.92	uncharacterized protein LOC118261894
LOC118261910	2.72	uncharacterized protein LOC118261910
LOC118261914	4.27	uncharacterized protein LOC118261914
LOC118261922	3.42	uncharacterized protein LOC118261922
LOC118261925	5.73	uncharacterized protein LOC118261925
LOC118261949	4.22	uncharacterized protein LOC118261949
LOC118261959	-4.75	uncharacterized protein LOC118261959
LOC118261961	3.57	uncharacterized protein LOC118261961
LOC118262017	4.53	uncharacterized protein LOC118262017
LOC118262018	7.87	uncharacterized protein LOC118262018
LOC118262045	-2.68	uncharacterized protein LOC118262045
LOC118262047	6.88	uncharacterized protein LOC118262047
LOC118262064	6.32	uncharacterized protein LOC118262064
LOC118262100	2.14	uncharacterized protein LOC118262100
LOC118262101	2.51	uncharacterized protein LOC118262101 isoform X1
LOC118262134	-3.15	uncharacterized protein LOC118262134
LOC118262158	-3.15	uncharacterized protein LOC118262158
LOC118262181	5.10	uncharacterized protein LOC118262181
LOC118262276	8.51	uncharacterized protein LOC118262276 isoform X1
LOC118262279	2.05	uncharacterized protein LOC118262279 isoform X1
LOC118262360	-2.42	uncharacterized protein LOC118262360
LOC118262361	-2.27	uncharacterized protein LOC118262361
LOC118262425	-3.80	uncharacterized protein LOC118262425
LOC118262460	2.40	uncharacterized protein LOC118262460
LOC118262475	2.37	uncharacterized protein LOC118262475 isoform X1
LOC118262499	3.75	uncharacterized protein LOC118262499
LOC118262681	-3.42	uncharacterized protein LOC118262681
LOC118262682	-3.78	uncharacterized protein LOC118262682
LOC118262705	2.24	uncharacterized protein LOC118262705
LOC118262746	2.10	uncharacterized protein LOC118262746 isoform X1
LOC118262818	2.05	uncharacterized protein LOC118262818

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118262914	6.54	uncharacterized protein LOC118262914 isoform X1
LOC118262929	7.09	uncharacterized protein LOC118262929
LOC118262930	2.37	uncharacterized protein LOC118262930
LOC118262935	6.57	uncharacterized protein LOC118262935
LOC118262936	3.16	uncharacterized protein LOC118262936
LOC118262954	3.89	uncharacterized protein LOC118262954
LOC118262989	7.01	uncharacterized protein LOC118262989
LOC118263008	3.46	uncharacterized protein LOC118263008 isoform X1
LOC118263052	-4.70	uncharacterized protein LOC118263052
LOC118263053	3.73	uncharacterized protein LOC118263053
LOC118263054	-4.11	uncharacterized protein LOC118263054
LOC118263084	-3.43	uncharacterized protein LOC118263084 isoform X1
LOC118263088	5.91	uncharacterized protein LOC118263088
LOC118263093	4.78	uncharacterized protein LOC118263093
LOC118263139	2.40	uncharacterized protein LOC118263139
LOC118263303	-3.16	uncharacterized protein LOC118263303
LOC118263304	-3.56	uncharacterized protein LOC118263304
LOC118263341	-2.03	uncharacterized protein LOC118263341
LOC118263348	3.34	uncharacterized protein LOC118263348
LOC118263416	-2.93	uncharacterized protein LOC118263416
LOC118263417	-2.23	uncharacterized protein LOC118263417
LOC118263438	4.70	uncharacterized protein LOC118263438
LOC118263477	5.56	uncharacterized protein LOC118263477
LOC118263504	2.85	uncharacterized protein LOC118263504
LOC118263537	2.44	uncharacterized protein LOC118263537
LOC118263579	4.12	uncharacterized protein LOC118263579
LOC118263589	2.88	uncharacterized protein LOC118263589
LOC118263737	3.75	uncharacterized protein LOC118263737 isoform X1
LOC118263758	-2.01	uncharacterized protein LOC118263758
LOC118263773	-2.53	uncharacterized protein LOC118263773
LOC118263800	-4.04	uncharacterized protein LOC118263800
LOC118263817	-3.68	uncharacterized protein LOC118263817
LOC118263851	-2.36	uncharacterized protein LOC118263851
LOC118263861	-5.33	uncharacterized protein LOC118263861
LOC118263875	5.85	uncharacterized protein LOC118263875 isoform X1
LOC118263877	3.43	uncharacterized protein LOC118263877 isoform X1
LOC118263899	2.93	uncharacterized protein LOC118263899
LOC118263982	6.88	uncharacterized protein LOC118263982
LOC118263992	7.59	uncharacterized protein LOC118263992
LOC118264151	2.95	uncharacterized protein LOC118264151
LOC118264174	3.01	uncharacterized protein LOC118264174
LOC118264179	2.42	uncharacterized protein LOC118264179
LOC118264228	-3.52	uncharacterized protein LOC118264228
LOC118264231	3.44	uncharacterized protein LOC118264231
LOC118264238	4.46	uncharacterized protein LOC118264238
LOC118264246	2.37	uncharacterized protein LOC118264246
LOC118264284	3.40	uncharacterized protein LOC118264284
LOC118264332	5.94	uncharacterized protein LOC118264332
LOC118264347	-2.71	uncharacterized protein LOC118264347
LOC118264369	-2.06	uncharacterized protein LOC118264369
LOC118264393	6.85	uncharacterized protein LOC118264393
LOC118264468	-3.32	uncharacterized protein LOC118264468
LOC118264469	4.17	uncharacterized protein LOC118264469
LOC118264508	-3.61	uncharacterized protein LOC118264508 isoform X1
LOC118264514	4.89	uncharacterized protein LOC118264514 isoform X1
LOC118264530	-5.81	uncharacterized protein LOC118264530
LOC118264532	4.05	uncharacterized protein LOC118264532
LOC118264539	-3.56	uncharacterized protein LOC118264539
LOC118264546	5.08	uncharacterized protein LOC118264546 isoform X1
LOC118264568	3.48	uncharacterized protein LOC118264568
LOC118264623	-2.85	uncharacterized protein LOC118264623
LOC118264701	-2.79	uncharacterized protein LOC118264701
LOC118264702	-3.34	uncharacterized protein LOC118264702
LOC118264731	2.58	uncharacterized protein LOC118264731
LOC118264740	-2.10	uncharacterized protein LOC118264740
LOC118264823	4.57	uncharacterized protein LOC118264823
LOC118264836	2.70	uncharacterized protein LOC118264836
LOC118264844	-3.15	uncharacterized protein LOC118264844
LOC118264846	-2.62	uncharacterized protein LOC118264846
LOC118264853	2.47	uncharacterized protein LOC118264853
LOC118264906	4.97	uncharacterized protein LOC118264906

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118264922	-2.37	uncharacterized protein LOC118264922
LOC118264934	7.77	uncharacterized protein LOC118264934
LOC118264937	-5.41	uncharacterized protein LOC118264937
LOC118264988	2.24	uncharacterized protein LOC118264988
LOC118265004	2.13	uncharacterized protein LOC118265004
LOC118265019	3.01	uncharacterized protein LOC118265019
LOC118265040	-3.52	uncharacterized protein LOC118265040
LOC118265072	3.92	uncharacterized protein LOC118265072
LOC118265073	4.57	uncharacterized protein LOC118265073
LOC118265076	-2.98	uncharacterized protein LOC118265076
LOC118265096	3.44	uncharacterized protein LOC118265096
LOC118265098	4.61	uncharacterized protein LOC118265098
LOC118265114	6.53	uncharacterized protein LOC118265114
LOC118265116	4.16	uncharacterized protein LOC118265116
LOC118265175	4.82	uncharacterized protein LOC118265175
LOC118265224	6.69	uncharacterized protein LOC118265224
LOC118265234	-2.71	uncharacterized protein LOC118265234 isoform X1
LOC118265396	-3.38	uncharacterized protein LOC118265396 isoform X1
LOC118265410	-4.76	uncharacterized protein LOC118265410 isoform X1
LOC118265434	6.37	uncharacterized protein LOC118265434
LOC118265463	3.87	uncharacterized protein LOC118265463 isoform X1
LOC118265464	4.50	uncharacterized protein LOC118265464
LOC118265465	2.44	uncharacterized protein LOC118265465 isoform X1
LOC118265569	3.52	uncharacterized protein LOC118265569 isoform X1
LOC118265716	-3.73	uncharacterized protein LOC118265716
LOC118265717	-3.13	uncharacterized protein LOC118265717
LOC118265788	6.69	uncharacterized protein LOC118265788
LOC118265789	7.15	uncharacterized protein LOC118265789
LOC118265863	10.23	uncharacterized protein LOC118265863
LOC118265992	-2.32	uncharacterized protein LOC118265992
LOC118265994	-3.17	uncharacterized protein LOC118265994
LOC118266024	-2.14	uncharacterized protein LOC118266024
LOC118266040	5.74	uncharacterized protein LOC118266040
LOC118266063	-5.15	uncharacterized protein LOC118266063
LOC118266093	3.15	uncharacterized protein LOC118266093
LOC118266178	-2.13	uncharacterized protein LOC118266178
LOC118266187	5.20	uncharacterized protein LOC118266187
LOC118266193	4.42	uncharacterized protein LOC118266193
LOC118266246	-3.14	uncharacterized protein LOC118266246
LOC118266249	-3.63	uncharacterized protein LOC118266249
LOC118266269	7.13	uncharacterized protein LOC118266269
LOC118266287	-2.21	uncharacterized protein LOC118266287 isoform X1
LOC118266301	4.83	uncharacterized protein LOC118266301
LOC118266310	3.40	uncharacterized protein LOC118266310
LOC118266319	5.85	uncharacterized protein LOC118266319
LOC118266335	5.40	uncharacterized protein LOC118266335 isoform X1
LOC118266347	-2.36	uncharacterized protein LOC118266347 isoform X1
LOC118266369	9.18	uncharacterized protein LOC118266369
LOC118266383	8.38	uncharacterized protein LOC118266383 isoform X1
LOC118266385	-5.15	uncharacterized protein LOC118266385
LOC118266434	5.09	uncharacterized protein LOC118266434
LOC118266437	-2.41	uncharacterized protein LOC118266437
LOC118266480	2.14	uncharacterized protein LOC118266480
LOC118266491	2.15	uncharacterized protein LOC118266491
LOC118266509	3.66	uncharacterized protein LOC118266509
LOC118266513	-2.10	uncharacterized protein LOC118266513
LOC118266522	-2.20	uncharacterized protein LOC118266522
LOC118266606	10.44	uncharacterized protein LOC118266606
LOC118266612	7.08	uncharacterized protein LOC118266612
LOC118266650	2.40	uncharacterized protein LOC118266650
LOC118266663	-5.80	uncharacterized protein LOC118266663
LOC118266693	2.33	uncharacterized protein LOC118266693
LOC118266771	-2.64	uncharacterized protein LOC118266771
LOC118266786	3.57	uncharacterized protein LOC118266786
LOC118266802	-2.22	uncharacterized protein LOC118266802
LOC118266845	-5.49	uncharacterized protein LOC118266845
LOC118266910	4.31	uncharacterized protein LOC118266910
LOC118266929	-2.24	uncharacterized protein LOC118266929
LOC118266955	2.04	uncharacterized protein LOC118266955
LOC118266985	11.12	uncharacterized protein LOC118266985 isoform X1

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118267101	10.54	uncharacterized protein LOC118267101
LOC118267195	2.43	uncharacterized protein LOC118267195
LOC118267218	3.23	uncharacterized protein LOC118267218
LOC118267221	2.48	uncharacterized protein LOC118267221
LOC118267248	2.30	uncharacterized protein LOC118267248 isoform X1
LOC118267296	2.99	uncharacterized protein LOC118267296
LOC118267306	9.05	uncharacterized protein LOC118267306
LOC118267317	3.40	uncharacterized protein LOC118267317
LOC118267326	-4.45	uncharacterized protein LOC118267326
LOC118267364	8.54	uncharacterized protein LOC118267364
LOC118267396	-3.35	uncharacterized protein LOC118267396 isoform X1
LOC118267423	10.67	uncharacterized protein LOC118267423 isoform X1
LOC118267432	9.25	uncharacterized protein LOC118267432
LOC118267445	11.65	uncharacterized protein LOC118267445 isoform X1
LOC118267549	10.06	uncharacterized protein LOC118267549
LOC118267552	2.31	uncharacterized protein LOC118267552
LOC118267565	7.96	uncharacterized protein LOC118267565
LOC118267575	2.31	uncharacterized protein LOC118267575
LOC118267577	9.34	uncharacterized protein LOC118267577
LOC118267594	-3.08	uncharacterized protein LOC118267594
LOC118267595	-3.01	uncharacterized protein LOC118267595
LOC118267647	6.90	uncharacterized protein LOC118267647
LOC118267664	7.14	uncharacterized protein LOC118267664
LOC118267679	6.16	uncharacterized protein LOC118267679 isoform X1
LOC118267721	4.35	uncharacterized protein LOC118267721 isoform X1
LOC118267722	2.20	uncharacterized protein LOC118267722
LOC118267733	3.10	uncharacterized protein LOC118267733
LOC118267749	2.67	uncharacterized protein LOC118267749
LOC118267779	4.28	uncharacterized protein LOC118267779
LOC118267783	-3.76	uncharacterized protein LOC118267783
LOC118267785	4.86	uncharacterized protein LOC118267785
LOC118267833	5.96	uncharacterized protein LOC118267833
LOC118267858	9.97	uncharacterized protein LOC118267858
LOC118267865	-3.94	uncharacterized protein LOC118267865
LOC118267876	-2.03	uncharacterized protein LOC118267876
LOC118267877	-4.58	uncharacterized protein LOC118267877
LOC118267886	-5.24	uncharacterized protein LOC118267886
LOC118267887	-3.67	uncharacterized protein LOC118267887
LOC118267928	-3.89	uncharacterized protein LOC118267928
LOC118267929	-2.76	uncharacterized protein LOC118267929
LOC118267931	-2.01	uncharacterized protein LOC118267931
LOC118267952	6.20	uncharacterized protein LOC118267952
LOC118267979	-3.44	uncharacterized protein LOC118267979 isoform X1
LOC118267981	-4.52	uncharacterized protein LOC118267981
LOC118267982	-2.12	uncharacterized protein LOC118267982
LOC118267986	-5.11	uncharacterized protein LOC118267986
LOC118267988	-3.81	uncharacterized protein LOC118267988
LOC118267991	-4.38	uncharacterized protein LOC118267991
LOC118268003	8.99	uncharacterized protein LOC118268003
LOC118268133	2.07	uncharacterized protein LOC118268133 isoform X1
LOC118268147	2.20	uncharacterized protein LOC118268147 isoform X1
LOC118268189	-2.69	uncharacterized protein LOC118268189
LOC118268215	3.41	uncharacterized protein LOC118268215
LOC118268327	3.85	uncharacterized protein LOC118268327
LOC118268357	2.69	uncharacterized protein LOC118268357
LOC118268402	4.63	uncharacterized protein LOC118268402
LOC118268494	-3.23	uncharacterized protein LOC118268494
LOC118268588	-3.72	uncharacterized protein LOC118268588
LOC118268630	3.20	uncharacterized protein LOC118268630 isoform X1
LOC118268672	2.08	uncharacterized protein LOC118268672
LOC118268891	3.55	uncharacterized protein LOC118268891
LOC118268943	7.90	uncharacterized protein LOC118268943
LOC118268949	8.93	uncharacterized protein LOC118268949
LOC118269044	-3.22	uncharacterized protein LOC118269044
LOC118269096	3.75	uncharacterized protein LOC118269096
LOC118269163	2.75	uncharacterized protein LOC118269163
LOC118269194	-2.22	uncharacterized protein LOC118269194 isoform X1
LOC118269211	-2.96	uncharacterized protein LOC118269211
LOC118269238	8.40	uncharacterized protein LOC118269238
LOC118269258	-5.21	uncharacterized protein LOC118269258 isoform X1
LOC118269259	-4.28	uncharacterized protein LOC118269259

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118269261	2.10	uncharacterized protein LOC118269261
LOC118269278	2.34	uncharacterized protein LOC118269278
LOC118269329	4.95	uncharacterized protein LOC118269329
LOC118269342	-3.55	uncharacterized protein LOC118269342
LOC118269345	5.46	uncharacterized protein LOC118269345
LOC118269350	-2.04	uncharacterized protein LOC118269350
LOC118269363	5.73	uncharacterized protein LOC118269363 isoform X1
LOC118269408	-3.83	uncharacterized protein LOC118269408
LOC118269424	-2.52	uncharacterized protein LOC118269424
LOC118269444	2.70	uncharacterized protein LOC118269444
LOC118269448	3.85	uncharacterized protein LOC118269448
LOC118269494	2.14	uncharacterized protein LOC118269494
LOC118269597	3.22	uncharacterized protein LOC118269597
LOC118269606	-3.23	uncharacterized protein LOC118269606
LOC118269612	-3.04	uncharacterized protein LOC118269612
LOC118269652	2.16	uncharacterized protein LOC118269652
LOC118269665	-3.42	uncharacterized protein LOC118269665 isoform X1
LOC118269701	-3.36	uncharacterized protein LOC118269701
LOC118269728	2.32	uncharacterized protein LOC118269728
LOC118269744	5.47	uncharacterized protein LOC118269744
LOC118269759	2.05	uncharacterized protein LOC118269759
LOC118269790	7.07	uncharacterized protein LOC118269790
LOC118269793	5.26	uncharacterized protein LOC118269793
LOC118269832	3.71	uncharacterized protein LOC118269832
LOC118269903	7.27	uncharacterized protein LOC118269903
LOC118269905	3.60	uncharacterized protein LOC118269905
LOC118269909	2.83	uncharacterized protein LOC118269909
LOC118269934	6.08	uncharacterized protein LOC118269934
LOC118269985	3.83	uncharacterized protein LOC118269985
LOC118269994	5.52	uncharacterized protein LOC118269994
LOC118270007	-5.45	uncharacterized protein LOC118270007 isoform X1
LOC118270040	8.05	uncharacterized protein LOC118270040
LOC118270049	2.47	uncharacterized protein LOC118270049
LOC118270054	8.65	uncharacterized protein LOC118270054
LOC118270077	5.77	uncharacterized protein LOC118270077
LOC118270115	2.14	uncharacterized protein LOC118270115
LOC118270121	4.76	uncharacterized protein LOC118270121
LOC118270141	5.04	uncharacterized protein LOC118270141
LOC118270149	-2.46	uncharacterized protein LOC118270149
LOC118270150	2.28	uncharacterized protein LOC118270150
LOC118270190	-3.09	uncharacterized protein LOC118270190
LOC118270293	2.50	uncharacterized protein LOC118270293
LOC118270295	2.77	uncharacterized protein LOC118270295
LOC118270399	5.03	uncharacterized protein LOC118270399
LOC118270401	-3.37	uncharacterized protein LOC118270401
LOC118270408	4.34	uncharacterized protein LOC118270408 isoform X1
LOC118270432	10.52	uncharacterized protein LOC118270432
LOC118270433	-3.08	uncharacterized protein LOC118270433
LOC118270437	9.25	uncharacterized protein LOC118270437
LOC118270447	3.72	uncharacterized protein LOC118270447 isoform X1
LOC118270455	10.87	uncharacterized protein LOC118270455
LOC118270487	6.03	uncharacterized protein LOC118270487
LOC118270503	9.32	uncharacterized protein LOC118270503
LOC118270504	4.08	uncharacterized protein LOC118270504
LOC118270510	11.09	uncharacterized protein LOC118270510
LOC118270511	13.12	uncharacterized protein LOC118270511
LOC118270513	9.10	uncharacterized protein LOC118270513
LOC118270517	11.26	uncharacterized protein LOC118270517
LOC118270525	11.25	uncharacterized protein LOC118270525 isoform X1
LOC118270528	13.86	uncharacterized protein LOC118270528
LOC118270531	5.02	uncharacterized protein LOC118270531
LOC118270538	10.78	uncharacterized protein LOC118270538 isoform X1
LOC118270546	12.24	uncharacterized protein LOC118270546
LOC118270551	12.52	uncharacterized protein LOC118270551
LOC118270558	10.95	uncharacterized protein LOC118270558 isoform X1
LOC118270567	9.89	uncharacterized protein LOC118270567
LOC118270591	8.07	uncharacterized protein LOC118270591 isoform X1
LOC118270592	9.44	uncharacterized protein LOC118270592
LOC118270596	-2.22	uncharacterized protein LOC118270596
LOC118270622	7.70	uncharacterized protein LOC118270622 isoform X1

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118270625	7.44	uncharacterized protein LOC118270625 isoform X1
LOC118270626	4.40	uncharacterized protein LOC118270626 isoform X1
LOC118270655	8.24	uncharacterized protein LOC118270655
LOC118270660	6.60	uncharacterized protein LOC118270660
LOC118270675	9.03	uncharacterized protein LOC118270675
LOC118270676	14.10	uncharacterized protein LOC118270676
LOC118270699	2.88	uncharacterized protein LOC118270699
LOC118270723	2.19	uncharacterized protein LOC118270723
LOC118270727	6.14	uncharacterized protein LOC118270727
LOC118270745	5.32	uncharacterized protein LOC118270745
LOC118270760	10.72	uncharacterized protein LOC118270760
LOC118270762	-9.87	uncharacterized protein LOC118270762
LOC118270770	9.21	uncharacterized protein LOC118270770
LOC118270784	6.07	uncharacterized protein LOC118270784
LOC118270786	11.88	uncharacterized protein LOC118270786
LOC118270787	7.69	uncharacterized protein LOC118270787
LOC118270788	11.78	uncharacterized protein LOC118270788
LOC118270789	9.08	uncharacterized protein LOC118270789
LOC118270805	12.15	uncharacterized protein LOC118270805
LOC118270819	9.74	uncharacterized protein LOC118270819
LOC118270824	4.24	uncharacterized protein LOC118270824
LOC118270825	5.28	uncharacterized protein LOC118270825
LOC118270841	8.47	uncharacterized protein LOC118270841
LOC118270842	7.70	uncharacterized protein LOC118270842
LOC118270853	2.48	uncharacterized protein LOC118270853
LOC118270862	-7.34	uncharacterized protein LOC118270862
LOC118270928	-5.56	uncharacterized protein LOC118270928
LOC118270947	-3.71	uncharacterized protein LOC118270947
LOC118270961	7.36	uncharacterized protein LOC118270961
LOC118270979	-2.51	uncharacterized protein LOC118270979
LOC118271006	-2.66	uncharacterized protein LOC118271006
LOC118271015	3.38	uncharacterized protein LOC118271015
LOC118271016	-2.04	uncharacterized protein LOC118271016
LOC118271019	-3.52	uncharacterized protein LOC118271019
LOC118271036	2.61	uncharacterized protein LOC118271036
LOC118271045	-3.38	uncharacterized protein LOC118271045 isoform X1
LOC118271110	2.54	uncharacterized protein LOC118271110
LOC118271160	2.14	uncharacterized protein LOC118271160
LOC118271210	4.86	uncharacterized protein LOC118271210
LOC118271266	-2.51	uncharacterized protein LOC118271266
LOC118271331	8.11	uncharacterized protein LOC118271331
LOC118271338	2.19	uncharacterized protein LOC118271338
LOC118271353	-4.05	uncharacterized protein LOC118271353
LOC118271360	6.36	uncharacterized protein LOC118271360 isoform X1
LOC118271377	2.32	uncharacterized protein LOC118271377
LOC118271384	-3.13	uncharacterized protein LOC118271384
LOC118271405	-3.37	uncharacterized protein LOC118271405
LOC118271409	4.12	uncharacterized protein LOC118271409
LOC118271410	2.68	uncharacterized protein LOC118271410
LOC118271428	3.02	uncharacterized protein LOC118271428
LOC118271439	3.00	uncharacterized protein LOC118271439
LOC118271444	-4.55	uncharacterized protein LOC118271444
LOC118271453	-2.49	uncharacterized protein LOC118271453
LOC118271468	2.93	uncharacterized protein LOC118271468
LOC118271481	2.70	uncharacterized protein LOC118271481
LOC118271498	2.03	uncharacterized protein LOC118271498
LOC118271589	2.38	uncharacterized protein LOC118271589 isoform X1
LOC118271706	2.42	uncharacterized protein LOC118271706 isoform X1
LOC118271797	3.43	uncharacterized protein LOC118271797
LOC118271800	2.49	uncharacterized protein LOC118271800 isoform X1
LOC118271819	-3.36	uncharacterized protein LOC118271819
LOC118271829	2.49	uncharacterized protein LOC118271829
LOC118271840	3.26	uncharacterized protein LOC118271840
LOC118271875	2.45	uncharacterized protein LOC118271875
LOC118271903	2.27	uncharacterized protein LOC118271903 isoform X1
LOC118271906	-4.42	uncharacterized protein LOC118271906
LOC118271975	5.24	uncharacterized protein LOC118271975
LOC118271977	-2.84	uncharacterized protein LOC118271977
LOC118271978	-2.75	uncharacterized protein LOC118271978
LOC118272061	4.07	uncharacterized protein LOC118272061
LOC118272138	-5.05	uncharacterized protein LOC118272138

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118272139	5.56	uncharacterized protein LOC118272139
LOC118272207	2.49	uncharacterized protein LOC118272207
LOC118272230	2.62	uncharacterized protein LOC118272230 isoform X1
LOC118272238	3.05	uncharacterized protein LOC118272238 isoform X1
LOC118272249	-2.91	uncharacterized protein LOC118272249
LOC118272279	-2.34	uncharacterized protein LOC118272279 isoform X1
LOC118272346	-3.73	uncharacterized protein LOC118272346
LOC118272368	-4.75	uncharacterized protein LOC118272368
LOC118272384	3.88	uncharacterized protein LOC118272384 isoform X1
LOC118272531	10.30	uncharacterized protein LOC118272531 isoform X1
LOC118272534	-4.72	uncharacterized protein LOC118272534
LOC118272535	-4.13	uncharacterized protein LOC118272535
LOC118272543	-3.52	uncharacterized protein LOC118272543
LOC118272573	2.85	uncharacterized protein LOC118272573
LOC118272582	-2.11	uncharacterized protein LOC118272582
LOC118272626	5.17	uncharacterized protein LOC118272626 isoform X1
LOC118272637	2.55	uncharacterized protein LOC118272637
LOC118272651	4.09	uncharacterized protein LOC118272651 isoform X1
LOC118272702	9.70	uncharacterized protein LOC118272702
LOC118272705	-3.86	uncharacterized protein LOC118272705
LOC118272732	4.56	uncharacterized protein LOC118272732
LOC118272768	2.41	uncharacterized protein LOC118272768
LOC118272877	7.85	uncharacterized protein LOC118272877
LOC118272887	-4.33	uncharacterized protein LOC118272887
LOC118272893	-2.90	uncharacterized protein LOC118272893
LOC118272948	-3.01	uncharacterized protein LOC118272948
LOC118272997	2.26	uncharacterized protein LOC118272997
LOC118273045	2.61	uncharacterized protein LOC118273045
LOC118273046	-2.13	uncharacterized protein LOC118273046
LOC118273062	7.41	uncharacterized protein LOC118273062
LOC118273134	9.34	uncharacterized protein LOC118273134
LOC118273243	8.16	uncharacterized protein LOC118273243
LOC118273281	-5.00	uncharacterized protein LOC118273281
LOC118273335	3.75	uncharacterized protein LOC118273335
LOC118273355	8.79	uncharacterized protein LOC118273355
LOC118273357	-2.70	uncharacterized protein LOC118273357
LOC118273361	9.15	uncharacterized protein LOC118273361
LOC118273394	2.87	uncharacterized protein LOC118273394
LOC118273479	4.46	uncharacterized protein LOC118273479
LOC118273695	-2.26	uncharacterized protein LOC118273695
LOC118273711	3.69	uncharacterized protein LOC118273711 isoform X1
LOC118273736	3.77	uncharacterized protein LOC118273736 isoform X1
LOC118273805	-4.92	uncharacterized protein LOC118273805
LOC118273832	-3.53	uncharacterized protein LOC118273832
LOC118273840	9.82	uncharacterized protein LOC118273840
LOC118273859	-5.72	uncharacterized protein LOC118273859
LOC118273870	-3.83	uncharacterized protein LOC118273870
LOC118273888	-2.88	uncharacterized protein LOC118273888 isoform X1
LOC118273950	-5.29	uncharacterized protein LOC118273950
LOC118273989	-2.25	uncharacterized protein LOC118273989
LOC118273998	4.54	uncharacterized protein LOC118273998
LOC118274026	7.05	uncharacterized protein LOC118274026
LOC118274027	5.07	uncharacterized protein LOC118274027
LOC118274034	6.67	uncharacterized protein LOC118274034
LOC118274037	3.99	uncharacterized protein LOC118274037
LOC118274096	-3.12	uncharacterized protein LOC118274096
LOC118274101	3.81	uncharacterized protein LOC118274101
LOC118274103	2.35	uncharacterized protein LOC118274103
LOC118274110	-3.07	uncharacterized protein LOC118274110
LOC118274129	7.15	uncharacterized protein LOC118274129
LOC118274142	-2.24	uncharacterized protein LOC118274142 isoform X1
LOC118274176	5.83	uncharacterized protein LOC118274176
LOC118274179	-3.29	uncharacterized protein LOC118274179
LOC118274196	-3.65	uncharacterized protein LOC118274196
LOC118274228	6.68	uncharacterized protein LOC118274228
LOC118274294	-3.07	uncharacterized protein LOC118274294
LOC118274319	3.39	uncharacterized protein LOC118274319
LOC118274343	4.13	uncharacterized protein LOC118274343
LOC118274363	6.43	uncharacterized protein LOC118274363
LOC118274366	2.53	uncharacterized protein LOC118274366

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118274367	6.30	uncharacterized protein LOC118274367
LOC118274368	7.20	uncharacterized protein LOC118274368
LOC118274369	5.38	uncharacterized protein LOC118274369
LOC118274372	7.23	uncharacterized protein LOC118274372
LOC118274373	5.18	uncharacterized protein LOC118274373
LOC118274469	-4.04	uncharacterized protein LOC118274469
LOC118274472	-3.41	uncharacterized protein LOC118274472
LOC118274473	3.11	uncharacterized protein LOC118274473
LOC118274532	3.41	uncharacterized protein LOC118274532
LOC118274576	2.81	uncharacterized protein LOC118274576
LOC118274598	3.83	uncharacterized protein LOC118274598
LOC118274600	-4.46	uncharacterized protein LOC118274600
LOC118274622	-2.14	uncharacterized protein LOC118274622
LOC118274662	6.24	uncharacterized protein LOC118274662
LOC118274701	2.43	uncharacterized protein LOC118274701
LOC118274757	2.17	uncharacterized protein LOC118274757
LOC118274762	-5.23	uncharacterized protein LOC118274762
LOC118274765	-4.78	uncharacterized protein LOC118274765
LOC118274771	3.34	uncharacterized protein LOC118274771
LOC118274808	-2.36	uncharacterized protein LOC118274808
LOC118274810	2.07	uncharacterized protein LOC118274810
LOC118274842	2.37	uncharacterized protein LOC118274842
LOC118274889	-2.69	uncharacterized protein LOC118274889
LOC118274913	-2.79	uncharacterized protein LOC118274913 isoform X1
LOC118274922	-3.60	uncharacterized protein LOC118274922
LOC118274924	-3.52	uncharacterized protein LOC118274924
LOC118274937	10.62	uncharacterized protein LOC118274937
LOC118274971	-4.53	uncharacterized protein LOC118274971
LOC118274973	9.47	uncharacterized protein LOC118274973
LOC118275001	-5.32	uncharacterized protein LOC118275001
LOC118275020	3.53	uncharacterized protein LOC118275020
LOC118275058	-2.66	uncharacterized protein LOC118275058 isoform X1
LOC118275072	-2.20	uncharacterized protein LOC118275072
LOC118275096	5.87	uncharacterized protein LOC118275096 isoform X1
LOC118275106	-4.38	uncharacterized protein LOC118275106
LOC118275134	-3.66	uncharacterized protein LOC118275134
LOC118275157	4.93	uncharacterized protein LOC118275157 isoform X1
LOC118275165	-2.51	uncharacterized protein LOC118275165
LOC118275189	4.43	uncharacterized protein LOC118275189
LOC118275199	-2.96	uncharacterized protein LOC118275199
LOC118275230	3.60	uncharacterized protein LOC118275230
LOC118275232	2.30	uncharacterized protein LOC118275232
LOC118275257	-2.51	uncharacterized protein LOC118275257
LOC118275353	-4.33	uncharacterized protein LOC118275353
LOC118275356	-2.62	uncharacterized protein LOC118275356
LOC118275357	-2.59	uncharacterized protein LOC118275357
LOC118275360	-2.44	uncharacterized protein LOC118275360
LOC118275506	-2.35	uncharacterized protein LOC118275506
LOC118275523	2.65	uncharacterized protein LOC118275523
LOC118275587	-2.76	uncharacterized protein LOC118275587 isoform X1
LOC118275630	-3.13	uncharacterized protein LOC118275630
LOC118275631	-2.81	uncharacterized protein LOC118275631
LOC118275643	-2.55	uncharacterized protein LOC118275643
LOC118275665	-2.67	uncharacterized protein LOC118275665
LOC118275681	2.52	uncharacterized protein LOC118275681
LOC118275682	2.34	uncharacterized protein LOC118275682
LOC118275703	4.90	uncharacterized protein LOC118275703 isoform X1
LOC118275740	2.38	uncharacterized protein LOC118275740
LOC118275764	-2.52	uncharacterized protein LOC118275764
LOC118275770	-4.58	uncharacterized protein LOC118275770
LOC118275827	-2.22	uncharacterized protein LOC118275827
LOC118275928	-3.42	uncharacterized protein LOC118275928
LOC118275982	2.05	uncharacterized protein LOC118275982
LOC118275983	-3.42	uncharacterized protein LOC118275983
LOC118275992	-4.32	uncharacterized protein LOC118275992
LOC118275997	2.42	uncharacterized protein LOC118275997
LOC118275998	3.45	uncharacterized protein LOC118275998
LOC118275999	-4.44	uncharacterized protein LOC118275999
LOC118276062	2.70	uncharacterized protein LOC118276062 isoform X1
LOC118276102	2.61	uncharacterized protein LOC118276102 isoform X1
LOC118276175	-5.14	uncharacterized protein LOC118276175

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118276237	8.45	uncharacterized protein LOC118276237
LOC118276264	2.42	uncharacterized protein LOC118276264
LOC118276283	-3.12	uncharacterized protein LOC118276283
LOC118276292	4.79	uncharacterized protein LOC118276292
LOC118276296	2.08	uncharacterized protein LOC118276296 isoform X1
LOC118276303	-2.12	uncharacterized protein LOC118276303
LOC118276310	8.48	uncharacterized protein LOC118276310
LOC118276311	8.81	uncharacterized protein LOC118276311
LOC118276339	-5.06	uncharacterized protein LOC118276339
LOC118276352	-2.90	uncharacterized protein LOC118276352
LOC118276377	9.41	uncharacterized protein LOC118276377
LOC118276382	-2.53	uncharacterized protein LOC118276382
LOC118276383	10.24	uncharacterized protein LOC118276383 isoform X1
LOC118276385	6.17	uncharacterized protein LOC118276385
LOC118276391	-4.66	uncharacterized protein LOC118276391
LOC118276408	4.49	uncharacterized protein LOC118276408
LOC118276449	2.38	uncharacterized protein LOC118276449 isoform X1
LOC118276456	-3.32	uncharacterized protein LOC118276456
LOC118276480	-2.70	uncharacterized protein LOC118276480
LOC118276504	2.28	uncharacterized protein LOC118276504
LOC118276548	2.49	uncharacterized protein LOC118276548
LOC118276569	-3.08	uncharacterized protein LOC118276569
LOC118276600	2.43	uncharacterized protein LOC118276600 isoform X1
LOC118276652	2.19	uncharacterized protein LOC118276652
LOC118276719	-4.73	uncharacterized protein LOC118276719
LOC118276750	-3.56	uncharacterized protein LOC118276750
LOC118276770	2.51	uncharacterized protein LOC118276770
LOC118276776	-3.95	uncharacterized protein LOC118276776 isoform X1
LOC118276799	4.08	uncharacterized protein LOC118276799
LOC118276823	-5.92	uncharacterized protein LOC118276823
LOC118276824	2.54	uncharacterized protein LOC118276824
LOC118276865	2.27	uncharacterized protein LOC118276865
LOC118276871	-4.68	uncharacterized protein LOC118276871
LOC118276938	3.74	uncharacterized protein LOC118276938 isoform X1
LOC118276965	4.98	uncharacterized protein LOC118276965
LOC118276971	6.99	uncharacterized protein LOC118276971
LOC118276992	3.12	uncharacterized protein LOC118276992 isoform X1
LOC118277015	4.46	uncharacterized protein LOC118277015 isoform X1
LOC118277123	7.27	uncharacterized protein LOC118277123
LOC118277128	2.59	uncharacterized protein LOC118277128
LOC118277130	-2.82	uncharacterized protein LOC118277130
LOC118277131	9.20	uncharacterized protein LOC118277131
LOC118277141	4.66	uncharacterized protein LOC118277141
LOC118277143	4.33	uncharacterized protein LOC118277143 isoform X1
LOC118277153	-2.47	uncharacterized protein LOC118277153
LOC118277160	-4.13	uncharacterized protein LOC118277160
LOC118277169	2.22	uncharacterized protein LOC118277169
LOC118277170	-3.07	uncharacterized protein LOC118277170
LOC118277173	4.61	uncharacterized protein LOC118277173
LOC118277184	-6.41	uncharacterized protein LOC118277184
LOC118277194	-3.13	uncharacterized protein LOC118277194
LOC118277288	-7.65	uncharacterized protein LOC118277288
LOC118277478	8.97	uncharacterized protein LOC118277478 isoform X1
LOC118277507	6.84	uncharacterized protein LOC118277507
LOC118277540	2.53	uncharacterized protein LOC118277540 isoform X1
LOC118277546	3.83	uncharacterized protein LOC118277546 isoform X1
LOC118277637	-5.59	uncharacterized protein LOC118277637
LOC118277645	2.79	uncharacterized protein LOC118277645
LOC118277727	-3.53	uncharacterized protein LOC118277727
LOC118277743	7.54	uncharacterized protein LOC118277743 isoform X1
LOC118277809	-3.67	uncharacterized protein LOC118277809
LOC118277812	-3.63	uncharacterized protein LOC118277812
LOC118277813	6.63	uncharacterized protein LOC118277813
LOC118277817	4.90	uncharacterized protein LOC118277817
LOC118277818	-3.35	uncharacterized protein LOC118277818
LOC118277820	-2.35	uncharacterized protein LOC118277820
LOC118277862	6.05	uncharacterized protein LOC118277862 isoform X1
LOC118277910	-5.97	uncharacterized protein LOC118277910
LOC118278009	3.72	uncharacterized protein LOC118278009
LOC118278020	-2.28	uncharacterized protein LOC118278020

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118278049	2.60	uncharacterized protein LOC118278049
LOC118278064	-4.93	uncharacterized protein LOC118278064
LOC118278080	5.61	uncharacterized protein LOC118278080
LOC118278128	7.23	uncharacterized protein LOC118278128
LOC118278131	6.97	uncharacterized protein LOC118278131
LOC118278139	-4.93	uncharacterized protein LOC118278139
LOC118278167	3.71	uncharacterized protein LOC118278167
LOC118278193	-2.81	uncharacterized protein LOC118278193
LOC118278196	6.09	uncharacterized protein LOC118278196 isoform X1
LOC118278206	-8.68	uncharacterized protein LOC118278206
LOC118278223	-3.51	uncharacterized protein LOC118278223
LOC118278233	7.82	uncharacterized protein LOC118278233 isoform X1
LOC118278240	2.05	uncharacterized protein LOC118278240
LOC118278250	-2.03	uncharacterized protein LOC118278250
LOC118278259	10.03	uncharacterized protein LOC118278259
LOC118278261	2.24	uncharacterized protein LOC118278261 isoform X1
LOC118278596	-2.66	uncharacterized protein LOC118278596
LOC118278613	2.01	uncharacterized protein LOC118278613
LOC118278633	2.51	uncharacterized protein LOC118278633
LOC118278644	-3.62	uncharacterized protein LOC118278644
LOC118278688	2.52	uncharacterized protein LOC118278688
LOC118278713	-2.49	uncharacterized protein LOC118278713
LOC118278746	-2.00	uncharacterized protein LOC118278746
LOC118278749	3.34	uncharacterized protein LOC118278749 isoform X1
LOC118278798	-3.53	uncharacterized protein LOC118278798
LOC118278944	8.01	uncharacterized protein LOC118278944
LOC118278951	2.66	uncharacterized protein LOC118278951
LOC118278958	2.79	uncharacterized protein LOC118278958
LOC118278961	2.98	uncharacterized protein LOC118278961
LOC118278963	-2.05	uncharacterized protein LOC118278963
LOC118278983	2.49	uncharacterized protein LOC118278983
LOC118278984	2.22	uncharacterized protein LOC118278984
LOC118279020	-2.03	uncharacterized protein LOC118279020
LOC118279028	-2.40	uncharacterized protein LOC118279028
LOC118279047	2.17	uncharacterized protein LOC118279047 isoform X1
LOC118279065	2.84	uncharacterized protein LOC118279065 isoform X1
LOC118279089	-7.98	uncharacterized protein LOC118279089
LOC118279091	2.48	uncharacterized protein LOC118279091
LOC118279092	-3.35	uncharacterized protein LOC118279092
LOC118279111	-2.47	uncharacterized protein LOC118279111
LOC118279146	-7.28	uncharacterized protein LOC118279146
LOC118279165	-2.46	uncharacterized protein LOC118279165
LOC118279188	2.73	uncharacterized protein LOC118279188
LOC118279214	5.95	uncharacterized protein LOC118279214
LOC118279220	-2.63	uncharacterized protein LOC118279220
LOC118279221	11.29	uncharacterized protein LOC118279221
LOC118279260	-2.44	uncharacterized protein LOC118279260
LOC118279281	-3.01	uncharacterized protein LOC118279281
LOC118279282	7.11	uncharacterized protein LOC118279282
LOC118279305	2.15	uncharacterized protein LOC118279305
LOC118279341	-2.32	uncharacterized protein LOC118279341
LOC118279350	2.31	uncharacterized protein LOC118279350 isoform X1
LOC118279406	-3.06	uncharacterized protein LOC118279406
LOC118279543	-2.45	uncharacterized protein LOC118279543
LOC118279617	5.42	uncharacterized protein LOC118279617 isoform X1
LOC118279624	-4.52	uncharacterized protein LOC118279624
LOC118279636	5.71	uncharacterized protein LOC118279636 isoform X1
LOC118279637	3.80	uncharacterized protein LOC118279637 isoform X1
LOC118279797	-2.87	uncharacterized protein LOC118279797 isoform X1
LOC118279817	-3.28	uncharacterized protein LOC118279817 isoform X1
LOC118279833	5.54	uncharacterized protein LOC118279833 isoform X1
LOC118279864	3.07	uncharacterized protein LOC118279864
LOC118279895	4.34	uncharacterized protein LOC118279895
LOC118279918	3.89	uncharacterized protein LOC118279918
LOC118279923	-3.17	uncharacterized protein LOC118279923 isoform X1
LOC118279973	5.12	uncharacterized protein LOC118279973
LOC118279984	4.91	uncharacterized protein LOC118279984 isoform X1
LOC118280028	3.36	uncharacterized protein LOC118280028
LOC118280034	2.24	uncharacterized protein LOC118280034 isoform X1
LOC118280039	8.81	uncharacterized protein LOC118280039
LOC118280057	7.68	uncharacterized protein LOC118280057 isoform X1

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118280067	8.58	uncharacterized protein LOC118280067 isoform X1
LOC118280183	3.18	uncharacterized protein LOC118280183
LOC118280191	-2.01	uncharacterized protein LOC118280191
LOC118280218	4.06	uncharacterized protein LOC118280218
LOC118280326	-2.38	uncharacterized protein LOC118280326
LOC118280353	-3.94	uncharacterized protein LOC118280353 isoform X1
LOC118280383	2.36	uncharacterized protein LOC118280383
LOC118280388	2.83	uncharacterized protein LOC118280388
LOC118280393	-2.04	uncharacterized protein LOC118280393
LOC118280418	2.25	uncharacterized protein LOC118280418 isoform X1
LOC118280446	-3.25	uncharacterized protein LOC118280446
LOC118280499	2.04	uncharacterized protein LOC118280499
LOC118280506	5.77	uncharacterized protein LOC118280506
LOC118280523	-2.80	uncharacterized protein LOC118280523
LOC118280580	4.87	uncharacterized protein LOC118280580
LOC118280648	-2.82	uncharacterized protein LOC118280648
LOC118280649	-3.18	uncharacterized protein LOC118280649
LOC118280686	-2.08	uncharacterized protein LOC118280686
LOC118280763	-3.41	uncharacterized protein LOC118280763
LOC118280768	-6.69	uncharacterized protein LOC118280768
LOC118280776	4.65	uncharacterized protein LOC118280776
LOC118280833	-3.26	uncharacterized protein LOC118280833
LOC118280844	-4.32	uncharacterized protein LOC118280844
LOC118280854	-2.72	uncharacterized protein LOC118280854
LOC118280969	4.76	uncharacterized protein LOC118280969
LOC118280979	3.44	uncharacterized protein LOC118280979
LOC118281023	2.67	uncharacterized protein LOC118281023
LOC118281025	2.86	uncharacterized protein LOC118281025
LOC118281067	2.28	uncharacterized protein LOC118281067
LOC118281069	-3.49	uncharacterized protein LOC118281069
LOC118281147	4.63	uncharacterized protein LOC118281147
LOC118281156	-2.01	uncharacterized protein LOC118281156
LOC118281162	-3.12	uncharacterized protein LOC118281162
LOC118281163	-2.67	uncharacterized protein LOC118281163
LOC118281185	4.01	uncharacterized protein LOC118281185
LOC118281277	-3.05	uncharacterized protein LOC118281277
LOC118281306	2.16	uncharacterized protein LOC118281306
LOC118281352	3.70	uncharacterized protein LOC118281352
LOC118281353	4.95	uncharacterized protein LOC118281353
LOC118281385	-4.63	uncharacterized protein LOC118281385
LOC118281390	3.09	uncharacterized protein LOC118281390 isoform X1
LOC118281397	-2.05	uncharacterized protein LOC118281397
LOC118281403	-2.91	uncharacterized protein LOC118281403
LOC118281410	3.97	uncharacterized protein LOC118281410
LOC118281430	-2.55	uncharacterized protein LOC118281430
LOC118281431	-2.39	uncharacterized protein LOC118281431
LOC118281436	4.79	uncharacterized protein LOC118281436
LOC118281465	-2.08	uncharacterized protein LOC118281465
LOC118281485	7.51	uncharacterized protein LOC118281485
LOC118281493	-3.76	uncharacterized protein LOC118281493
LOC118281518	-4.58	uncharacterized protein LOC118281518
LOC118281567	3.48	uncharacterized protein LOC118281567
LOC118281574	3.63	uncharacterized protein LOC118281574
LOC118281692	6.39	uncharacterized protein LOC118281692
LOC118281695	-3.08	uncharacterized protein LOC118281695
LOC118281722	2.16	uncharacterized protein LOC118281722
LOC118281755	3.34	uncharacterized protein LOC118281755
LOC118281784	-2.31	uncharacterized protein LOC118281784 isoform X1
LOC118281889	6.66	uncharacterized protein LOC118281889 isoform X1
LOC118281890	7.85	uncharacterized protein LOC118281890 isoform X1
LOC118281915	-2.06	uncharacterized protein LOC118281915
LOC118281926	4.67	uncharacterized protein LOC118281926
LOC118281927	-3.49	uncharacterized protein LOC118281927
LOC118281942	2.19	uncharacterized protein LOC118281942
LOC118281945	-8.00	uncharacterized protein LOC118281945
LOC118282073	2.61	uncharacterized protein LOC118282073
LOC118282214	3.06	uncharacterized protein LOC118282214
LOC118282226	5.57	uncharacterized protein LOC118282226
LOC118282315	4.69	uncharacterized protein LOC118282315
LOC118282341	-4.98	uncharacterized protein LOC118282341

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118282357	8.85	uncharacterized protein LOC118282357
LOC118282387	-3.66	uncharacterized protein LOC118282387 isoform X1
LOC118282432	2.39	uncharacterized protein LOC118282432
LOC118282438	3.06	uncharacterized protein LOC118282438
LOC118282480	2.08	uncharacterized protein LOC118282480
LOC118262715	-2.26	uncharacterized protein PB18E9.04c-like
LOC118262535	5.50	UPF0605 protein CG18335-like
LOC118273334	2.51	uricase-like
LOC118279986	2.90	U-scoloptoxin(01)-Cw1a-like
LOC118279993	4.59	U-scoloptoxin(01)-Cw1a-like
LOC118263625	6.51	U-scoloptoxin(01)-Cw1a-like
LOC118263556	9.76	U-scoloptoxin(01)-Cw1a-like
LOC118262758	2.08	U-scoloptoxin(19)-Sm1a-like
LOC118262745	2.30	U-scoloptoxin(19)-Sm1a-like
LOC118263156	2.70	U-scoloptoxin(19)-Sm1a-like
LOC118262197	3.49	U-scoloptoxin(19)-Sm1a-like
LOC118277941	-2.00	UTP--glucose-1-phosphate uridylyltransferase-like isoform X1
LOC118281610	2.03	vacuolar protein sorting-associated protein 4A-like
LOC118271773	-2.55	vasoactive intestinal polypeptide receptor 2-like
LOC118273013	5.23	vasorin-like isoform X1
LOC118278418	4.82	vegetative cell wall protein gp1-like
LOC118267908	8.70	vegetative cell wall protein gp1-like
LOC118273858	12.55	vegetative cell wall protein gp1-like
LOC118272696	13.34	vegetative cell wall protein gp1-like
LOC118270627	2.22	vegetative cell wall protein gp1-like
LOC118268300	3.37	venom allergen 5.02-like
LOC118268283	4.22	venom allergen 5.02-like
LOC118262636	-2.36	venom carboxylesterase-6-like
LOC118265778	2.22	venom carboxylesterase-6-like
LOC118275668	4.96	venom carboxylesterase-6-like
LOC118270895	-2.01	venom carboxylesterase-6-like isoform X1
LOC118273663	2.63	venom dipeptidyl peptidase 4-like isoform X1
LOC118273505	2.64	venom dipeptidyl peptidase 4-like isoform X1
LOC118282292	-4.63	venom peptide CtAPI-like isoform X1
LOC118282209	-3.06	venom peptide CtAPI-like isoform X1
LOC118278956	-5.21	venom protease-like
LOC118278920	-4.75	venom protease-like isoform X1
LOC118274807	-2.38	venom serine carboxypeptidase-like
LOC118269911	-6.54	venom serine protease inhibitor-like
LOC118269891	-3.72	venom serine protease inhibitor-like
LOC118268742	-3.34	vitamin K epoxide reductase complex subunit 1-like protein 1
LOC118268852	-2.13	vitamin K epoxide reductase complex subunit 1-like protein 1
LOC118279270	5.13	vitellin-degrading protease-like
LOC118280769	-6.58	vitellogenin-like
LOC118280767	-5.92	vitellogenin-like
LOC118277091	2.21	von Hippel-Lindau disease tumor suppressor-like
LOC118277089	3.13	von Hippel-Lindau disease tumor suppressor-like
LOC118271079	2.13	WD repeat domain phosphoinositide-interacting protein 4-like
LOC118266962	-2.37	WD repeat-containing protein 78-like
LOC118267673	-2.42	xanthine dehydrogenase 1-like
LOC118267950	-3.33	xanthine dehydrogenase 2-like
LOC118267938	-3.07	xanthine dehydrogenase-like
LOC118265469	-2.39	xanthine dehydrogenase-like
LOC118267672	-2.21	xanthine dehydrogenase-like
LOC118267651	-2.14	xanthine dehydrogenase-like
LOC118267793	5.51	xanthine dehydrogenase-like
LOC118267951	6.30	xanthine dehydrogenase-like
LOC118269899	-2.08	xylulose kinase-like
LOC118264722	3.90	zinc carboxypeptidase A 1-like
LOC118266727	2.73	zinc carboxypeptidase A 1-like isoform X1
LOC118270911	-4.67	zinc finger BED domain-containing protein 6-like
LOC118264260	-2.35	zinc finger BED domain-containing protein 6-like
LOC118262249	2.20	zinc finger CCHC domain-containing protein 24-like
LOC118265342	2.53	zinc finger CCHC domain-containing protein 24-like
LOC118277602	2.02	zinc finger MYM-type protein 1-like
LOC118264678	2.13	zinc finger MYM-type protein 1-like
LOC118272602	2.28	zinc finger MYM-type protein 1-like
LOC118270336	3.06	zinc finger MYM-type protein 1-like
LOC118267857	5.07	zinc finger MYM-type protein 5-like
LOC118282327	3.79	zinc finger protein 112-like isoform X1
LOC118263161	3.81	zinc finger protein 395-like

Appendix A. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118282082	-2.26	zinc finger protein 567-like
LOC118280641	-2.54	zinc finger protein rotund-like isoform X1
LOC118280470	2.31	zinc finger protein swm-like isoform X1
LOC118263591	2.25	zinc transporter 1-like
LOC118275735	-2.44	zinc transporter ZIP1-like
LOC118263330	2.67	zinc/cadmium resistance protein-like isoform X1
LOC118264517	-3.59	zinc-type alcohol dehydrogenase-like protein SERP1785
LOC118264683	-2.84	zinc-type alcohol dehydrogenase-like protein SERP1785
LOC118264652	-2.83	zinc-type alcohol dehydrogenase-like protein SERP1785
LOC118282477	2.39	zonadhesin-like
LOC118282451	2.78	zonadhesin-like
LOC118271594	3.02	zonadhesin-like
LOC118264895	6.57	zonadhesin-like
LOC118275467	4.09	zonadhesin-like isoform X1
LOC118261970	4.15	zonadhesin-like isoform X1

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains.

Gene ID	log2FC	Description
LOC118266460	-5.09	(2R)-3-sulfolactate dehydrogenase (NADP(+))-like
LOC118271698	-2.30	1,4-alpha-glucan-branching enzyme-like
LOC118273853	3.58	15-hydroxyprostaglandin dehydrogenase [NAD(+)
LOC118264063	-4.77	15-hydroxyprostaglandin dehydrogenase [NAD(+)-like
LOC118264062	-4.65	15-hydroxyprostaglandin dehydrogenase [NAD(+)-like
LOC118264064	-3.50	15-hydroxyprostaglandin dehydrogenase [NAD(+)-like
LOC118263962	-2.82	15-hydroxyprostaglandin dehydrogenase [NAD(+)-like
LOC118269957	-2.21	17-beta-hydroxysteroid dehydrogenase 13-like isoform X1
LOC118268885	-3.87	17-beta-hydroxysteroid dehydrogenase 14-like
LOC118269450	-2.49	17-beta-hydroxysteroid dehydrogenase 14-like
LOC118269452	-2.39	17-beta-hydroxysteroid dehydrogenase 14-like
LOC118262433	-4.85	1-acyl-sn-glycerol-3-phosphate acyltransferase beta-like
LOC118262431	2.90	1-acyl-sn-glycerol-3-phosphate acyltransferase beta-like
LOC118267056	2.32	23 kDa integral membrane protein-like
LOC118276616	2.82	23 kDa integral membrane protein-like
LOC118279051	3.74	32 kDa beta-galactoside-binding lectin-like
LOC118278788	5.78	32 kDa beta-galactoside-binding lectin-like
LOC118278787	3.00	32 kDa beta-galactoside-binding lectin-like isoform X1
LOC118279782	2.42	3-hydroxy-3-methylglutaryl-coenzyme A reductase
LOC118266304	-3.92	3-ketoacyl-CoA thiolase, mitochondrial-like
LOC118266245	-3.63	3-ketoacyl-CoA thiolase, mitochondrial-like
LOC118267137	-4.62	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
LOC118271177	-4.13	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
LOC118275088	-3.94	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
LOC118275021	-3.66	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
LOC118275066	-3.64	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
LOC118275087	-3.05	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
LOC118274902	-2.84	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
LOC118268882	-2.67	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
LOC118269451	-2.54	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
LOC118268886	-2.12	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
LOC118269453	-2.11	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
LOC118278663	-2.77	4-coumarate--CoA ligase 1-like
LOC118269139	-4.74	4-hydroxyphenylpyruvate dioxygenase-like
LOC118268976	-4.25	4-hydroxyphenylpyruvate dioxygenase-like
LOC118279423	2.07	5.8S ribosomal RNA
LOC118279425	2.19	5.8S ribosomal RNA
LOC118279426	2.21	5.8S ribosomal RNA
LOC118264873	2.61	5.8S ribosomal RNA
LOC118266517	2.90	A disintegrin and metalloproteinase with thrombospondin motifs 16-like
LOC118266126	2.93	A disintegrin and metalloproteinase with thrombospondin motifs 16-like
LOC118275258	2.53	A disintegrin and metalloproteinase with thrombospondin motifs adt-2-like isoform X1
LOC118270767	2.37	ABC transporter G family member 23-like
LOC118270222	2.40	ABC transporter G family member 23-like
LOC118278886	-2.83	acanthoscurrin-1-like
LOC118278083	-3.49	acanthoscurrin-2-like
LOC118274025	5.03	acetylcholine receptor subunit beta-like 2 isoform X1
LOC118276152	-2.75	acetylcholinesterase-like
LOC118276155	-2.45	acetylcholinesterase-like
LOC118276153	-2.19	acetylcholinesterase-like
LOC118264687	9.38	acidic repeat-containing protein-like
LOC118281870	9.39	acidic repeat-containing protein-like
LOC118275009	-3.57	acrosin-like
LOC118270032	3.52	actin cytoskeleton-regulatory complex protein PAN1-like
LOC118270598	11.89	actin cytoskeleton-regulatory complex protein PAN1-like
LOC118279603	4.46	actin-like protein 6B
LOC118273023	2.77	activating signal cointegrator 1 complex subunit 1-like isoform X1
LOC118264933	-3.99	acyl-CoA Delta(11) desaturase-like
LOC118269215	10.96	acyl-CoA Delta(11) desaturase-like
LOC118269154	14.05	acyl-CoA Delta(11) desaturase-like
LOC118269923	6.32	acyl-CoA desaturase 1-like
LOC118269922	13.45	acyl-CoA desaturase 1-like
LOC118278116	-2.82	acyl-CoA synthetase short-chain family member 3, mitochondrial-like
LOC118274253	2.08	acyl-coenzyme A thioesterase 13-like
LOC118275125	4.01	adenosine deaminase 2-like
LOC118275163	-2.69	adenosine deaminase AGSA-like
LOC118279912	2.03	adenosylhomocysteinase-like 1 isoform X1
LOC118264822	-2.32	adenylosuccinate lyase-like
LOC118264826	-2.02	adenylosuccinate lyase-like
LOC118270960	2.20	adiponectin receptor protein-like
LOC118281460	6.00	adult-specific cuticular protein ACP-20-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118261995	6.80	adult-specific cuticular protein ACP-20-like
LOC118262128	8.62	adult-specific cuticular protein ACP-20-like
LOC118275749	9.21	adult-specific cuticular protein ACP-20-like
LOC118264590	2.88	alcohol dehydrogenase [acceptor-like
LOC118264589	4.22	alcohol dehydrogenase [acceptor-like
LOC118264588	4.58	alcohol dehydrogenase [acceptor-like
LOC118263961	-3.44	alcohol dehydrogenase 1-like
LOC118272357	-3.97	alcohol dehydrogenase class-3 chain L-like
LOC118265216	-2.12	aldehyde dehydrogenase X, mitochondrial-like isoform X1
LOC118268489	-2.61	aldehyde dehydrogenase, cytosolic 1-like
LOC118265756	-2.01	aldehyde dehydrogenase, dimeric NADP-preferring-like isoform X1
LOC118273932	-2.78	aldehyde dehydrogenase, mitochondrial-like
LOC118267799	2.41	aldehyde oxidase 1-like
LOC118279607	-5.08	aldo-keto reductase AKR2E4-like
LOC118279519	-5.02	aldo-keto reductase AKR2E4-like
LOC118274940	-2.53	aldo-keto reductase AKR2E4-like
LOC118274962	-2.45	aldo-keto reductase AKR2E4-like
LOC118280048	-2.02	aldo-keto reductase AKR2E4-like
LOC118279988	-2.17	aldo-keto reductase AKR2E4-like isoform X1
LOC118264688	-5.09	aldo-keto reductase family 1 member B1-like
LOC118278592	-2.51	aldo-keto reductase family 1 member B1-like
LOC118269437	4.43	alkaline phosphatase, tissue-nonspecific isozyme-like
LOC118267498	-2.39	alkaline phosphatase-like isoform X1
LOC118264112	4.11	alkyldihydroxyacetonephosphate synthase-like
LOC118268332	-2.14	alkylglycerol monooxygenase-like
LOC118268627	-2.53	allantoicase-like
LOC118265699	-6.26	allergen Tha p 1-like
LOC118266455	-6.12	allergen Tha p 1-like
LOC118265697	-2.28	allergen Tha p 1-like
LOC118265698	-3.27	allergen Tha p 1-like isoform X1
LOC118265695	3.90	allergen Tha p 1-like isoform X1
LOC118266098	4.75	allergen Tha p 1-like isoform X1
LOC118265620	2.01	alpha-aminoadipic semialdehyde synthase, mitochondrial-like
LOC118266156	-2.84	alpha-amylase 4N-like
LOC118266145	-2.49	alpha-amylase 4N-like
LOC118277109	4.43	alpha-crystallin A chain-like
LOC118276752	4.72	alpha-crystallin A chain-like
LOC118267030	-2.46	alpha-mannosidase 2-like
LOC118266499	5.40	alpha-N-acetylgalactosaminidase-like
LOC118266307	5.55	alpha-N-acetylgalactosaminidase-like
LOC118271281	-2.98	alpha-N-acetylglucosaminidase-like
LOC118271305	-2.77	alpha-N-acetylglucosaminidase-like
LOC118274753	-4.21	alpha-tocopherol transfer protein-like
LOC118274760	-3.90	alpha-tocopherol transfer protein-like
LOC118274796	-3.29	alpha-tocopherol transfer protein-like
LOC118274755	-2.60	alpha-tocopherol transfer protein-like
LOC118274737	-2.46	alpha-tocopherol transfer protein-like
LOC118274072	2.36	alpha-tocopherol transfer protein-like
LOC118274939	2.88	alpha-tocopherol transfer protein-like
LOC118263738	3.16	alpha-tocopherol transfer protein-like
LOC118274015	3.17	alpha-tocopherol transfer protein-like
LOC118274961	3.35	alpha-tocopherol transfer protein-like
LOC118275108	3.44	alpha-tocopherol transfer protein-like
LOC118263381	4.59	alpha-tocopherol transfer protein-like
LOC118275225	4.99	alpha-tocopherol transfer protein-like
LOC118273546	2.42	alpha-tocopherol transfer protein-like isoform X1
LOC118273542	3.23	alpha-tocopherol transfer protein-like isoform X1
LOC118273544	4.50	alpha-tocopherol transfer protein-like isoform X1
LOC118275177	6.11	alpha-tocopherol transfer protein-like isoform X1
LOC118275090	6.18	alpha-tocopherol transfer protein-like isoform X1
LOC118265489	5.43	altered inheritance of mitochondria protein 3-like
LOC118264312	-2.32	amino acid transporter AVT1A-like
LOC118261808	-3.08	aminoacylase-1-like
LOC118265511	-2.28	aminoacylase-1-like
LOC118278202	-2.73	aminomethyltransferase, mitochondrial-like
LOC118269054	2.20	amyloid protein-binding protein 2-like isoform X1
LOC118279866	-3.11	androgen-dependent TFPI-regulating protein-like
LOC118273698	-2.54	androgen-dependent TFPI-regulating protein-like
LOC118279898	-2.32	androgen-dependent TFPI-regulating protein-like
LOC118281823	-2.20	androgen-induced gene 1 protein-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118267158	3.23	angiopoietin-related protein 2-like
LOC118270470	2.56	ankyrin repeat and MYND domain-containing protein 1-like
LOC118280221	-2.27	anoctamin-4-like isoform X1
LOC118265780	-3.86	antichymotrypsin-1-like isoform X1
LOC118265781	-3.39	antichymotrypsin-1-like isoform X1
LOC118274630	-3.20	apolipophorin-3
LOC118280748	-4.43	apolipophorins-like isoform X1
LOC118276696	4.38	apolipoprotein D-like
LOC118279537	-2.27	aromatic-L-amino-acid decarboxylase-like
LOC118265398	2.71	arrestin domain-containing protein 2-like
LOC118268635	2.04	arylsulfatase B-like
LOC118268296	2.07	arylsulfatase B-like
LOC118268302	3.02	arylsulfatase J-like
LOC118268295	3.18	arylsulfatase J-like
LOC118263189	-2.18	aspartate aminotransferase, cytoplasmic-like isoform X1
LOC118262037	2.14	aspartate--tRNA ligase, mitochondrial-like
LOC118278708	5.33	ATP synthase subunit beta, mitochondrial-like
LOC118278986	6.72	ATP synthase subunit beta, mitochondrial-like
LOC118265120	2.06	ATP-binding cassette sub-family G member 1-like
LOC118270306	-2.50	ATP-dependent 6-phosphofructokinase-like isoform X1
LOC118282422	4.21	ATP-dependent DNA helicase pif1-like
LOC118276278	6.40	ATP-dependent RNA helicase glh-1-like
LOC118279379	-4.02	ATP-sensitive inward rectifier potassium channel 15-like isoform X1
LOC118279386	2.49	ATP-sensitive inward rectifier potassium channel 1-like
LOC118267152	3.21	atrial natriuretic peptide-converting enzyme-like
LOC118264419	2.03	autophagy protein 12-like
LOC118261904	3.54	band 7 protein AGAP004871-like isoform X1
LOC118261942	6.72	band 7 protein AGAP004871-like isoform X1
LOC118282051	-4.32	B-cell CLL/lymphoma 6 member B protein-like
LOC118277435	3.26	beta-1,3-galactosyltransferase 5-like
LOC118272701	-2.47	beta-1,3-glucan-binding protein-like
LOC118281636	-2.38	beta-1,3-glucan-binding protein-like
LOC118271849	5.48	beta-1,4-galactosyltransferase 4-like
LOC118274075	-4.70	beta-ureidopropionase-like
LOC118273984	-3.47	beta-ureidopropionase-like
LOC118262803	-5.19	bile salt-activated lipase-like
LOC118282211	-3.19	bile salt-activated lipase-like
LOC118263255	3.90	bombyxin A-1 homolog
LOC118268312	3.59	bombyxin A-3 homolog
LOC118267724	-2.13	brachyurin-like
LOC118280118	5.76	brain-specific serine protease 4-like isoform X1
LOC118266456	8.74	bromodomain-containing protein 4-like
LOC118275625	-3.34	C-1-tetrahydrofolate synthase, cytoplasmic isoform X1
LOC118281677	-2.08	cadherin-related tumor suppressor-like
LOC118278470	2.29	calcium-binding protein P-like
LOC118269568	-3.80	calmodulin-1-like
LOC118274847	-3.25	calmodulin-like isoform X1
LOC118281029	2.01	calmodulin-like protein 4
LOC118274334	-3.51	calphotin-like
LOC118263689	-2.65	capon-like protein isoform X1
LOC118270569	-2.07	carbonic anhydrase 1-like
LOC118268288	-2.77	carbonic anhydrase 1-like isoform X1
LOC118268251	-3.42	carbonic anhydrase 7-like
LOC118280653	-2.13	carbonyl reductase [NADPH 3-like
LOC118276151	-3.28	carboxylesterase 1C-like
LOC118272141	-2.66	carboxylesterase 1E-like
LOC118272142	-3.39	carboxylesterase 5A-like
LOC118279505	-3.03	carboxylesterase 5A-like
LOC118271478	-5.03	carboxypeptidase B-like
LOC118271425	-4.74	carboxypeptidase B-like
LOC118271477	-4.08	carboxypeptidase B-like
LOC118271474	-3.30	carboxypeptidase B-like
LOC118271473	-2.06	carboxypeptidase B-like
LOC118275055	2.10	carboxypeptidase B-like
LOC118266420	5.14	carboxypeptidase B-like
LOC118271974	6.50	carboxypeptidase B-like
LOC118271913	6.56	carboxypeptidase B-like
LOC118271475	-2.66	carboxypeptidase B-like isoform X1
LOC118269492	2.44	carboxypeptidase M-like
LOC118267946	-4.92	carcinine transporter-like
LOC118280466	-3.98	carcinine transporter-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118280478	-3.34	carcinine transporter-like
LOC118282333	3.86	cardioacceleratory peptide receptor-like isoform X1
LOC118261782	3.98	cardioacceleratory peptide receptor-like isoform X1
LOC118277523	2.39	caspase-1-like
LOC118267266	3.24	caspase-1-like
LOC118276022	-3.63	catalase-like
LOC118262513	-2.30	catalase-like
LOC118261852	3.74	catalase-like
LOC118261836	4.48	catalase-like
LOC118262151	4.69	catalase-like
LOC118282418	5.24	catalase-like
LOC118262153	5.71	catalase-like
LOC118262150	6.49	catalase-like
LOC118261834	6.96	catalase-like
LOC118282430	8.99	catalase-like
LOC118276442	2.21	cathepsin L1-like
LOC118271292	-2.49	cathepsin O-like
LOC118271264	-2.48	cathepsin O-like
LOC118271291	-2.47	cathepsin O-like
LOC118269235	2.12	cationic amino acid transporter 2-like isoform X1
LOC118277463	7.47	CCAAT/enhancer-binding protein-like
LOC118266494	-3.25	CD109 antigen-like
LOC118279053	2.32	cell surface glycoprotein 1-like
LOC118269430	2.52	cell surface glycoprotein 1-like isoform X1
LOC118280675	2.90	cell wall protein DAN4-like
LOC118267654	7.75	cell wall protein DAN4-like
LOC118269446	2.21	centromere protein S-like isoform X1
LOC118275077	-2.37	ceramide synthase 6-like
LOC118275180	-2.28	ceramide synthase 6-like
LOC118268439	2.39	chaoptin-like
LOC118269637	2.34	chaoptin-like isoform X1
LOC118269698	2.57	chaoptin-like isoform X1
LOC118273193	2.37	chitin deacetylase 1
LOC118272095	7.90	chitin deacetylase 1-like
LOC118273685	2.19	chitin deacetylase 1-like isoform X1
LOC118279269	2.55	chitin deacetylase 8-like
LOC118282002	4.74	chitinase A-like
LOC118277800	5.55	chitinase A-like
LOC118281054	2.07	cholesterol 7-desaturase-like
LOC118263178	-4.85	cholinesterase 1-like
LOC118265448	2.98	chorion class B protein Ld34-like
LOC118276246	-3.46	chorion peroxidase-like
LOC118264035	3.48	chorion peroxidase-like
LOC118276450	5.54	chromatin modification-related protein eaf-1-like
LOC118267662	-4.18	chymotrypsin-1-like
LOC118267815	-4.08	chymotrypsin-1-like
LOC118267939	-3.04	chymotrypsin-1-like
LOC118267584	-2.99	chymotrypsin-1-like
LOC118267797	-2.74	chymotrypsin-1-like
LOC118267816	-2.63	chymotrypsin-1-like
LOC118267770	-2.49	chymotrypsin-1-like
LOC118267822	-2.09	chymotrypsin-1-like
LOC118267759	-3.55	chymotrypsin-2-like
LOC118267597	-3.25	chymotrypsin-2-like
LOC118267771	-3.11	chymotrypsin-2-like
LOC118267593	-2.56	chymotrypsin-2-like
LOC118267586	-2.55	chymotrypsin-2-like
LOC118267760	-2.50	chymotrypsin-2-like
LOC118282047	-2.77	cilia- and flagella-associated protein 36-like
LOC118276492	-5.77	circadian clock-controlled protein daywake-like
LOC118275991	-3.64	circadian clock-controlled protein daywake-like
LOC118276100	-3.52	circadian clock-controlled protein daywake-like
LOC118276479	-3.48	circadian clock-controlled protein daywake-like
LOC118263879	-3.10	circadian clock-controlled protein daywake-like
LOC118276477	-2.58	circadian clock-controlled protein daywake-like
LOC118263001	4.32	circadian clock-controlled protein daywake-like
LOC118276328	6.63	circadian clock-controlled protein daywake-like
LOC118264172	2.33	class A basic helix-loop-helix protein 15-like
LOC118274706	-2.02	clavesin-1-like
LOC118265087	2.87	clavesin-1-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118273241	-2.85	clavesin-2-like
LOC118267845	-2.33	CLIP domain-containing serine protease 14D-like
LOC118279314	4.92	CLIP domain-containing serine protease B15-like
LOC118280568	-3.15	coagulation factor IX-like
LOC118276373	-2.17	coiled-coil domain-containing protein 130 homolog
LOC118266475	2.38	collagen alpha-1(I) chain-like
LOC118262957	2.40	collagen alpha-1(I) chain-like
LOC118265974	2.49	collagen alpha-1(I) chain-like
LOC118262955	2.25	collagen alpha-1(I) chain-like isoform X1
LOC118267918	-2.05	connectin-like
LOC118281831	2.25	COX assembly mitochondrial protein homolog
LOC118281407	4.47	craniofacial development protein 2-like
LOC118272895	8.13	craniofacial development protein 2-like
LOC118267587	-2.86	ctenidin-3-like
LOC118270464	2.02	C-type lectin domain family 4 member E-like
LOC118264375	-2.14	C-type mannose receptor 2-like
LOC118267044	-5.40	C-type mannose receptor 2-like isoform X1
LOC118265693	6.37	CUB and sushi domain-containing protein 3-like isoform X1
LOC118279659	2.09	cuticle protein 16.5-like
LOC118279658	2.28	cuticle protein 16.5-like
LOC118276092	4.42	cuticle protein 16.5-like
LOC118277907	5.59	cuticle protein 16.5-like
LOC118276281	5.68	cuticle protein 16.5-like
LOC118272646	9.11	cuticle protein 16.5-like
LOC118272879	9.75	cuticle protein 16.5-like
LOC118273867	9.82	cuticle protein 16.5-like
LOC118273866	11.76	cuticle protein 16.5-like
LOC118261734	5.37	cuticle protein 18.6-like
LOC118261733	5.73	cuticle protein 18.6-like
LOC118261732	8.40	cuticle protein 18.6-like
LOC118274137	9.30	cuticle protein 18.6-like
LOC118274138	11.62	cuticle protein 18.6-like
LOC118277977	9.14	cuticle protein 19.8-like
LOC118277978	9.81	cuticle protein 19.8-like
LOC118282419	4.16	cuticle protein 19-like
LOC118261786	5.01	cuticle protein 19-like
LOC118266418	5.20	cuticle protein 19-like
LOC118261962	5.45	cuticle protein 19-like
LOC118261992	5.65	cuticle protein 19-like
LOC118261804	6.71	cuticle protein 19-like
LOC118281467	8.36	cuticle protein 19-like
LOC118262072	10.67	cuticle protein 19-like
LOC118281454	11.11	cuticle protein 19-like
LOC118262025	11.43	cuticle protein 19-like
LOC118272371	-5.32	cuticle protein 21-like
LOC118272373	-5.10	cuticle protein 21-like
LOC118266485	-2.70	cuticle protein 3-like
LOC118265978	6.87	cuticle protein 3-like
LOC118265851	7.31	cuticle protein 3-like
LOC118266512	7.92	cuticle protein 3-like
LOC118265980	8.42	cuticle protein 3-like
LOC118265844	9.44	cuticle protein 3-like
LOC118265845	9.53	cuticle protein 3-like
LOC118265979	7.64	cuticle protein 3-like isoform X1
LOC118272743	11.11	cuticle protein 63-like
LOC118273869	11.24	cuticle protein 63-like
LOC118273856	-5.86	cuticle protein 65-like
LOC118273653	-2.40	cuticle protein 7-like
LOC118262030	4.15	cuticle protein 7-like
LOC118262028	4.52	cuticle protein 7-like
LOC118281445	5.23	cuticle protein 7-like
LOC118264710	5.49	cuticle protein 7-like
LOC118281381	7.16	cuticle protein 7-like
LOC118262023	7.54	cuticle protein 7-like
LOC118262024	8.28	cuticle protein 7-like
LOC118277981	8.35	cuticle protein 7-like
LOC118281406	8.53	cuticle protein 7-like
LOC118261774	8.63	cuticle protein 7-like
LOC118262033	8.81	cuticle protein 7-like
LOC118262026	9.30	cuticle protein 7-like
LOC118281416	11.26	cuticle protein 7-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118281423	9.67	cuticle protein 7-like isoform X1
LOC118262022	4.26	cuticle protein 8-like
LOC118281401	5.30	cuticle protein 8-like
LOC118261907	8.84	cuticle protein 8-like
LOC118274135	9.65	cuticle protein 8-like
LOC118281439	9.68	cuticle protein 8-like
LOC118281375	9.81	cuticle protein 8-like
LOC118261945	10.41	cuticle protein 8-like
LOC118262019	10.48	cuticle protein 8-like
LOC118262027	11.15	cuticle protein 8-like
LOC118281391	11.98	cuticle protein 8-like
LOC118262020	12.34	cuticle protein 8-like
LOC118282313	8.36	cuticle protein 8-like isoform X1
LOC118262125	9.04	cuticle protein 8-like isoform X1
LOC118274134	9.36	cuticle protein 8-like isoform X1
LOC118272369	-4.59	cuticle protein LPCP-23-like
LOC118261759	6.30	cuticle protein-like
LOC118261775	6.69	cuticle protein-like
LOC118274403	7.40	cuticle protein-like
LOC118278046	7.71	cuticle protein-like
LOC118261779	7.73	cuticle protein-like
LOC118261780	8.72	cuticle protein-like
LOC118261737	9.50	cuticle protein-like
LOC118274136	11.27	cuticle protein-like
LOC118275589	2.51	cyclin-dependent kinase-like 1 isoform X1
LOC118277020	-2.19	cystathionine gamma-lyase-like
LOC118272798	2.92	cysteine sulfinic acid decarboxylase-like
LOC118276728	-2.25	cytadherence high molecular weight protein 1-like
LOC118281691	5.06	cytadherence high molecular weight protein 3-like
LOC118265393	5.11	cytadherence high molecular weight protein 3-like
LOC118267804	-3.08	cytochrome b561 domain-containing protein 1-like
LOC118271394	-2.45	cytochrome b5-like
LOC118268104	-3.05	cytochrome b5-related protein-like
LOC118268419	-2.38	cytochrome b5-related protein-like
LOC118268438	-2.36	cytochrome b5-related protein-like
LOC118268452	-2.35	cytochrome b5-related protein-like
LOC118268105	2.10	cytochrome b5-related protein-like
LOC118268107	-2.67	cytochrome b5-related protein-like isoform X1
LOC118269113	-3.14	cytochrome P450 315a1, mitochondrial-like
LOC118270459	-9.53	cytochrome P450 4C1-like
LOC118270823	-8.29	cytochrome P450 4C1-like
LOC118270313	-8.15	cytochrome P450 4C1-like
LOC118270314	-5.64	cytochrome P450 4C1-like
LOC118270312	-5.24	cytochrome P450 4C1-like
LOC118282305	-5.23	cytochrome P450 4C1-like
LOC118270689	-4.64	cytochrome P450 4C1-like
LOC118282379	-4.58	cytochrome P450 4C1-like
LOC118270860	-4.30	cytochrome P450 4C1-like
LOC118270758	-4.08	cytochrome P450 4C1-like
LOC118270695	-2.80	cytochrome P450 4C1-like
LOC118273959	-2.23	cytochrome P450 4C1-like
LOC118281716	2.15	cytochrome P450 4C1-like
LOC118275081	2.54	cytochrome P450 4C1-like
LOC118281717	2.80	cytochrome P450 4C1-like
LOC118270310	3.37	cytochrome P450 4C1-like
LOC118270578	3.74	cytochrome P450 4C1-like
LOC118270461	6.49	cytochrome P450 4C1-like
LOC118270719	-7.40	cytochrome P450 4C1-like isoform X1
LOC118270718	-2.81	cytochrome P450 4C1-like isoform X1
LOC118270458	2.75	cytochrome P450 4c21-like
LOC118270308	4.75	cytochrome P450 4c21-like
LOC118272240	-5.15	cytochrome P450 4c3-like
LOC118270750	-5.14	cytochrome P450 4c3-like
LOC118281843	-3.34	cytochrome P450 4c3-like
LOC118270311	-3.87	cytochrome P450 4d1-like isoform X1
LOC118261999	-4.72	cytochrome P450 4d2-like
LOC118282337	-4.31	cytochrome P450 4d2-like
LOC118263710	-2.57	cytochrome P450 4d2-like
LOC118263397	-2.09	cytochrome P450 4d2-like
LOC118263448	-3.94	cytochrome P450 4g15-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118263457	-2.67	cytochrome P450 4g15-like
LOC118282334	-5.71	cytochrome P450 4V2-like
LOC118262004	-5.02	cytochrome P450 4V2-like
LOC118270854	-4.58	cytochrome P450 4V2-like
LOC118281824	-4.38	cytochrome P450 4V2-like
LOC118282338	-3.79	cytochrome P450 4V2-like
LOC118270575	-3.29	cytochrome P450 4V2-like
LOC118271683	-3.29	cytochrome P450 4V2-like
LOC118270460	-9.10	cytochrome P450 4V2-like isoform X1
LOC118270694	-3.98	cytochrome P450 4V2-like isoform X1
LOC118274185	-3.62	cytochrome P450 6a9-like
LOC118274106	6.53	cytochrome P450 6B1-like
LOC118272349	-3.09	cytochrome P450 6B2-like
LOC118273914	-2.73	cytochrome P450 6B2-like
LOC118273915	-2.08	cytochrome P450 6B2-like
LOC118274504	-2.39	cytochrome P450 6B4-like
LOC118282199	-2.97	cytochrome P450 6B5-like
LOC118274503	-2.80	cytochrome P450 6B5-like
LOC118281490	-2.32	cytochrome P450 6B5-like
LOC118274506	-2.06	cytochrome P450 6B5-like
LOC118262947	-8.74	cytochrome P450 6B6-like
LOC118263005	-7.57	cytochrome P450 6B6-like
LOC118262642	-5.69	cytochrome P450 6B6-like
LOC118263048	-5.44	cytochrome P450 6B6-like
LOC118273912	-2.93	cytochrome P450 6B6-like
LOC118274094	-2.47	cytochrome P450 6B6-like
LOC118265346	2.46	cytochrome P450 6j1-like
LOC118265371	3.03	cytochrome P450 6j1-like
LOC118263077	-4.37	cytochrome P450 6k1-like
LOC118263083	-4.11	cytochrome P450 6k1-like
LOC118274285	-3.96	cytochrome P450 6k1-like
LOC118274242	-2.35	cytochrome P450 6k1-like
LOC118264058	-2.46	cytochrome P450 9e2-like
LOC118264410	-2.25	cytochrome P450 9e2-like
LOC118264788	5.60	cytochrome P450 9e2-like
LOC118263547	-2.42	cytochrome P450 CYP12A2-like
LOC118264200	-2.43	cytoglobin-1-like isoform X1
LOC118276126	2.42	cytosol aminopeptidase-like
LOC118280252	-5.24	D-arabinitol dehydrogenase 1-like
LOC118280432	-4.69	D-arabinitol dehydrogenase 1-like
LOC118265945	-2.58	D-aspartate oxidase-like
LOC118268135	2.97	decaprenyl-diphosphate synthase subunit 1-like
LOC118279850	4.62	decaprenyl-diphosphate synthase subunit 2-like
LOC118279842	5.29	decaprenyl-diphosphate synthase subunit 2-like
LOC118280239	-4.25	dehydrogenase-like
LOC118276294	-4.08	dehydrogenase-like
LOC118266266	2.74	dehydrogenase-like
LOC118280738	-3.26	delta(24)-sterol reductase-like
LOC118265731	-2.92	delta(24)-sterol reductase-like
LOC118265730	-2.76	delta(24)-sterol reductase-like
LOC118268457	-3.49	delta(7)-sterol 5(6)-desaturase erg32-like
LOC118276214	-2.42	delta-1-pyrroline-5-carboxylate synthase-like isoform X1
LOC118280533	-3.78	dentin sialophosphoprotein-like
LOC118264591	4.06	dentin sialophosphoprotein-like isoform X1
LOC118264622	-4.69	D-erythronate dehydrogenase-like
LOC118264400	-4.45	D-erythronate dehydrogenase-like
LOC118267631	2.28	disheveled-associated activator of morphogenesis 1-like isoform X1
LOC118267630	2.87	disheveled-associated activator of morphogenesis 1-like isoform X1
LOC118265573	2.00	DNA translocase FtsK-like isoform X1
LOC118267610	-2.31	dopamine N-acetyltransferase-like
LOC118265067	5.05	drebrin-like protein
LOC118269141	2.08	dual oxidase-like isoform X1
LOC118264986	4.25	dynein heavy chain 2, axonemal-like
LOC118264984	6.39	dynein heavy chain 2, axonemal-like
LOC118278254	-3.79	dynein light chain Tctex-type 1-like
LOC118262808	5.35	dynein regulatory complex subunit 5-like
LOC118263091	5.36	dynein regulatory complex subunit 5-like
LOC118278842	2.03	E3 ubiquitin-protein ligase CIP8-like isoform X1
LOC118265527	-4.27	early nodulin-75-like
LOC118269902	3.80	eclosion hormone
LOC118266097	-4.73	ejaculatory bulb-specific protein 3-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118265694	-4.67	ejaculatory bulb-specific protein 3-like
LOC118266106	-3.60	ejaculatory bulb-specific protein 3-like
LOC118265701	-3.51	ejaculatory bulb-specific protein 3-like
LOC118266100	-2.83	ejaculatory bulb-specific protein 3-like
LOC118266099	-2.37	ejaculatory bulb-specific protein 3-like
LOC118266102	-2.26	ejaculatory bulb-specific protein 3-like
LOC118266101	-2.07	ejaculatory bulb-specific protein 3-like
LOC118274267	3.48	ejaculatory bulb-specific protein 3-like
LOC118265700	5.71	ejaculatory bulb-specific protein 3-like
LOC118272832	9.55	elongation of very long chain fatty acids protein 1-like
LOC118272394	9.68	elongation of very long chain fatty acids protein 1-like
LOC118263756	3.14	elongation of very long chain fatty acids protein 4-like
LOC118263487	3.25	elongation of very long chain fatty acids protein 4-like
LOC118261977	2.10	elongation of very long chain fatty acids protein 7-like
LOC118262043	2.15	elongation of very long chain fatty acids protein 7-like
LOC118261956	2.54	elongation of very long chain fatty acids protein 7-like
LOC118282375	7.54	elongation of very long chain fatty acids protein 7-like
LOC118282383	8.02	elongation of very long chain fatty acids protein 7-like
LOC118261979	5.61	elongation of very long chain fatty acids protein 7-like isoform X1
LOC118261900	5.92	elongation of very long chain fatty acids protein 7-like isoform X1
LOC118282225	-5.97	elongation of very long chain fatty acids protein AAEL008004-like
LOC118262109	-5.48	elongation of very long chain fatty acids protein AAEL008004-like
LOC118282252	-5.14	elongation of very long chain fatty acids protein AAEL008004-like
LOC118262067	-5.07	elongation of very long chain fatty acids protein AAEL008004-like
LOC118262083	-3.63	elongation of very long chain fatty acids protein AAEL008004-like
LOC118262014	-3.57	elongation of very long chain fatty acids protein AAEL008004-like
LOC118282220	-2.96	elongation of very long chain fatty acids protein AAEL008004-like
LOC118281500	2.01	elongation of very long chain fatty acids protein AAEL008004-like
LOC118275867	-4.22	elongation of very long chain fatty acids protein-like
LOC118275898	7.25	endochitinase A-like isoform X1
LOC118278006	5.27	endochitinase-like
LOC118278717	2.82	endocuticle structural glycoprotein ABD-4-like
LOC118282348	3.65	endocuticle structural glycoprotein ABD-4-like
LOC118282374	4.24	endocuticle structural glycoprotein ABD-5-like
LOC118275283	12.64	endocuticle structural glycoprotein ABD-5-like
LOC118261896	5.56	endocuticle structural glycoprotein SgAbd-2-like
LOC118261769	-3.77	endocuticle structural glycoprotein SgAbd-5-like
LOC118282330	-2.77	endocuticle structural glycoprotein SgAbd-5-like
LOC118282356	-2.68	endocuticle structural glycoprotein SgAbd-5-like
LOC118282407	5.74	endocuticle structural glycoprotein SgAbd-5-like
LOC118261870	7.75	endocuticle structural glycoprotein SgAbd-5-like
LOC118261868	8.22	endocuticle structural glycoprotein SgAbd-5-like
LOC118261848	-4.58	endocuticle structural glycoprotein SgAbd-5-like isoform X1
LOC118282354	-2.23	endocuticle structural glycoprotein SgAbd-5-like isoform X1
LOC118282349	5.17	endocuticle structural glycoprotein SgAbd-8-like
LOC118282304	6.43	endocuticle structural glycoprotein SgAbd-8-like
LOC118282343	8.01	endocuticle structural glycoprotein SgAbd-8-like
LOC118269470	-2.07	enolase-like isoform X1
LOC118279735	-2.00	ephrin-B2a-like
LOC118271971	3.17	epidermal retinol dehydrogenase 2-like isoform X1
LOC118271766	6.86	espin-like isoform X1
LOC118267335	-3.96	ester hydrolase C11orf54 homolog
LOC118277582	-3.29	esterase B1-like
LOC118265499	-2.19	esterase B1-like isoform X1
LOC118276233	-8.85	esterase FE4-like
LOC118276232	-8.18	esterase FE4-like
LOC118276149	-4.32	esterase FE4-like
LOC118276230	-3.66	esterase FE4-like
LOC118265387	-2.88	esterase FE4-like
LOC118262722	-2.69	esterase FE4-like
LOC118276150	-2.51	esterase FE4-like isoform X1
LOC118271630	2.35	estradiol 17-beta-dehydrogenase 11-like
LOC118277327	2.23	ethanolaminephosphotransferase 1-like
LOC118282394	-3.78	eukaryotic peptide chain release factor GTP-binding subunit ERF3A-like
LOC118262073	2.34	eukaryotic translation initiation factor 4E1-like
LOC118265547	-2.67	excitatory amino acid transporter-like isoform X1
LOC118269090	2.39	exonuclease GOR-like
LOC118267658	6.23	extensin-like
LOC118263017	9.86	extensin-like
LOC118277657	-5.43	facilitated trehalose transporter Tret1-2 homolog

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118277673	-4.21	facilitated trehalose transporter Tret1-2 homolog
LOC118270022	-7.65	facilitated trehalose transporter Tret1-like
LOC118277593	-4.85	facilitated trehalose transporter Tret1-like
LOC118277644	-4.50	facilitated trehalose transporter Tret1-like
LOC118277596	-3.74	facilitated trehalose transporter Tret1-like
LOC118277392	-3.66	facilitated trehalose transporter Tret1-like
LOC118277648	-3.59	facilitated trehalose transporter Tret1-like
LOC118277658	-3.55	facilitated trehalose transporter Tret1-like
LOC118270686	-3.39	facilitated trehalose transporter Tret1-like
LOC118277661	-3.30	facilitated trehalose transporter Tret1-like
LOC118264956	-3.24	facilitated trehalose transporter Tret1-like
LOC118270389	-2.90	facilitated trehalose transporter Tret1-like
LOC118265246	-2.89	facilitated trehalose transporter Tret1-like
LOC118265245	-2.75	facilitated trehalose transporter Tret1-like
LOC118278124	-2.19	facilitated trehalose transporter Tret1-like
LOC118277640	-2.16	facilitated trehalose transporter Tret1-like
LOC118270807	-2.06	facilitated trehalose transporter Tret1-like
LOC118270205	-2.04	facilitated trehalose transporter Tret1-like
LOC118280805	2.01	facilitated trehalose transporter Tret1-like
LOC118264155	2.02	facilitated trehalose transporter Tret1-like
LOC118270388	4.34	facilitated trehalose transporter Tret1-like
LOC118277887	4.53	facilitated trehalose transporter Tret1-like
LOC118270601	6.14	facilitated trehalose transporter Tret1-like
LOC118270392	6.30	facilitated trehalose transporter Tret1-like
LOC118277850	7.27	facilitated trehalose transporter Tret1-like
LOC118269337	-3.78	farnesol dehydrogenase-like
LOC118266039	2.70	farnesyl pyrophosphate synthase-like
LOC118268284	-3.03	fasciclin-1-like isoform X1
LOC118268287	-2.78	fasciclin-1-like isoform X1
LOC118274969	-4.19	fatty acid synthase-like
LOC118275042	-4.10	fatty acid synthase-like
LOC118275041	-3.86	fatty acid synthase-like
LOC118274634	-3.59	fatty acid synthase-like
LOC118274778	-3.59	fatty acid synthase-like
LOC118274970	-3.58	fatty acid synthase-like
LOC118274609	-3.52	fatty acid synthase-like
LOC118274998	-3.47	fatty acid synthase-like
LOC118274779	-3.24	fatty acid synthase-like
LOC118274999	-2.44	fatty acid synthase-like
LOC118274989	-2.34	fatty acid synthase-like
LOC118275043	4.75	fatty acid synthase-like
LOC118274972	5.80	fatty acid synthase-like
LOC118267601	8.84	fatty acid synthase-like
LOC118274557	-4.24	fatty acid synthase-like isoform X1
LOC118274601	-3.77	fatty acid synthase-like isoform X1
LOC118275711	6.93	fatty acid-binding protein-like
LOC118265386	-4.63	fatty acyl-CoA reductase 1-like
LOC118265399	-4.57	fatty acyl-CoA reductase 1-like
LOC118265401	-3.19	fatty acyl-CoA reductase 1-like
LOC118280282	2.04	fatty acyl-CoA reductase 1-like
LOC118280456	-6.91	fatty acyl-CoA reductase wat-like
LOC118267780	-5.68	fatty acyl-CoA reductase wat-like
LOC118280298	-3.62	fatty acyl-CoA reductase wat-like
LOC118280458	2.61	fatty acyl-CoA reductase wat-like
LOC118280319	5.11	fatty acyl-CoA reductase wat-like
LOC118280321	5.75	fatty acyl-CoA reductase wat-like
LOC118280723	9.22	fatty acyl-CoA reductase wat-like
LOC118268523	2.09	fatty-acid amide hydrolase 2-B-like
LOC118272338	3.43	F-box only protein 32-like isoform X1
LOC118269908	2.77	fibril-forming collagen alpha chain-like
LOC118275600	3.79	fibroin heavy chain-like
LOC118274569	4.72	fibroin heavy chain-like
LOC118270722	4.92	fibroin heavy chain-like
LOC118270804	4.99	fibroin heavy chain-like
LOC118275411	5.25	fibroin heavy chain-like
LOC118270733	4.69	fibroin heavy chain-like isoform X1
LOC118280656	-2.14	fibulin-1-like
LOC118262265	3.51	flocculation protein FLO11-like isoform X1
LOC118262695	-3.18	follicle cell protein 3C-1-like
LOC118266807	2.03	fork head domain-containing protein crocodile-like
LOC118274056	3.52	forkhead box protein C1-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118263848	2.96	forkhead box protein I2-like
LOC118263857	4.15	forkhead box protein I2-like
LOC118275119	-3.77	fructose-bisphosphate aldolase-like
LOC118275099	-3.50	fructose-bisphosphate aldolase-like
LOC118274716	-2.01	fructose-bisphosphate aldolase-like isoform X1
LOC118272026	-3.01	fumarylacetoacetase-like
LOC118270444	-3.29	fumarylacetoacetate hydrolase domain-containing protein 2-like
LOC118271599	-2.76	fumarylacetoacetate hydrolase domain-containing protein 2-like
LOC118272227	-2.35	fumarylacetoacetate hydrolase domain-containing protein 2-like
LOC118270542	-2.09	fumarylacetoacetate hydrolase domain-containing protein 2-like
LOC118275890	-2.63	G protein-activated inward rectifier potassium channel 4-like
LOC118264621	-2.32	G protein-activated inward rectifier potassium channel 4-like
LOC118264704	-2.80	galactokinase-like
LOC118278868	-2.57	galectin-4-like
LOC118272840	-2.26	gamma-glutamyl hydrolase A-like isoform X1
LOC118270884	2.31	GAS2-like protein 3
LOC118280880	-4.78	gastrula zinc finger protein XlCGF49.1-like
LOC118265973	5.85	GATA zinc finger domain-containing protein 7-like
LOC118280966	-2.63	gelsolin-like
LOC118281011	-2.17	gelsolin-like
LOC118281217	-2.14	gelsolin-like
LOC118265042	-3.91	gelsolin-related protein of 125 kDa-like
LOC118267984	-3.20	general odorant-binding protein 28a-like
LOC118267782	-3.95	general odorant-binding protein 69a-like isoform X1
LOC118261908	3.13	general odorant-binding protein 70-like
LOC118267992	-6.35	general odorant-binding protein 72-like
LOC118270815	-2.47	general odorant-binding protein 83a-like
LOC118278869	2.32	GILT-like protein 1 isoform X1
LOC118268426	-4.70	girdin-like isoform X1
LOC118269449	-2.22	glucose 1-dehydrogenase-like
LOC118274655	-6.41	glucose dehydrogenase [FAD, quinone
LOC118276420	-5.48	glucose dehydrogenase [FAD, quinone
LOC118265894	-5.45	glucose dehydrogenase [FAD, quinone
LOC118265750	-4.64	glucose dehydrogenase [FAD, quinone
LOC118276416	-4.50	glucose dehydrogenase [FAD, quinone
LOC118276929	-3.20	glucose dehydrogenase [FAD, quinone
LOC118274656	-2.99	glucose dehydrogenase [FAD, quinone
LOC118279078	-2.94	glucose dehydrogenase [FAD, quinone
LOC118274648	2.20	glucose dehydrogenase [FAD, quinone
LOC118279376	2.67	glucose dehydrogenase [FAD, quinone
LOC118279366	3.39	glucose dehydrogenase [FAD, quinone
LOC118271447	4.49	glucose dehydrogenase [FAD, quinone
LOC118274802	4.94	glucose dehydrogenase [FAD, quinone
LOC118279377	5.21	glucose dehydrogenase [FAD, quinone
LOC118274823	6.38	glucose dehydrogenase [FAD, quinone
LOC118271457	6.47	glucose dehydrogenase [FAD, quinone
LOC118274660	6.48	glucose dehydrogenase [FAD, quinone
LOC118274658	7.70	glucose dehydrogenase [FAD, quinone
LOC118271446	8.23	glucose dehydrogenase [FAD, quinone
LOC118274651	8.43	glucose dehydrogenase [FAD, quinone
LOC118274653	9.57	glucose dehydrogenase [FAD, quinone
LOC118265594	-6.55	glucose dehydrogenase [FAD, quinone-like
LOC118265598	-5.78	glucose dehydrogenase [FAD, quinone-like
LOC118264728	-4.54	glucose dehydrogenase [FAD, quinone-like
LOC118265561	-2.53	glucose dehydrogenase [FAD, quinone-like
LOC118265591	-2.13	glucose dehydrogenase [FAD, quinone-like
LOC118264299	-2.01	glucose dehydrogenase [FAD, quinone-like
LOC118264389	2.29	glucose dehydrogenase [FAD, quinone-like
LOC118264860	2.72	glucose dehydrogenase [FAD, quinone-like
LOC118263014	3.94	glucose dehydrogenase [FAD, quinone-like
LOC118264388	4.32	glucose dehydrogenase [FAD, quinone-like
LOC118263006	4.35	glucose dehydrogenase [FAD, quinone-like
LOC118265446	6.19	glucose dehydrogenase [FAD, quinone-like
LOC118264453	6.52	glucose dehydrogenase [FAD, quinone-like
LOC118280186	2.35	glucose-1-phosphatase-like
LOC118280537	2.85	glucose-1-phosphatase-like
LOC118277306	-2.35	glucose-6-phosphate isomerase-like
LOC118269835	-3.39	glutamate dehydrogenase, mitochondrial-like
LOC118266855	-3.27	glutamate receptor ionotropic, delta-2-like
LOC118277778	-5.09	glutathione S-transferase 1-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118277779	-4.86	glutathione S-transferase 1-like
LOC118261929	-3.66	glutathione S-transferase 1-like
LOC118282243	-3.18	glutathione S-transferase 1-like
LOC118261932	-3.13	glutathione S-transferase 1-like
LOC118282244	-2.82	glutathione S-transferase 1-like
LOC118261931	-2.81	glutathione S-transferase 1-like
LOC118261930	-2.55	glutathione S-transferase 1-like
LOC118270502	4.08	glutathione S-transferase 1-like
LOC118266709	-2.60	glutathione S-transferase 1-like isoform X1
LOC118271639	-2.69	glutathione S-transferase 2-like
LOC118272015	-2.52	glutathione S-transferase 2-like
LOC118272232	2.04	glutathione S-transferase 2-like
LOC118271636	3.04	glutathione S-transferase 2-like
LOC118270053	-2.85	glutathione S-transferase S1-like
LOC118270030	-3.34	glutathione S-transferase-like
LOC118278457	4.26	glutenin, low molecular weight subunit-like
LOC118278459	4.67	glutenin, low molecular weight subunit-like
LOC118281669	-2.36	glycine dehydrogenase (decarboxylating), mitochondrial-like
LOC118263297	-2.49	glycine N-methyltransferase-like
LOC118263254	-2.33	glycine N-methyltransferase-like
LOC118281892	3.42	glycine receptor subunit alpha-2-like
LOC118278076	3.50	glycine, alanine and asparagine-rich protein-like
LOC118279384	9.69	glycine-rich cell wall structural protein 1.0-like
LOC118274210	-5.33	glycine-rich cell wall structural protein 1.8-like
LOC118278606	2.50	glycine-rich cell wall structural protein 1.8-like
LOC118278016	7.83	glycine-rich cell wall structural protein 1.8-like
LOC118273737	-5.51	glycine-rich cell wall structural protein 1.8-like isoform X1
LOC118267835	2.22	glycine-rich cell wall structural protein-like
LOC118265961	2.72	glycine-rich cell wall structural protein-like
LOC118268964	8.69	glycine-rich cell wall structural protein-like
LOC118269040	11.50	glycine-rich cell wall structural protein-like
LOC118275779	-5.51	glycine-rich protein DOT1-like
LOC118276030	-4.06	glycine-rich protein DOT1-like
LOC118267709	7.01	glycine-rich protein-like
LOC118277916	-4.04	glycine-rich RNA-binding protein 2-like
LOC118265847	-2.72	glycine-rich RNA-binding protein 3, mitochondrial-like
LOC118280330	-3.21	glycogen [starch synthase-like
LOC118280302	-3.37	glycogen [starch synthase-like isoform X1
LOC118280331	-2.13	glycogen [starch synthase-like isoform X1
LOC118266715	2.26	glycolipid transfer protein-like
LOC118266636	-2.42	glyoxalase domain-containing protein 4-like
LOC118271727	-2.50	glyoxylate reductase/hydroxypyruvate reductase-like
LOC118271984	-2.71	glyoxylate reductase/hydroxypyruvate reductase-like isoform X1
LOC118267756	-2.37	G-protein coupled receptor moody-like
LOC118270547	-3.11	G-protein coupled receptor Mth2-like isoform X1
LOC118270698	-3.07	G-protein coupled receptor Mth2-like isoform X1
LOC118280678	-2.30	granzyme-like protein 1
LOC118266836	3.44	granzyme-like protein 1
LOC118265482	-2.16	gremlin-1-like isoform X1
LOC118272831	2.61	GTP-binding protein REM 1-like
LOC118280660	-2.51	heat shock protein 68-like
LOC118280663	-2.13	heat shock protein 68-like
LOC118281868	2.14	heme peroxidase 2-like
LOC118271465	-2.88	hemicentin-1-like
LOC118271466	-2.08	hemicentin-2-like
LOC118271414	2.02	hemicentin-2-like
LOC118272929	4.23	heparan sulfate 2-O-sulfotransferase pipe-like
LOC118263480	2.28	heparan-alpha-glucosaminide N-acetyltransferase-like isoform X1
LOC118268703	2.68	hepatic leukemia factor-like isoform X1
LOC118265352	6.40	hepatic triacylglycerol lipase-like
LOC118278739	4.36	hepatocyte growth factor-regulated tyrosine kinase substrate-like
LOC118271288	3.23	heterogeneous nuclear ribonucleoprotein A2 homolog 1-like
LOC118276284	3.39	heterogeneous nuclear ribonucleoprotein A2 homolog 1-like
LOC118276130	-5.17	heterogeneous nuclear ribonucleoprotein A2 homolog 1-like isoform X1
LOC118262485	-2.41	HIG1 domain family member 1A, mitochondrial-like
LOC118261742	5.47	histidine-rich glycoprotein-like
LOC118261791	5.58	histidine-rich glycoprotein-like
LOC118261746	5.93	histidine-rich glycoprotein-like
LOC118281584	6.52	histidine-rich glycoprotein-like
LOC118281476	6.89	histidine-rich glycoprotein-like
LOC118261800	8.30	histidine-rich glycoprotein-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118261751	8.97	histidine-rich glycoprotein-like
LOC118261795	9.27	histidine-rich glycoprotein-like
LOC118261788	9.35	histidine-rich glycoprotein-like
LOC118261793	9.49	histidine-rich glycoprotein-like
LOC118261752	9.64	histidine-rich glycoprotein-like
LOC118265472	10.47	histidine-rich glycoprotein-like
LOC118265442	11.34	histidine-rich glycoprotein-like
LOC118281568	11.77	histidine-rich glycoprotein-like
LOC118265488	11.81	histidine-rich glycoprotein-like
LOC118281596	11.87	histidine-rich glycoprotein-like
LOC118265441	12.17	histidine-rich glycoprotein-like
LOC118281597	12.86	histidine-rich glycoprotein-like
LOC118265473	12.97	histidine-rich glycoprotein-like
LOC118281572	13.11	histidine-rich glycoprotein-like
LOC118262126	10.40	histidine-rich protein PFHRP-II-like
LOC118261991	10.46	histidine-rich protein PFHRP-II-like
LOC118280946	7.34	histone-lysine N-methyltransferase 2D-like
LOC118272764	3.35	histone-lysine N-methyltransferase, H3 lysine-79 specific-like isoform X1
LOC118277569	-3.08	holotricin-3-like
LOC118268309	3.71	homeobox protein engrailed-2-B-like
LOC118279865	2.20	homeobox protein Hox-A1-like
LOC118273125	2.21	homeobox protein Mohawk-like
LOC118281914	2.08	homeobox protein Nkx-2.2-like
LOC118273254	-2.19	homocysteine S-methyltransferase-like
LOC118272070	-2.96	homogentisate 1,2-dioxygenase-like
LOC118262489	7.69	hormone receptor 4-like isoform X1
LOC118279116	4.36	hyaluronidase-like
LOC118265848	-2.71	hyphally-regulated protein-like isoform X1
LOC118277388	4.03	hypodermin-A-like
LOC118276002	4.51	ice-structuring glycoprotein-like
LOC118262918	9.67	ichor-like
LOC118270327	-2.21	ileal sodium/bile acid cotransporter-like isoform X1
LOC118273522	2.29	inactive hydroxysteroid dehydrogenase-like protein 1
LOC118267675	-2.70	indole-3-acetaldehyde oxidase-like
LOC118267674	-2.29	indole-3-acetaldehyde oxidase-like
LOC118267470	-2.13	indole-3-acetaldehyde oxidase-like
LOC118267487	-2.02	indole-3-acetaldehyde oxidase-like
LOC118261862	-3.74	inducible metalloproteinase inhibitor protein-like
LOC118282397	2.70	inducible metalloproteinase inhibitor protein-like
LOC118282478	3.57	inducible metalloproteinase inhibitor protein-like
LOC118261951	4.07	inducible metalloproteinase inhibitor protein-like
LOC118279816	4.33	inosine triphosphate pyrophosphatase-like
LOC118262557	-2.64	inosine-uridine preferring nucleoside hydrolase-like
LOC118275434	-2.67	insecticyanin-B-like
LOC118276404	2.37	insulin-like growth factor-binding protein complex acid labile subunit
LOC118275904	2.62	insulin-like growth factor-binding protein complex acid labile subunit
LOC118280820	4.70	integrator complex subunit 3 homolog
LOC118262522	-2.29	inter-alpha-trypsin inhibitor heavy chain H4-like isoform X1
LOC118264699	4.49	interaptin-like isoform X1
LOC118264697	4.52	interaptin-like isoform X1
LOC118268731	2.82	intraflagellar transport protein 22 homolog
LOC118269814	2.61	iodotyrosine deiodinase 1-like
LOC118261941	-3.49	ionotropic receptor 21a-like
LOC118276822	-2.32	irregular chiasm C-roughest protein-like isoform X1
LOC118272200	3.41	IST1-like protein
LOC118263778	-5.12	junctional adhesion molecule A-like
LOC118279322	-3.39	juvenile hormone epoxide hydrolase-like
LOC118279351	-3.38	juvenile hormone epoxide hydrolase-like
LOC118279248	2.83	juvenile hormone epoxide hydrolase-like
LOC118276231	-4.83	juvenile hormone esterase-like
LOC118276234	-4.03	juvenile hormone esterase-like
LOC118281026	4.30	juvenile hormone esterase-like
LOC118266127	2.50	juvenile hormone esterase-like isoform X1
LOC118276400	-2.51	juvenile hormone-binding protein-like
LOC118276399	-2.03	juvenile hormone-binding protein-like
LOC118275326	-2.06	kelch repeat and BTB domain-containing protein 2-like
LOC118272812	-3.70	kelch-like protein 2
LOC118272760	-2.24	kelch-like protein 2
LOC118275334	-3.39	keratin, type I cytoskeletal 10-like
LOC118274496	-3.06	keratin, type I cytoskeletal 10-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118268908	10.68	keratin, type I cytoskeletal 10-like
LOC118278260	-5.22	keratin, type I cytoskeletal 9-like
LOC118266481	-2.66	keratin, type I cytoskeletal 9-like
LOC118266476	-3.67	keratin, type II cytoskeletal 2 epidermal-like
LOC118281713	3.50	keratin, type II cytoskeletal I-like
LOC118266488	-2.84	keratin-3, type I cytoskeletal 51 kDa-like
LOC118274402	2.88	keratin-associated protein 19-2-like
LOC118276093	6.01	keratin-associated protein 19-2-like
LOC118269409	2.59	kinesin-like protein KIF12 isoform X1
LOC118275761	4.29	kinesin-like protein KIF18A
LOC118274147	-4.93	kynureninase-like
LOC118267147	-4.80	kynurenine 3-monooxygenase-like
LOC118279380	-2.71	kynurenine/alpha-aminoadipate aminotransferase, mitochondrial-like
LOC118267107	2.19	laccase-2-like
LOC118266894	5.96	laccase-5-like isoform X1
LOC118280431	-2.12	lachesin-like
LOC118282275	-2.27	lambda-crystallin homolog
LOC118279156	5.10	la-related protein 6-like
LOC118273122	-2.11	large neutral amino acids transporter small subunit 2-like
LOC118279431	2.03	large subunit ribosomal RNA
LOC118264871	2.07	large subunit ribosomal RNA
LOC118279433	2.08	large subunit ribosomal RNA
LOC118282151	-4.47	larval cuticle protein 16/17-like
LOC118282159	-7.57	larval cuticle protein 1-like
LOC118261853	-4.41	larval cuticle protein 1-like
LOC118282167	-3.94	larval cuticle protein 1-like
LOC118282178	-3.94	larval cuticle protein 1-like isoform X1
LOC118277988	6.70	larval cuticle protein A1A-like
LOC118277984	3.45	larval cuticle protein A2B-like
LOC118273296	3.49	larval cuticle protein A2B-like
LOC118277985	12.69	larval cuticle protein A2B-like
LOC118277982	13.12	larval cuticle protein A2B-like
LOC118277980	7.01	larval cuticle protein A3A-like
LOC118277983	7.49	larval cuticle protein A3A-like
LOC118279159	8.81	larval cuticle protein A3A-like
LOC118269434	-4.93	larval cuticle protein LCP-14-like
LOC118269179	-4.43	larval cuticle protein LCP-14-like
LOC118282344	-4.82	larval cuticle protein LCP-17-like
LOC118282346	2.34	larval cuticle protein LCP-22-like
LOC118282347	3.03	larval cuticle protein LCP-22-like isoform X1
LOC118282342	-2.35	larval cuticle protein LCP-30-like
LOC118272499	-4.33	larval/pupal cuticle protein H1C-like
LOC118273864	-4.15	larval/pupal cuticle protein H1C-like
LOC118276091	5.06	larval/pupal cuticle protein H1C-like
LOC118273370	-6.61	larval/pupal rigid cuticle protein 66-like
LOC118273654	-3.73	larval/pupal rigid cuticle protein 66-like
LOC118273319	-3.47	larval/pupal rigid cuticle protein 66-like
LOC118273336	-3.33	larval/pupal rigid cuticle protein 66-like
LOC118273639	-3.19	larval/pupal rigid cuticle protein 66-like
LOC118275158	-2.73	L-asparaginase-like
LOC118268498	-3.24	lathosterol oxidase-like isoform X1
LOC118281154	-2.54	L-dopachrome tautomerase yellow-f2-like
LOC118281155	-2.53	L-dopachrome tautomerase yellow-f2-like
LOC118280999	-2.18	L-dopachrome tautomerase yellow-f2-like
LOC118282274	2.32	L-dopachrome tautomerase yellow-f2-like
LOC118280606	3.01	lebocin-4-like
LOC118280911	2.40	leishmanolysin-like peptidase isoform X1
LOC118269675	2.84	leucine-rich repeat transmembrane protein FLRT3-like
LOC118271352	3.61	leucine-rich repeat-containing protein 24-like
LOC118263065	3.10	leucine-rich repeat-containing protein 57-like isoform X1
LOC118278050	-2.46	leukocyte elastase inhibitor-like
LOC118277884	-2.39	leukocyte elastase inhibitor-like
LOC118267564	2.25	leukocyte surface antigen CD53-like
LOC118279152	2.25	LHFPL tetraspan subfamily member 3 protein-like
LOC118264586	-3.57	lipase 1-like
LOC118271511	-3.55	lipase 1-like
LOC118277642	-3.29	lipase 1-like
LOC118264583	-3.25	lipase 1-like
LOC118264830	-2.52	lipase 1-like
LOC118272791	-5.57	lipase 3-like
LOC118272788	-5.15	lipase 3-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118272789	-4.44	lipase 3-like
LOC118275653	-3.49	lipase 3-like
LOC118275483	-2.84	lipase 3-like
LOC118268083	3.48	lipase 3-like
LOC118268348	3.48	lipase 3-like
LOC118262771	4.57	lipase 3-like
LOC118273710	2.75	lipase 3-like isoform X1
LOC118265419	7.50	lipase member H-A-like isoform X1
LOC118273252	-3.50	lipase member H-like
LOC118273148	-3.10	lipase member H-like
LOC118273140	-2.98	lipase member H-like
LOC118273242	-2.95	lipase member H-like
LOC118265609	6.75	lipase member H-like
LOC118275811	5.82	lipase member I-like
LOC118272575	3.89	lipase member I-like isoform X1
LOC118272619	5.38	lipase member I-like isoform X1
LOC118281624	-2.26	lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial-like
LOC118263908	2.08	lipopolysaccharide-induced tumor necrosis factor-alpha factor homolog
LOC118277908	-5.52	loricrin-like
LOC118265619	4.93	loricrin-like
LOC118272241	7.01	low density lipoprotein receptor adapter protein 1-B-like
LOC118276125	-3.67	LOW QUALITY PROTEIN: acyl-CoA Delta(11) desaturase-like
LOC118271573	-2.96	LOW QUALITY PROTEIN: adenosine kinase-like
LOC118279947	-2.05	LOW QUALITY PROTEIN: aldo-keto reductase AKR2E4-like
LOC118274159	-2.13	LOW QUALITY PROTEIN: arrestin domain-containing protein 17-like
LOC118269941	9.76	LOW QUALITY PROTEIN: cadherin-89D-like
LOC118264954	-2.00	LOW QUALITY PROTEIN: cadherin-related tumor suppressor-like
LOC118273450	-2.50	LOW QUALITY PROTEIN: carbonyl reductase [NADPH 3-like
LOC118271482	-5.34	LOW QUALITY PROTEIN: carboxypeptidase B-like
LOC118274156	-3.37	LOW QUALITY PROTEIN: cell surface glycoprotein 1-like
LOC118265222	6.95	LOW QUALITY PROTEIN: circadian clock-controlled protein daywake-like
LOC118269093	3.84	LOW QUALITY PROTEIN: coiled-coil-helix-coiled-coil-helix domain-containing protein 10, mitochondrial-like
LOC118268156	-2.61	LOW QUALITY PROTEIN: contactin-like
LOC118267194	2.34	LOW QUALITY PROTEIN: cytochrome P450 18a1-like
LOC118263350	-2.61	LOW QUALITY PROTEIN: cytochrome P450 4g15-like
LOC118261903	5.52	LOW QUALITY PROTEIN: decaprenyl-diphosphate synthase subunit 2-like
LOC118277633	5.41	LOW QUALITY PROTEIN: E3 ubiquitin-protein ligase RNF123-like
LOC118266191	5.26	LOW QUALITY PROTEIN: esterase E4-like
LOC118279601	-2.57	LOW QUALITY PROTEIN: fibroin heavy chain-like
LOC118263841	2.90	LOW QUALITY PROTEIN: G1/S-specific cyclin-D2-like
LOC118264707	-2.54	LOW QUALITY PROTEIN: galactokinase-like
LOC118281562	2.30	LOW QUALITY PROTEIN: geranylgeranyl pyrophosphate synthase-like
LOC118276784	2.90	LOW QUALITY PROTEIN: glucose dehydrogenase [FAD, quinone
LOC118269821	-3.56	LOW QUALITY PROTEIN: glutamate dehydrogenase, mitochondrial-like
LOC118267113	-3.58	LOW QUALITY PROTEIN: glutathione S-transferase 1-like
LOC118267525	2.00	LOW QUALITY PROTEIN: heme transporter hrg1-B-like
LOC118266137	2.10	LOW QUALITY PROTEIN: hemolymph lipopolysaccharide-binding protein-like
LOC118272663	3.58	LOW QUALITY PROTEIN: histamine H2 receptor-like
LOC118261744	7.40	LOW QUALITY PROTEIN: histidine-rich glycoprotein-like
LOC118268000	9.49	LOW QUALITY PROTEIN: histone acetyltransferase p300-like
LOC118270109	2.21	LOW QUALITY PROTEIN: kinesin-like protein KIF21B
LOC118276760	2.53	LOW QUALITY PROTEIN: low-density lipoprotein receptor-like
LOC118275005	-3.11	LOW QUALITY PROTEIN: luciferin 4-monooxygenase-like
LOC118273878	4.73	LOW QUALITY PROTEIN: mucin-3A-like
LOC118280674	2.29	LOW QUALITY PROTEIN: mucin-5AC-like
LOC118268973	2.79	LOW QUALITY PROTEIN: mutS protein homolog 4-like
LOC118263793	3.18	LOW QUALITY PROTEIN: N-acetylglucosamine-6-phosphate deacetylase-like
LOC118268159	-2.07	LOW QUALITY PROTEIN: neurexin-4-like
LOC118267427	3.90	LOW QUALITY PROTEIN: nuclear hormone receptor FTZ-F1-like
LOC118275260	4.25	LOW QUALITY PROTEIN: protein doublesex-like
LOC118280038	2.37	LOW QUALITY PROTEIN: protein FAM214A-like
LOC118263458	-2.52	LOW QUALITY PROTEIN: protein UBASH3A homolog
LOC118269800	7.82	LOW QUALITY PROTEIN: pupal cuticle protein C1B-like
LOC118261789	9.47	LOW QUALITY PROTEIN: pupal cuticle protein Edg-84A-like
LOC118281339	7.15	LOW QUALITY PROTEIN: putative GPI-anchored protein pfl2
LOC118273838	-3.41	LOW QUALITY PROTEIN: regulating synaptic membrane exocytosis protein 2-like
LOC118266607	-3.44	LOW QUALITY PROTEIN: sulfotransferase 1E1-like
LOC118265105	2.59	LOW QUALITY PROTEIN: thyrostimulin beta-5 subunit-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118279630	2.37	LOW QUALITY PROTEIN: transcription factor SPT20 homolog
LOC118269739	6.31	LOW QUALITY PROTEIN: trypsin-like
LOC118262222	8.28	LOW QUALITY PROTEIN: uncharacterized protein LOC118262222
LOC118263418	-3.32	LOW QUALITY PROTEIN: uncharacterized protein LOC118263418
LOC118263558	-5.17	LOW QUALITY PROTEIN: uncharacterized protein LOC118263558
LOC118264824	2.60	LOW QUALITY PROTEIN: uncharacterized protein LOC118264824
LOC118265044	8.03	LOW QUALITY PROTEIN: uncharacterized protein LOC118265044
LOC118265094	4.45	LOW QUALITY PROTEIN: uncharacterized protein LOC118265094
LOC118267020	2.91	LOW QUALITY PROTEIN: uncharacterized protein LOC118267020
LOC118267328	4.34	LOW QUALITY PROTEIN: uncharacterized protein LOC118267328
LOC118267615	6.32	LOW QUALITY PROTEIN: uncharacterized protein LOC118267615
LOC118267755	5.48	LOW QUALITY PROTEIN: uncharacterized protein LOC118267755
LOC118269609	3.50	LOW QUALITY PROTEIN: uncharacterized protein LOC118269609
LOC118271043	9.16	LOW QUALITY PROTEIN: uncharacterized protein LOC118271043
LOC118273359	8.63	LOW QUALITY PROTEIN: uncharacterized protein LOC118273359
LOC118276079	8.85	LOW QUALITY PROTEIN: uncharacterized protein LOC118276079
LOC118276623	2.28	LOW QUALITY PROTEIN: uncharacterized protein LOC118276623
LOC118277148	-2.30	LOW QUALITY PROTEIN: uncharacterized protein LOC118277148
LOC118279621	2.30	LOW QUALITY PROTEIN: uncharacterized protein LOC118279621
LOC118280777	3.44	LOW QUALITY PROTEIN: uncharacterized protein LOC118280777
LOC118281364	4.29	LOW QUALITY PROTEIN: uncharacterized protein LOC118281364
LOC118282020	5.42	LOW QUALITY PROTEIN: uncharacterized protein LOC118282020
LOC118282282	-3.68	LOW QUALITY PROTEIN: uncharacterized protein LOC118282282
LOC118282440	3.43	LOW QUALITY PROTEIN: uncharacterized protein LOC118282440
LOC118273156	-2.40	LOW QUALITY PROTEIN: venom serine carboxypeptidase-like
LOC118273705	2.76	LOW QUALITY PROTEIN: villin-like protein quail
LOC118263636	-2.34	low-density lipoprotein receptor-related protein 4-like
LOC118263646	-2.29	low-density lipoprotein receptor-related protein 4-like
LOC118274873	-9.10	luciferin 4-monooxygenase-like
LOC118281710	-4.79	luciferin 4-monooxygenase-like
LOC118274486	-4.62	luciferin 4-monooxygenase-like
LOC118274572	-4.48	luciferin 4-monooxygenase-like
LOC118274574	-3.75	luciferin 4-monooxygenase-like
LOC118275118	-2.87	luciferin 4-monooxygenase-like
LOC118274571	-2.73	luciferin 4-monooxygenase-like
LOC118280070	-2.61	luciferin 4-monooxygenase-like
LOC118274573	-3.63	luciferin 4-monooxygenase-like isoform X1
LOC118266603	-5.72	luciferin sulfotransferase-like
LOC118266605	-4.87	luciferin sulfotransferase-like
LOC118266604	-2.97	luciferin sulfotransferase-like
LOC118281846	-4.54	lymphocyte antigen 75-like
LOC118272562	2.17	lysophosphatidylcholine acyltransferase-like
LOC118271261	3.38	lysoplasmalogenase-like
LOC118271619	-3.69	lysozyme-like
LOC118265277	3.63	lysozyme-like
LOC118265132	5.70	lysozyme-like
LOC118280708	-2.41	major heat shock 70 kDa protein Ba-like
LOC118280707	-2.30	major heat shock 70 kDa protein Ba-like
LOC118274552	-2.11	malate dehydrogenase, mitochondrial-like isoform X1
LOC118269324	4.56	malate dehydrogenase, mitochondrial-like isoform X1
LOC118273030	-3.19	maltase A1-like
LOC118267648	6.38	mantle protein-like
LOC118276238	2.88	MAPK-interacting and spindle-stabilizing protein-like
LOC118280570	-3.57	mast cell protease 1A-like
LOC118280681	-3.02	mast cell protease 1A-like
LOC118280760	-4.50	mast cell protease 3-like
LOC118280567	-4.32	mast cell protease 3-like
LOC118261986	5.80	MATH and LRR domain-containing protein PFE0570w-like
LOC118276931	8.80	mediator of RNA polymerase II transcription subunit 15-like
LOC118276902	9.30	mediator of RNA polymerase II transcription subunit 15-like isoform X1
LOC118265532	-2.22	medium-chain acyl-CoA ligase ACSF2, mitochondrial-like
LOC118270791	-2.59	melanotransferrin-like
LOC118271569	-2.89	membrane-bound alkaline phosphatase-like
LOC118271570	-2.48	membrane-bound alkaline phosphatase-like isoform X1
LOC118263027	-2.13	MFS-type transporter SLC18B1-like isoform X1
LOC118281239	-3.28	microvitellogenin-like
LOC118265038	9.55	midnolin homolog
LOC118271740	-2.26	mitochondrial 2-oxoglutarate/malate carrier protein-like
LOC118271793	-2.00	mitochondrial 2-oxoglutarate/malate carrier protein-like
LOC118276975	-2.46	mitochondrial enolase superfamily member 1-like
LOC118270416	-2.28	mitochondrial enolase superfamily member 1-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118278295	6.02	mitochondrial glutamate carrier 1-like
LOC118269613	-2.27	mitochondrial pyruvate carrier 1-like
LOC118269683	-2.22	mitochondrial pyruvate carrier 1-like
LOC118278440	-3.40	modular serine protease-like
LOC118274611	-4.73	monocarboxylate transporter 1-like
LOC118276496	-2.12	monocarboxylate transporter 3-like
LOC118271952	2.76	monocarboxylate transporter 4-like isoform X1
LOC118272007	2.91	monocarboxylate transporter 4-like isoform X1
LOC118263449	-3.99	monocarboxylate transporter 9-like
LOC118272336	3.43	mpv17-like protein
LOC118279179	5.83	mucin-17-like isoform X1
LOC118265872	-4.08	mucin-19-like isoform X1
LOC118266000	-3.86	mucin-19-like isoform X1
LOC118280089	-2.18	mucin-22-like isoform X1
LOC118276098	-2.01	mucin-2-like
LOC118265097	2.58	mucin-2-like
LOC118278048	4.07	mucin-2-like
LOC118278119	6.00	mucin-3A-like
LOC118268598	-2.14	mucin-5AC-like
LOC118274381	2.00	mucin-5AC-like
LOC118279275	2.79	mucin-5AC-like
LOC118276086	3.54	mucin-5AC-like
LOC118273996	3.93	mucin-5AC-like
LOC118268655	2.02	mucin-5AC-like isoform X1
LOC118268441	8.78	mucin-5AC-like isoform X1
LOC118269877	-2.94	mucin-5B-like
LOC118271848	2.49	mucin-6-like isoform X1
LOC118266209	-3.71	multidrug resistance protein homolog 49-like
LOC118262367	-2.60	multifunctional protein ADE2-like
LOC118262526	-2.44	multifunctional protein ADE2-like
LOC118268599	2.82	multiple epidermal growth factor-like domains protein 10
LOC118262074	-2.64	multiple inositol polyphosphate phosphatase 1-like
LOC118263808	-2.10	muscle LIM protein Mlp84B-like isoform X1
LOC118279279	2.86	muscle M-line assembly protein unc-89-like
LOC118264103	2.13	muscle M-line assembly protein unc-89-like isoform X1
LOC118280714	-2.32	myb/SANT-like DNA-binding domain-containing protein 3
LOC118267468	-3.49	myb/SANT-like DNA-binding domain-containing protein 4
LOC118267705	5.03	myb-like protein AA
LOC118261983	9.13	myb-like protein F isoform X1
LOC118270257	3.38	mycosubtilin synthase subunit C-like
LOC118270248	4.60	mycosubtilin synthase subunit C-like
LOC118278445	4.45	myoneurin-like
LOC118269287	2.11	myosin-11-like
LOC118272660	2.10	myosin-IIIb-like isoform X1
LOC118268569	-2.66	myrosinase 1-like
LOC118277638	2.02	myrosinase 1-like
LOC118277675	3.72	myrosinase 1-like
LOC118270227	-2.36	myrosinase 1-like isoform X1
LOC118270752	3.39	myrosinase 1-like isoform X1
LOC118270798	3.62	myrosinase 1-like isoform X1
LOC118276964	2.44	N-acetylgalactosamine kinase-like
LOC118275853	-4.56	N-acetylneuraminate lyase-like isoform X1
LOC118279333	3.09	NADPH oxidase 5-like
LOC118280864	4.39	nascent polypeptide-associated complex subunit alpha, muscle-specific form-like
LOC118262896	2.93	neprilysin-2-like isoform X1
LOC118263251	3.76	neprilysin-4-like
LOC118263294	4.63	neprilysin-4-like
LOC118276446	3.26	neurofilament medium polypeptide-like
LOC118274628	-4.71	neurogenic locus notch homolog protein 3-like isoform X1
LOC118267572	9.02	neurogenic locus protein delta-like isoform X1
LOC118262193	2.22	neuroligin-3-like
LOC118262827	3.97	neuroligin-4, X-linked-like isoform X1
LOC118275923	-4.86	neuropeptide-like protein 31
LOC118262123	6.34	neurotrophin 1-like
LOC118265404	2.52	neutral ceramidase-like
LOC118265043	2.71	neutral ceramidase-like
LOC118265117	-2.56	nidogen-like
LOC118266978	-2.96	nitric oxide synthase-like
LOC118278472	6.66	non-classical arabinogalactan protein 31-like
LOC118276608	-4.50	nose resistant to fluoxetine protein 6-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118266053	-3.84	nose resistant to fluoxetine protein 6-like
LOC118266008	-3.52	nose resistant to fluoxetine protein 6-like
LOC118266134	-3.42	nose resistant to fluoxetine protein 6-like
LOC118279120	-3.29	nose resistant to fluoxetine protein 6-like
LOC118266467	-3.02	nose resistant to fluoxetine protein 6-like
LOC118263671	2.24	nose resistant to fluoxetine protein 6-like
LOC118263678	2.88	nose resistant to fluoxetine protein 6-like
LOC118274733	5.36	nose resistant to fluoxetine protein 6-like
LOC118262496	6.91	nose resistant to fluoxetine protein 6-like
LOC118266468	6.97	nose resistant to fluoxetine protein 6-like
LOC118262975	7.28	nose resistant to fluoxetine protein 6-like
LOC118266462	8.52	nose resistant to fluoxetine protein 6-like
LOC118275143	-2.09	NPC intracellular cholesterol transporter 2-like
LOC118275380	4.70	nucleoside diphosphate kinase 7-like
LOC118279400	-4.35	O-acyltransferase like protein-like
LOC118265078	-4.32	O-acyltransferase like protein-like
LOC118265077	-3.29	O-acyltransferase like protein-like
LOC118265308	-3.22	O-acyltransferase like protein-like
LOC118276609	2.94	O-acyltransferase like protein-like
LOC118270548	3.54	octopamine receptor beta-1R-like
LOC118270587	3.73	octopamine receptor beta-1R-like
LOC118262461	-3.04	odorant receptor 85c-like isoform X1
LOC118266412	-3.97	odorant-binding protein 59a-like
LOC118272567	-5.52	ommochrome-binding protein-like
LOC118268509	-2.85	opsin Rh3-like isoform X1
LOC118277314	2.07	orexin receptor type 1-like
LOC118282149	2.27	organic cation transporter protein-like
LOC118275981	2.94	organic cation transporter protein-like
LOC118280511	4.71	organic cation transporter protein-like
LOC118280301	4.92	organic cation transporter protein-like
LOC118282153	-2.28	organic cation transporter protein-like isoform X1
LOC118276256	2.45	organic cation transporter-like protein
LOC118277783	3.09	organic cation transporter-like protein
LOC118269968	-4.22	organic cation/carnitine transporter 7-like
LOC118270037	3.12	organic cation/carnitine transporter 7-like
LOC118279308	-2.62	ovalbumin-related protein X-like
LOC118263701	-3.89	paired mesoderm homeobox protein 2A-like isoform X1
LOC118265237	2.30	palmitoyltransferase ZDHHC23-like
LOC118273275	-6.01	pancreatic lipase-related protein 2-like
LOC118273267	-4.68	pancreatic lipase-related protein 2-like
LOC118274199	-4.21	pancreatic lipase-related protein 2-like
LOC118274201	-2.66	pancreatic lipase-related protein 2-like
LOC118273890	-2.65	pancreatic lipase-related protein 2-like
LOC118281197	-2.53	pancreatic lipase-related protein 2-like
LOC118278929	2.06	pancreatic lipase-related protein 2-like
LOC118265265	5.79	pancreatic lipase-related protein 2-like
LOC118274200	-5.33	pancreatic triacylglycerol lipase-like
LOC118273885	-5.27	pancreatic triacylglycerol lipase-like
LOC118277405	-5.14	pancreatic triacylglycerol lipase-like
LOC118273225	-4.40	pancreatic triacylglycerol lipase-like
LOC118273258	-4.20	pancreatic triacylglycerol lipase-like
LOC118273259	-4.09	pancreatic triacylglycerol lipase-like
LOC118277406	-4.01	pancreatic triacylglycerol lipase-like
LOC118273205	-3.99	pancreatic triacylglycerol lipase-like
LOC118273173	-3.86	pancreatic triacylglycerol lipase-like
LOC118273213	-3.43	pancreatic triacylglycerol lipase-like
LOC118281263	-2.52	pancreatic triacylglycerol lipase-like
LOC118281020	-2.37	pancreatic triacylglycerol lipase-like
LOC118273181	-2.25	pancreatic triacylglycerol lipase-like
LOC118281256	-2.16	pancreatic triacylglycerol lipase-like
LOC118273884	-2.00	pancreatic triacylglycerol lipase-like
LOC118273883	-4.47	pancreatic triacylglycerol lipase-like isoform X1
LOC118273882	-3.95	pancreatic triacylglycerol lipase-like isoform X1
LOC118277404	-3.91	pancreatic triacylglycerol lipase-like isoform X1
LOC118262060	3.99	pancreatic triacylglycerol lipase-like isoform X1
LOC118262239	-4.88	para-nitrobenzyl esterase-like
LOC118262756	-3.92	para-nitrobenzyl esterase-like
LOC118263044	-2.43	para-nitrobenzyl esterase-like
LOC118266705	3.12	patched domain-containing protein 3-like
LOC118266649	3.13	patched domain-containing protein 3-like
LOC118262097	6.76	paternally-expressed gene 3 protein-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118261899	-2.45	paxillin-like isoform X1
LOC118281639	-2.10	PDZ and LIM domain protein Zasp-like isoform X1
LOC118274491	4.22	PE-PGRS family protein PE_PGRS16-like
LOC118266470	8.84	PE-PGRS family protein PE_PGRS16-like
LOC118272698	-2.12	peptide methionine sulfoxide reductase-like
LOC118268059	2.15	peptide transporter family 1-like isoform X1
LOC118280597	-4.04	peroxidase-like
LOC118282278	-3.62	peroxidase-like
LOC118262077	-3.28	peroxidase-like
LOC118282279	-3.17	peroxidase-like
LOC118280613	-2.33	peroxidase-like
LOC118261998	-2.12	peroxidase-like
LOC118269917	4.07	peroxidase-like isoform X1
LOC118269931	5.46	peroxidase-like isoform X1
LOC118269806	-2.30	peroxisomal membrane protein 11C-like
LOC118279229	-2.94	phenoloxidase-activating factor 2-like
LOC118274872	-5.48	phosphatidylethanolamine-binding protein homolog F40A3.3-like
LOC118270638	2.24	phosphoacetylglucosamine mutase-like
LOC118277526	-2.15	phosphoenolpyruvate carboxykinase [GTP
LOC118262502	-2.22	phosphoglycerate kinase-like
LOC118264978	6.63	phospholipase A1 member A-like
LOC118265491	2.51	phospholipase A1 VesT1.02-like
LOC118265142	2.82	phospholipase A1-like
LOC118277646	3.00	phospholipase A1-like
LOC118276475	4.07	phospholipase A1-like
LOC118274943	5.74	phospholipase A2-like
LOC118268474	6.50	phospholipase B1, membrane-associated-like
LOC118268476	6.80	phospholipase B1, membrane-associated-like
LOC118281765	-3.03	phosphoribosylformylglycinamidine synthase-like
LOC118275868	-4.41	phytanoyl-CoA dioxygenase, peroxisomal-like
LOC118281922	-3.10	phytanoyl-CoA dioxygenase, peroxisomal-like
LOC118270917	-2.96	piggyBac transposable element-derived protein 3-like
LOC118264396	2.01	piggyBac transposable element-derived protein 3-like
LOC118281064	2.20	piggyBac transposable element-derived protein 3-like
LOC118265338	2.43	piggyBac transposable element-derived protein 3-like
LOC118280451	2.38	piggyBac transposable element-derived protein 4-like
LOC118267393	2.52	piggyBac transposable element-derived protein 4-like
LOC118263610	-2.08	pollen-specific leucine-rich repeat extensin-like protein 3
LOC118266692	10.83	pollen-specific leucine-rich repeat extensin-like protein 4
LOC118276552	-4.21	poly(A) polymerase type 3-like
LOC118281996	2.37	polyprenol reductase-like
LOC118263865	2.41	polyprenol reductase-like
LOC118263573	2.02	potassium channel subfamily K member 18-like isoform X1
LOC118276158	-2.13	potassium channel subfamily K member 1-like isoform X1
LOC118274833	2.02	poxin-like isoform X1
LOC118265185	-2.12	PR domain zinc finger protein 10-like
LOC118263665	11.90	pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16-like
LOC118266944	10.00	prisilkin-39-like
LOC118264573	-3.07	probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial
LOC118267776	-2.12	probable aldehyde oxidase gad-3
LOC118267996	2.32	probable cytochrome P450 301a1, mitochondrial
LOC118271250	6.85	probable cytochrome P450 301a1, mitochondrial
LOC118268212	2.77	probable cytochrome P450 304a1
LOC118268370	3.17	probable cytochrome P450 304a1
LOC118266520	3.95	probable cytochrome P450 305a1 isoform X1
LOC118266312	5.24	probable cytochrome P450 49a1
LOC118265707	6.61	probable cytochrome P450 49a1
LOC118268618	-3.43	probable cytochrome P450 6a13
LOC118268527	-3.10	probable cytochrome P450 6a13
LOC118268605	-2.68	probable cytochrome P450 6a13
LOC118268604	-2.24	probable cytochrome P450 6a13
LOC118275709	9.19	probable cytochrome P450 6a14
LOC118274407	6.76	probable cytochrome P450 6a17
LOC118281706	-2.03	probable DNA mismatch repair protein Msh6 isoform X1
LOC118281232	-2.04	probable galactose-1-phosphate uridylyltransferase
LOC118266977	2.09	probable G-protein coupled receptor Mth-like 1
LOC118275819	2.51	probable G-protein coupled receptor Mth-like 3
LOC118276040	-5.37	probable H/ACA ribonucleoprotein complex subunit 1
LOC118277652	-3.72	probable metabolite transport protein CsbC
LOC118277655	-3.42	probable metabolite transport protein CsbC

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118266428	-2.22	probable methylcrotonoyl-CoA carboxylase beta chain, mitochondrial
LOC118267546	-2.87	probable methylmalonate-semialdehyde dehydrogenase [acylating, mitochondrial
LOC118267560	-2.48	probable methylmalonate-semialdehyde dehydrogenase [acylating, mitochondrial
LOC118279845	5.86	probable nuclear hormone receptor HR3 isoform X1
LOC118279815	5.97	probable nuclear hormone receptor HR3 isoform X1
LOC118273391	2.72	probable nuclear hormone receptor HR38 isoform X1
LOC118270794	-2.74	probable peroxisomal acyl-coenzyme A oxidase 1
LOC118270783	-2.67	probable peroxisomal acyl-coenzyme A oxidase 1
LOC118270681	-2.44	probable peroxisomal acyl-coenzyme A oxidase 1
LOC118279187	-2.23	probable phytanoyl-CoA dioxygenase
LOC118264950	2.04	probable protein S-acyltransferase 23
LOC118277157	6.04	probable salivary secreted peptide
LOC118277155	6.13	probable salivary secreted peptide
LOC118277156	6.23	probable salivary secreted peptide
LOC118265976	5.21	probable serine/threonine-protein kinase clkA
LOC118282388	6.83	probable serine/threonine-protein kinase kinX isoform X1
LOC118282406	7.20	probable serine/threonine-protein kinase kinX isoform X1
LOC118266359	8.27	probable serine/threonine-protein kinase nek3
LOC118277175	-4.60	probable serine/threonine-protein kinase tsuA
LOC118277379	-4.28	probable sodium-coupled neutral amino acid transporter 6
LOC118267639	4.42	probable tubulin polyglutamylase ttll-15
LOC118267638	2.90	probable tubulin polyglutamylase ttll-15 isoform X1
LOC118282369	-2.34	probable tubulin polyglutamylase TTLL2 isoform X1
LOC118262556	-2.04	probable uridine nucleosidase 2 isoform X1
LOC118269929	4.45	proclotting enzyme-like
LOC118278272	7.34	proclotting enzyme-like isoform X1
LOC118280634	2.30	proline-, glutamic acid- and leucine-rich protein 1-like
LOC118272664	6.57	proline-rich protein 27-like
LOC118273865	7.43	proline-rich protein 27-like
LOC118268649	6.57	proline-rich protein 4-like
LOC118268648	10.50	proline-rich protein 4-like
LOC118275417	10.76	proline-rich protein 4-like
LOC118276089	-3.05	prominin-1-A-like isoform X1
LOC118279931	4.48	pro-neuropeptide Y-like
LOC118276983	2.29	pro-resilin-like
LOC118276590	4.66	pro-resilin-like
LOC118276697	6.17	pro-resilin-like
LOC118269958	6.25	pro-resilin-like
LOC118276732	6.28	pro-resilin-like
LOC118276729	7.41	pro-resilin-like
LOC118274217	9.44	pro-resilin-like
LOC118267795	11.41	pro-resilin-like
LOC118264792	-4.55	prostaglandin reductase 1-like
LOC118264101	-2.10	prostaglandin reductase 1-like
LOC118277375	-2.12	protein 4.1 homolog isoform X1
LOC118264936	11.82	protein apnoia-like
LOC118274055	3.55	protein CEPU-1-like
LOC118269723	-3.04	protein CREG1-like isoform X1
LOC118275195	-5.96	protein D3-like
LOC118265859	2.23	protein dead ringer-like
LOC118276076	-2.09	protein enabled homolog
LOC118272824	2.86	protein FAM166B-like
LOC118280037	2.43	protein FAM214A-like
LOC118280035	2.22	protein FAM214A-like isoform X1
LOC118273899	2.02	protein fem-1 homolog CG6966-like isoform X1
LOC118274024	2.10	protein fem-1 homolog CG6966-like isoform X1
LOC118265418	-2.47	protein fuzzy homolog
LOC118274834	2.25	protein GUCD1-like
LOC118272087	3.67	protein KIAA0556-like
LOC118276394	-4.22	protein lethal(2)essential for life-like
LOC118277229	-3.47	protein lethal(2)essential for life-like
LOC118280743	-3.03	protein lethal(2)essential for life-like
LOC118280753	-2.76	protein lethal(2)essential for life-like
LOC118280746	-2.30	protein lethal(2)essential for life-like
LOC118280747	-2.01	protein lethal(2)essential for life-like
LOC118282420	-2.71	protein lethal(3)malignant blood neoplasm 1-like isoform X1
LOC118277943	4.48	protein masquerade-like isoform X1
LOC118271033	2.50	protein mesh isoform X1
LOC118279541	-5.96	protein mono-ADP-ribosyltransferase PARP16-like
LOC118265375	2.31	protein nubbin-like
LOC118263121	2.03	protein obstructor-E-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118263126	2.80	protein obstructor-E-like
LOC118262892	3.00	protein obstructor-E-like
LOC118263124	6.51	protein obstructor-E-like
LOC118263123	3.52	protein obstructor-E-like isoform X1
LOC118263754	3.45	protein O-mannosyl-transferase TMTC1-like
LOC118265051	2.09	protein peste-like isoform X1
LOC118276104	6.79	protein piccolo-like
LOC118271418	2.94	protein rolling stone-like
LOC118277996	-3.13	protein scarlet-like
LOC118267201	-2.75	protein scarlet-like
LOC118276911	-2.69	protein scarlet-like
LOC118267200	-2.34	protein scarlet-like isoform X1
LOC118267228	4.48	protein singles bar-like
LOC118270780	3.46	protein Skeletor, isoforms D/E-like isoform X1
LOC118272064	3.24	protein spaetzle 3-like
LOC118272073	6.34	protein spaetzle 4-like isoform X1
LOC118281631	2.36	protein spaetzle 5-like
LOC118262012	2.54	protein spaetzle 5-like
LOC118262191	-4.25	protein takeout-like
LOC118276515	-4.21	protein takeout-like
LOC118262190	-3.44	protein takeout-like
LOC118263049	3.66	protein takeout-like
LOC118262192	3.97	protein takeout-like
LOC118262220	4.47	protein takeout-like
LOC118263038	5.10	protein takeout-like
LOC118275183	8.39	protein takeout-like
LOC118276042	2.46	protein TANC2-like isoform X1
LOC118278759	-2.08	protein TEX261-like
LOC118262046	-2.34	protein THEM6-like
LOC118278641	2.13	protein tramtrack, alpha isoform-like isoform X1
LOC118277290	-2.26	protein tyrosine phosphatase domain-containing protein 1-like
LOC118267199	-3.62	protein white-like
LOC118267197	-3.60	protein white-like isoform X1
LOC118263618	-3.48	protein Ycf2-like
LOC118264029	3.65	protein yellow-like
LOC118264592	5.58	protein yellow-like
LOC118263854	9.12	protein yellow-like
LOC118264674	4.93	protein yellow-like isoform X1
LOC118268714	2.60	protein yippee-like 2 isoform X1
LOC118268388	2.39	proteoglycan 4-like
LOC118267805	6.98	proteoglycan 4-like isoform X1
LOC118262912	2.24	protocadherin-16-like isoform X1
LOC118263852	2.32	proton-coupled amino acid transporter-like protein CG1139
LOC118263727	2.41	proton-coupled amino acid transporter-like protein CG1139 isoform X1
LOC118263387	2.60	proton-coupled amino acid transporter-like protein CG1139 isoform X2
LOC118263666	2.41	proton-coupled amino acid transporter-like protein pathetic
LOC118263719	3.52	proton-coupled amino acid transporter-like protein pathetic
LOC118266474	-3.56	proton-coupled folate transporter-like
LOC118262041	-3.19	proton-coupled folate transporter-like
LOC118265959	-2.79	proton-coupled folate transporter-like
LOC118282461	-2.58	proton-coupled folate transporter-like
LOC118265965	3.43	proton-coupled folate transporter-like
LOC118266345	4.19	proton-coupled folate transporter-like
LOC118262804	-2.19	proton-coupled folate transporter-like isoform X1
LOC118263987	2.31	pupal cuticle protein 20-like
LOC118263985	3.30	pupal cuticle protein 20-like
LOC118263980	6.63	pupal cuticle protein 20-like
LOC118263981	7.04	pupal cuticle protein 20-like
LOC118263986	3.39	pupal cuticle protein 20-like isoform X1
LOC118265850	-5.16	pupal cuticle protein 27-like
LOC118266107	-4.17	pupal cuticle protein 27-like
LOC118265977	4.76	pupal cuticle protein 36a-like
LOC118265842	5.96	pupal cuticle protein 36a-like isoform X1
LOC118266482	-4.32	pupal cuticle protein 36-like
LOC118265849	-3.78	pupal cuticle protein 36-like
LOC118266051	-2.92	pupal cuticle protein 36-like
LOC118265846	2.63	pupal cuticle protein 36-like
LOC118266013	2.73	pupal cuticle protein 36-like
LOC118272785	6.58	pupal cuticle protein C1B-like
LOC118272876	7.45	pupal cuticle protein C1B-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118272659	7.91	pupal cuticle protein C1B-like
LOC118279656	-7.60	pupal cuticle protein PCP52-like
LOC118279657	-6.55	pupal cuticle protein PCP52-like
LOC118281116	-2.14	putative aminopeptidase W07G4.4
LOC118269972	-3.20	putative carbonic anhydrase 5
LOC118275034	-2.67	putative cystathionine gamma-lyase 2
LOC118268608	4.35	putative defense protein 3
LOC118268170	5.47	putative defense protein 3
LOC118280404	-5.59	putative fatty acyl-CoA reductase CG5065
LOC118265377	-4.95	putative fatty acyl-CoA reductase CG5065
LOC118265535	-3.16	putative fatty acyl-CoA reductase CG5065
LOC118280549	-2.59	putative fatty acyl-CoA reductase CG5065
LOC118280222	2.09	putative fatty acyl-CoA reductase CG5065
LOC118265593	3.04	putative fatty acyl-CoA reductase CG5065
LOC118280439	4.65	putative fatty acyl-CoA reductase CG5065
LOC118280297	4.66	putative fatty acyl-CoA reductase CG5065
LOC118280261	4.76	putative fatty acyl-CoA reductase CG5065
LOC118280293	5.09	putative fatty acyl-CoA reductase CG5065
LOC118280550	5.45	putative fatty acyl-CoA reductase CG5065
LOC118265382	-5.60	putative fatty acyl-CoA reductase CG5065 isoform X1
LOC118280263	-5.01	putative fatty acyl-CoA reductase CG5065 isoform X1
LOC118265028	9.28	putative glycine-rich cell wall structural protein 1
LOC118275766	3.08	putative helicase mov-10-B.1
LOC118275634	3.04	putative helicase mov-10-B.2
LOC118272630	-2.72	putative inactive cysteine synthase 2
LOC118268994	-4.30	putative inorganic phosphate cotransporter
LOC118269246	-3.81	putative inorganic phosphate cotransporter
LOC118266059	6.99	putative mediator of RNA polymerase II transcription subunit 29 isoform X1
LOC118264274	-4.15	putative nuclease HARBI1
LOC118276580	-3.84	putative nuclease HARBI1
LOC118262881	-2.47	putative nuclease HARBI1
LOC118280688	-2.12	putative nuclease HARBI1
LOC118269992	2.97	putative nuclease HARBI1
LOC118266103	-2.82	putative odorant-binding protein A10
LOC118275436	-2.08	putative phosphoenolpyruvate synthase
LOC118269720	-2.66	putative transporter svop-1
LOC118269969	-2.09	putative transporter svop-1
LOC118274621	2.27	putative uncharacterized protein DDB_G0277255
LOC118264923	-2.03	pyrokinin-1 receptor-like isoform X1
LOC118280754	-2.14	pyrroline-5-carboxylate reductase-like isoform X1
LOC118268451	5.10	ras-related and estrogen-regulated growth inhibitor-like protein
LOC118268315	3.94	ras-related and estrogen-regulated growth inhibitor-like protein isoform X1
LOC118265898	2.00	ras-related protein Rab-23-like isoform X1
LOC118268789	-2.06	ras-related protein Rab-28-like
LOC118278299	-3.60	regucalcin-like
LOC118276390	-3.30	regucalcin-like
LOC118276488	-2.39	regucalcin-like isoform X1
LOC118272352	-3.49	regulating synaptic membrane exocytosis protein 2-like isoform X1
LOC118279228	2.62	regulator of hypoxia-inducible factor 1-like
LOC118268491	-3.84	retinal dehydrogenase 1-like
LOC118268490	-3.97	retinal dehydrogenase 1-like isoform X1
LOC118277209	2.87	retinaldehyde-binding protein 1-like
LOC118262117	-5.46	retinol dehydrogenase 11-like
LOC118262510	-5.44	retinol dehydrogenase 11-like
LOC118277338	-5.42	retinol dehydrogenase 11-like
LOC118282297	-3.63	retinol dehydrogenase 11-like
LOC118261967	-3.31	retinol dehydrogenase 11-like
LOC118261968	-3.08	retinol dehydrogenase 11-like
LOC118282377	-2.88	retinol dehydrogenase 11-like
LOC118272390	2.72	retinol dehydrogenase 11-like
LOC118282233	3.54	retinol dehydrogenase 11-like
LOC118282026	5.19	retinol dehydrogenase 11-like
LOC118277341	-4.69	retinol dehydrogenase 12-like
LOC118277340	-3.33	retinol dehydrogenase 12-like
LOC118277339	-2.22	retinol dehydrogenase 12-like
LOC118274079	4.34	retinol dehydrogenase 12-like
LOC118274286	-5.67	retinol dehydrogenase 13-like
LOC118262082	-4.84	retinol dehydrogenase 13-like
LOC118282234	-4.37	retinol dehydrogenase 13-like
LOC118274246	-2.00	retinol dehydrogenase 13-like
LOC118270713	5.34	retinol dehydrogenase 14-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118274074	-3.63	ribose-phosphate pyrophosphokinase 2-like
LOC118270885	10.48	RNA polymerase II degradation factor 1-like
LOC118274336	11.53	RNA-binding protein 33-like
LOC118272878	12.35	RNA-binding protein 33-like
LOC118268638	2.73	RYamide receptor-like
LOC118269868	-2.79	saccharopine dehydrogenase-like oxidoreductase
LOC118269870	-2.29	saccharopine dehydrogenase-like oxidoreductase
LOC118262257	-2.17	saccharopine dehydrogenase-like oxidoreductase
LOC118282479	2.20	salivary glue protein Sgs-3-like
LOC118271756	-2.44	sarcoplasmic calcium-binding protein 1-like isoform X1
LOC118272231	-2.30	sarcoplasmic calcium-binding protein 1-like isoform X1
LOC118271854	-5.02	sarcoplasmic calcium-binding proteins I, III, and IV-like
LOC118278096	6.00	sarcoplasmic reticulum histidine-rich calcium-binding protein-like
LOC118269815	-3.00	scavenger receptor class B member 1-like
LOC118270036	2.07	scavenger receptor class B member 1-like
LOC118280352	2.11	scavenger receptor class B member 1-like
LOC118272226	2.00	segmentation protein Runt-like
LOC118262634	2.93	seminal metalloprotease 1-like
LOC118262711	4.61	seminal metalloprotease 1-like
LOC118281999	-2.49	sensory neuron membrane protein 2
LOC118263803	-2.63	sensory neuron membrane protein 2-like
LOC118273096	2.10	sequestosome-1-like isoform X1
LOC118279688	9.58	serine protease filzig-like
LOC118280078	9.94	serine protease filzig-like
LOC118275138	-3.54	serine protease gd-like isoform X1
LOC118274841	-3.08	serine protease gd-like isoform X1
LOC118274860	-2.26	serine protease gd-like isoform X1
LOC118262736	3.31	serine protease inhibitor 88Ea-like
LOC118277572	5.39	serine protease inhibitor dipetalogastin-like
LOC118277508	5.20	serine protease inhibitor dipetalogastin-like isoform X1
LOC118278559	-3.53	serine protease snake-like
LOC118278673	-3.32	serine protease snake-like
LOC118280676	-3.28	serine protease snake-like
LOC118274057	-3.08	serine protease snake-like
LOC118278662	-2.69	serine protease snake-like
LOC118280677	-2.41	serine protease snake-like
LOC118278810	-2.26	serine protease snake-like
LOC118278647	-2.26	serine protease snake-like
LOC118278721	-2.21	serine protease snake-like
LOC118280569	-2.99	serine protease snake-like isoform X1
LOC118278809	-2.79	serine protease snake-like isoform X1
LOC118279751	5.93	serine proteinase stubble-like
LOC118279917	6.64	serine proteinase stubble-like
LOC118279890	7.59	serine proteinase stubble-like
LOC118282258	2.08	serine/threonine-protein kinase STE20-like
LOC118282259	2.48	serine/threonine-protein kinase STE20-like
LOC118265560	2.06	serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A-like isoform X1
LOC118269184	-2.19	serine--pyruvate aminotransferase, mitochondrial-like
LOC118269185	2.68	serine--pyruvate aminotransferase, mitochondrial-like
LOC118269371	2.08	serine--pyruvate aminotransferase, mitochondrial-like isoform X1
LOC118263302	-3.33	serine-rich adhesin for platelets-like
LOC118281918	2.49	serine-rich adhesin for platelets-like
LOC118277885	4.52	serpin B12-like
LOC118279148	-10.18	serpin E3-like
LOC118279088	-7.46	serpin I2-like
LOC118276297	-2.18	short/branched chain specific acyl-CoA dehydrogenase, mitochondrial-like
LOC118267710	5.81	sialidase-like
LOC118271691	2.51	sialin-like isoform X1
LOC118274040	-3.48	SKI family transcriptional corepressor 2-like
LOC118268651	8.37	skin secretory protein xP2-like
LOC118272289	3.88	small nucleolar RNA U3
LOC118269286	-2.55	sodium channel protein Nach-like isoform X1
LOC118279643	3.29	sodium/nucleoside cotransporter 2-like
LOC118279642	3.38	sodium/nucleoside cotransporter 2-like isoform X1
LOC118265215	-2.17	sodium/potassium/calcium exchanger 4-like
LOC118266274	3.01	sodium/potassium/calcium exchanger Nckx30C-like
LOC118273245	-2.27	sodium/potassium-transporting ATPase subunit beta-2-like
LOC118270430	5.98	sodium-coupled monocarboxylate transporter 1-like
LOC118272746	-2.07	sodium-coupled monocarboxylate transporter 2-like
LOC118269386	2.23	sodium-dependent serotonin transporter-like isoform X1

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118264614	-2.37	sodium-independent sulfate anion transporter-like
LOC118264613	-2.27	sodium-independent sulfate anion transporter-like isoform X1
LOC118274591	2.43	solute carrier family 12 member 4-like
LOC118277595	-2.96	solute carrier family 2, facilitated glucose transporter member 6-like
LOC118277592	-2.73	solute carrier family 2, facilitated glucose transporter member 6-like
LOC118265729	-2.27	solute carrier family 22 member 1-like
LOC118282147	4.81	solute carrier family 22 member 1-like
LOC118261875	3.00	solute carrier family 46 member 3-like
LOC118274558	2.10	solute carrier organic anion transporter family member 4A1-like isoform X1
LOC118275137	4.09	somatomedin-B and thrombospondin type-1 domain-containing protein-like
LOC118275147	4.26	somatomedin-B and thrombospondin type-1 domain-containing protein-like
LOC118274164	-3.11	sorbitol dehydrogenase-like
LOC118272944	-2.46	sperm-associated antigen 6-like isoform X1
LOC118273944	-2.41	spermine oxidase-like
LOC118276989	-3.57	spherulin-2A-like
LOC118276734	-3.55	spherulin-2A-like
LOC118276584	-2.22	spherulin-2A-like
LOC118281045	3.97	spherulin-2A-like
LOC118270137	3.22	sphingomyelin phosphodiesterase-like isoform X1
LOC118272367	-5.96	spidroin-1-like
LOC118277836	8.13	spidroin-2-like
LOC118279342	4.87	stabilizer of axonemal microtubules 1-like
LOC118265276	2.93	START domain-containing protein 10-like
LOC118264926	3.46	stearoyl-CoA desaturase 5-like
LOC118265416	-4.01	succinate dehydrogenase cytochrome b560 subunit, mitochondrial-like
LOC118266608	-3.71	sulfotransferase 1C4-like
LOC118270564	-3.16	sulfotransferase 1C4-like
LOC118266602	-2.44	sulfotransferase 1C4-like
LOC118270544	-2.68	sulfotransferase family cytosolic 1B member 1-like
LOC118263505	-4.56	synaptic vesicle 2-related protein-like isoform X1
LOC118269963	6.09	synaptic vesicle glycoprotein 2B-like isoform X1
LOC118270044	-5.02	synaptic vesicle glycoprotein 2C-like
LOC118263868	-4.26	synaptic vesicle glycoprotein 2C-like
LOC118263902	-3.33	synaptic vesicle glycoprotein 2C-like
LOC118279149	4.09	tektin-4-like
LOC118263714	2.02	tenascin-X-like
LOC118268517	-2.12	tensin-1-like isoform X1
LOC118267666	12.63	tetra-peptide repeat homeobox protein 1-like
LOC118263709	2.54	tetraspanin-2A-like
LOC118271480	3.00	three prime repair exonuclease 2-like
LOC118262723	3.72	three prime repair exonuclease 2-like
LOC118275696	2.68	thyroid transcription factor 1-like
LOC118268680	2.12	titin-like
LOC118279372	10.53	titin-like
LOC118269398	11.41	titin-like
LOC118272158	-2.81	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase-like
LOC118271922	3.15	transcription factor hamlet-like
LOC118267262	-2.97	transcription factor Sp5-like
LOC118268460	8.19	transcription factor SPT20 homolog
LOC118278221	8.56	transcription factor SPT20 homolog
LOC118273521	8.38	transcription factor SPT20 homolog isoform X1
LOC118277989	5.30	transcription factor stalky-like
LOC118280719	6.14	transcriptional activator GLI3-like
LOC118278458	6.32	transcriptional regulatory protein AlgP-like
LOC118266018	-3.57	transcriptional regulatory protein LGE1-like
LOC118277790	-2.57	transketolase-like protein 2
LOC118269970	5.69	transmembrane protease serine 12-like
LOC118267882	2.79	transmembrane protease serine 9-like
LOC118270083	5.36	transmembrane protease serine 9-like
LOC118269693	9.15	transmembrane protease serine 9-like
LOC118264706	-3.45	trehalase-like
LOC118280551	-2.51	trehalase-like
LOC118264150	-2.91	trehalase-like isoform X1
LOC118268981	3.03	trichohyalin-like
LOC118263267	-2.55	trimethyllysine dioxygenase, mitochondrial-like
LOC118263239	-2.42	trimethyllysine dioxygenase, mitochondrial-like
LOC118265546	-2.88	triokinase/FMN cyclase-like
LOC118265049	-2.78	triokinase/FMN cyclase-like
LOC118273353	2.39	tripartite motif-containing protein 45-like
AOB78_gt10	2.18	tRNA-Gly
LOC118274264	2.23	tRNA-uridine aminocarboxypropyltransferase 2-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118263590	3.47	trypsin 3A1-like
LOC118274665	2.45	trypsin CFT-1-like
LOC118277917	2.35	trypsin CFT-1-like isoform X1
LOC118280050	4.27	trypsin inhibitor-like
LOC118280797	-2.96	trypsin, alkaline B-like
LOC118274659	5.85	trypsin, alkaline B-like
LOC118274623	5.02	trypsin, alkaline C-like
LOC118271895	7.21	trypsin-1-like
LOC118269924	10.49	trypsin-1-like isoform X1
LOC118263562	5.37	trypsin-3-like
LOC118280401	4.14	trypsin-like
LOC118280409	5.26	trypsin-like
LOC118281743	-2.40	tubulin polymerization-promoting protein homolog
LOC118266900	2.16	tumor protein p63-regulated gene 1-like protein isoform X1
LOC118263214	3.78	U1 spliceosomal RNA
LOC118275940	-5.53	UDP-glucuronosyltransferase 1-2-like
LOC118279191	-3.90	UDP-glucuronosyltransferase 1-7-like
LOC118279190	-3.87	UDP-glucuronosyltransferase 1-7-like
LOC118278122	-3.90	UDP-glucuronosyltransferase 1-8-like
LOC118269227	-2.53	UDP-glucuronosyltransferase 2B10-like
LOC118277904	-4.09	UDP-glucuronosyltransferase 2B15-like
LOC118277899	-3.29	UDP-glucuronosyltransferase 2B15-like
LOC118277906	-3.14	UDP-glucuronosyltransferase 2B15-like
LOC118277768	-2.57	UDP-glucuronosyltransferase 2B15-like
LOC118268440	-2.31	UDP-glucuronosyltransferase 2B15-like
LOC118279155	-3.89	UDP-glucuronosyltransferase 2B19-like
LOC118277903	-3.32	UDP-glucuronosyltransferase 2B19-like
LOC118265011	-4.40	UDP-glucuronosyltransferase 2B1-like
LOC118265425	2.49	UDP-glucuronosyltransferase 2B1-like
LOC118265297	3.23	UDP-glucuronosyltransferase 2B1-like
LOC118279415	-3.07	UDP-glucuronosyltransferase 2B20-like
LOC118277901	-4.18	UDP-glucuronosyltransferase 2B31-like
LOC118265039	-2.97	UDP-glucuronosyltransferase 2B31-like
LOC118279189	-4.04	UDP-glucuronosyltransferase 2B33-like isoform X1
LOC118279153	-3.09	UDP-glucuronosyltransferase 2B4-like
LOC118277900	-3.98	UDP-glucuronosyltransferase 2C1-like
LOC118277905	-2.60	UDP-glucuronosyltransferase 2C1-like
LOC118267687	4.55	UDP-glucuronosyltransferase 2C1-like
LOC118267688	4.80	UDP-glucuronosyltransferase 2C1-like
LOC118264242	2.67	UNC93-like protein MFSD11
LOC118264165	3.12	UNC93-like protein MFSD11
LOC118263484	-4.27	uncharacterized 30.3 kDa protein-like
LOC118263489	3.48	uncharacterized 30.3 kDa protein-like
LOC118263527	3.85	uncharacterized 30.3 kDa protein-like
LOC118278228	9.95	uncharacterized abhydrolase domain-containing protein DDB_G0269086-like isoform X1
LOC118276754	-5.70	uncharacterized GMC-type oxidoreductase Mb1310-like
LOC118261731	5.28	uncharacterized LOC118261731
LOC118261770	-4.78	uncharacterized LOC118261770
LOC118261933	-2.96	uncharacterized LOC118261933
LOC118262103	2.43	uncharacterized LOC118262103
LOC118262107	4.26	uncharacterized LOC118262107
LOC118262341	7.81	uncharacterized LOC118262341
LOC118262543	-4.68	uncharacterized LOC118262543
LOC118262817	5.25	uncharacterized LOC118262817
LOC118262908	4.48	uncharacterized LOC118262908
LOC118263526	4.52	uncharacterized LOC118263526
LOC118263869	-2.87	uncharacterized LOC118263869
LOC118264504	-4.48	uncharacterized LOC118264504
LOC118264505	-2.13	uncharacterized LOC118264505
LOC118264515	3.67	uncharacterized LOC118264515
LOC118264520	-3.64	uncharacterized LOC118264520
LOC118264552	4.93	uncharacterized LOC118264552
LOC118264665	-5.39	uncharacterized LOC118264665
LOC118264739	3.84	uncharacterized LOC118264739
LOC118264764	3.42	uncharacterized LOC118264764
LOC118264765	5.24	uncharacterized LOC118264765
LOC118264766	-4.18	uncharacterized LOC118264766
LOC118265451	3.20	uncharacterized LOC118265451
LOC118266108	-2.04	uncharacterized LOC118266108
LOC118266116	-3.25	uncharacterized LOC118266116

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118266117	-4.48	uncharacterized LOC118266117
LOC118266120	-4.16	uncharacterized LOC118266120
LOC118266138	-6.86	uncharacterized LOC118266138
LOC118266215	-6.77	uncharacterized LOC118266215
LOC118266387	-5.42	uncharacterized LOC118266387
LOC118266503	-3.90	uncharacterized LOC118266503
LOC118266537	-6.66	uncharacterized LOC118266537
LOC118266614	-4.22	uncharacterized LOC118266614
LOC118266631	-2.45	uncharacterized LOC118266631
LOC118266641	2.21	uncharacterized LOC118266641
LOC118266642	2.69	uncharacterized LOC118266642
LOC118266933	2.66	uncharacterized LOC118266933
LOC118267027	5.22	uncharacterized LOC118267027
LOC118267126	2.79	uncharacterized LOC118267126
LOC118267219	3.55	uncharacterized LOC118267219
LOC118267663	-6.71	uncharacterized LOC118267663
LOC118267667	3.22	uncharacterized LOC118267667
LOC118268735	2.69	uncharacterized LOC118268735
LOC118269402	4.29	uncharacterized LOC118269402
LOC118269767	4.18	uncharacterized LOC118269767
LOC118270017	2.81	uncharacterized LOC118270017
LOC118270019	2.07	uncharacterized LOC118270019
LOC118270118	2.44	uncharacterized LOC118270118
LOC118270597	-2.20	uncharacterized LOC118270597
LOC118271037	2.03	uncharacterized LOC118271037
LOC118271238	3.88	uncharacterized LOC118271238
LOC118271251	2.06	uncharacterized LOC118271251
LOC118271395	2.17	uncharacterized LOC118271395
LOC118271921	3.89	uncharacterized LOC118271921
LOC118271949	5.84	uncharacterized LOC118271949
LOC118272741	3.07	uncharacterized LOC118272741
LOC118272775	-4.94	uncharacterized LOC118272775
LOC118272808	-6.19	uncharacterized LOC118272808
LOC118273619	-2.03	uncharacterized LOC118273619
LOC118273916	-2.18	uncharacterized LOC118273916
LOC118274093	3.40	uncharacterized LOC118274093
LOC118274493	4.84	uncharacterized LOC118274493
LOC118274499	4.50	uncharacterized LOC118274499
LOC118274536	7.46	uncharacterized LOC118274536
LOC118274599	-2.11	uncharacterized LOC118274599
LOC118274620	-2.36	uncharacterized LOC118274620
LOC118274861	-2.28	uncharacterized LOC118274861
LOC118274915	-3.18	uncharacterized LOC118274915
LOC118275148	2.87	uncharacterized LOC118275148
LOC118275202	-3.21	uncharacterized LOC118275202
LOC118275559	-3.02	uncharacterized LOC118275559
LOC118275895	5.14	uncharacterized LOC118275895
LOC118276277	-2.15	uncharacterized LOC118276277
LOC118276387	4.99	uncharacterized LOC118276387
LOC118276638	5.74	uncharacterized LOC118276638
LOC118276921	4.77	uncharacterized LOC118276921
LOC118276928	5.15	uncharacterized LOC118276928
LOC118277147	6.27	uncharacterized LOC118277147
LOC118277168	-3.92	uncharacterized LOC118277168
LOC118277425	8.07	uncharacterized LOC118277425
LOC118277842	-4.06	uncharacterized LOC118277842
LOC118278597	3.15	uncharacterized LOC118278597
LOC118278694	-4.40	uncharacterized LOC118278694
LOC118279001	-3.09	uncharacterized LOC118279001
LOC118279402	-2.19	uncharacterized LOC118279402
LOC118279675	-2.78	uncharacterized LOC118279675
LOC118279684	-3.76	uncharacterized LOC118279684
LOC118279811	-4.38	uncharacterized LOC118279811
LOC118279812	-3.55	uncharacterized LOC118279812
LOC118280032	-4.21	uncharacterized LOC118280032
LOC118280052	-2.82	uncharacterized LOC118280052
LOC118280290	2.30	uncharacterized LOC118280290
LOC118280658	-2.57	uncharacterized LOC118280658
LOC118280798	3.82	uncharacterized LOC118280798
LOC118281386	6.81	uncharacterized LOC118281386
LOC118281395	5.92	uncharacterized LOC118281395

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118281866	-5.16	uncharacterized LOC118281866
LOC118282013	3.96	uncharacterized LOC118282013
LOC118282273	2.09	uncharacterized LOC118282273
LOC118275124	-2.93	uncharacterized oxidoreductase MexAM1_META1p0182-like
LOC118275122	-4.56	uncharacterized oxidoreductase TM_0325-like
LOC118269454	-3.80	uncharacterized oxidoreductase TM_0325-like
LOC118268887	-3.41	uncharacterized oxidoreductase TM_0325-like
LOC118276485	-2.56	uncharacterized oxidoreductase TM_0325-like
LOC118266443	-3.51	uncharacterized oxidoreductase YjmC-like
LOC118264328	-4.54	uncharacterized oxidoreductase YoxD-like
LOC118274010	-3.93	uncharacterized PE-PGRS family protein PE_PGRS36-like
LOC118278316	-2.99	uncharacterized PE-PGRS family protein PE_PGRS36-like
LOC118281712	4.50	uncharacterized PE-PGRS family protein PE_PGRS46-like
LOC118265037	-2.80	uncharacterized PE-PGRS family protein PE_PGRS54-like
LOC118275335	2.15	uncharacterized protein C14orf119 homolog isoform X1
LOC118273067	10.33	uncharacterized protein DDB_G0290587-like
LOC118262221	4.48	uncharacterized protein DDB_G0290685-like
LOC118278038	-8.95	uncharacterized protein K02A2.6-like
LOC118282007	-4.31	uncharacterized protein K02A2.6-like
LOC118281254	-3.83	uncharacterized protein K02A2.6-like
LOC118272595	-3.33	uncharacterized protein K02A2.6-like
LOC118278348	-2.85	uncharacterized protein K02A2.6-like
LOC118261738	9.12	uncharacterized protein LOC118261738
LOC118261776	9.54	uncharacterized protein LOC118261776
LOC118261777	9.02	uncharacterized protein LOC118261777
LOC118261794	9.32	uncharacterized protein LOC118261794
LOC118261809	3.50	uncharacterized protein LOC118261809
LOC118261817	3.29	uncharacterized protein LOC118261817 isoform X1
LOC118261820	-4.46	uncharacterized protein LOC118261820
LOC118261894	3.20	uncharacterized protein LOC118261894
LOC118261910	3.73	uncharacterized protein LOC118261910
LOC118261922	2.71	uncharacterized protein LOC118261922
LOC118261925	6.55	uncharacterized protein LOC118261925
LOC118261949	5.08	uncharacterized protein LOC118261949
LOC118261959	-4.94	uncharacterized protein LOC118261959
LOC118261961	2.97	uncharacterized protein LOC118261961
LOC118262018	8.00	uncharacterized protein LOC118262018
LOC118262047	5.74	uncharacterized protein LOC118262047
LOC118262064	7.48	uncharacterized protein LOC118262064
LOC118262098	2.44	uncharacterized protein LOC118262098
LOC118262118	2.31	uncharacterized protein LOC118262118
LOC118262134	-2.89	uncharacterized protein LOC118262134
LOC118262135	2.22	uncharacterized protein LOC118262135
LOC118262181	5.19	uncharacterized protein LOC118262181
LOC118262276	8.42	uncharacterized protein LOC118262276 isoform X1
LOC118262360	-2.16	uncharacterized protein LOC118262360
LOC118262361	-2.01	uncharacterized protein LOC118262361
LOC118262362	-2.03	uncharacterized protein LOC118262362
LOC118262425	-3.77	uncharacterized protein LOC118262425
LOC118262429	3.72	uncharacterized protein LOC118262429
LOC118262460	2.25	uncharacterized protein LOC118262460
LOC118262499	3.62	uncharacterized protein LOC118262499
LOC118262681	-3.52	uncharacterized protein LOC118262681
LOC118262682	-3.42	uncharacterized protein LOC118262682
LOC118262746	2.14	uncharacterized protein LOC118262746 isoform X1
LOC118262764	-2.06	uncharacterized protein LOC118262764
LOC118262818	2.17	uncharacterized protein LOC118262818
LOC118262914	6.73	uncharacterized protein LOC118262914 isoform X1
LOC118262929	7.33	uncharacterized protein LOC118262929
LOC118262930	3.27	uncharacterized protein LOC118262930
LOC118262935	6.71	uncharacterized protein LOC118262935
LOC118262936	3.58	uncharacterized protein LOC118262936
LOC118262954	3.75	uncharacterized protein LOC118262954
LOC118262956	-2.46	uncharacterized protein LOC118262956
LOC118262989	6.79	uncharacterized protein LOC118262989
LOC118263008	3.08	uncharacterized protein LOC118263008 isoform X1
LOC118263033	-2.23	uncharacterized protein LOC118263033
LOC118263051	2.75	uncharacterized protein LOC118263051
LOC118263052	-3.90	uncharacterized protein LOC118263052
LOC118263053	3.30	uncharacterized protein LOC118263053

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118263054	-3.98	uncharacterized protein LOC118263054
LOC118263075	3.72	uncharacterized protein LOC118263075
LOC118263084	-4.13	uncharacterized protein LOC118263084 isoform X1
LOC118263088	6.39	uncharacterized protein LOC118263088
LOC118263093	5.21	uncharacterized protein LOC118263093
LOC118263303	-3.67	uncharacterized protein LOC118263303
LOC118263304	-6.45	uncharacterized protein LOC118263304
LOC118263348	3.53	uncharacterized protein LOC118263348
LOC118263416	-3.08	uncharacterized protein LOC118263416
LOC118263417	-2.67	uncharacterized protein LOC118263417
LOC118263438	5.05	uncharacterized protein LOC118263438
LOC118263477	4.40	uncharacterized protein LOC118263477
LOC118263504	2.92	uncharacterized protein LOC118263504
LOC118263579	4.40	uncharacterized protein LOC118263579
LOC118263589	2.30	uncharacterized protein LOC118263589
LOC118263773	-2.63	uncharacterized protein LOC118263773
LOC118263817	-3.49	uncharacterized protein LOC118263817
LOC118263851	-2.18	uncharacterized protein LOC118263851
LOC118263861	-5.15	uncharacterized protein LOC118263861
LOC118263875	6.13	uncharacterized protein LOC118263875 isoform X1
LOC118263877	3.39	uncharacterized protein LOC118263877 isoform X1
LOC118263899	2.33	uncharacterized protein LOC118263899
LOC118263982	6.90	uncharacterized protein LOC118263982
LOC118263992	7.96	uncharacterized protein LOC118263992
LOC118264053	-2.30	uncharacterized protein LOC118264053
LOC118264151	3.39	uncharacterized protein LOC118264151
LOC118264174	3.22	uncharacterized protein LOC118264174
LOC118264238	4.64	uncharacterized protein LOC118264238
LOC118264246	2.70	uncharacterized protein LOC118264246
LOC118264284	4.37	uncharacterized protein LOC118264284
LOC118264332	6.52	uncharacterized protein LOC118264332
LOC118264347	-2.62	uncharacterized protein LOC118264347
LOC118264369	-2.87	uncharacterized protein LOC118264369
LOC118264393	5.96	uncharacterized protein LOC118264393
LOC118264401	-2.44	uncharacterized protein LOC118264401
LOC118264468	-4.02	uncharacterized protein LOC118264468
LOC118264469	4.07	uncharacterized protein LOC118264469
LOC118264485	-3.65	uncharacterized protein LOC118264485
LOC118264508	-6.10	uncharacterized protein LOC118264508 isoform X1
LOC118264514	5.06	uncharacterized protein LOC118264514 isoform X1
LOC118264530	-5.78	uncharacterized protein LOC118264530
LOC118264532	3.75	uncharacterized protein LOC118264532
LOC118264539	-3.27	uncharacterized protein LOC118264539
LOC118264546	5.68	uncharacterized protein LOC118264546 isoform X1
LOC118264568	3.29	uncharacterized protein LOC118264568
LOC118264623	-3.72	uncharacterized protein LOC118264623
LOC118264701	-2.16	uncharacterized protein LOC118264701
LOC118264702	-2.34	uncharacterized protein LOC118264702
LOC118264731	3.05	uncharacterized protein LOC118264731
LOC118264823	4.48	uncharacterized protein LOC118264823
LOC118264836	3.46	uncharacterized protein LOC118264836
LOC118264844	-5.54	uncharacterized protein LOC118264844
LOC118264846	-2.74	uncharacterized protein LOC118264846
LOC118264853	2.14	uncharacterized protein LOC118264853
LOC118264896	3.00	uncharacterized protein LOC118264896
LOC118264922	-2.06	uncharacterized protein LOC118264922
LOC118264934	8.00	uncharacterized protein LOC118264934
LOC118264937	-4.66	uncharacterized protein LOC118264937
LOC118265040	-2.80	uncharacterized protein LOC118265040
LOC118265073	3.93	uncharacterized protein LOC118265073
LOC118265076	-3.38	uncharacterized protein LOC118265076
LOC118265098	5.77	uncharacterized protein LOC118265098
LOC118265110	2.00	uncharacterized protein LOC118265110 isoform X1
LOC118265114	6.97	uncharacterized protein LOC118265114
LOC118265116	6.19	uncharacterized protein LOC118265116
LOC118265175	5.22	uncharacterized protein LOC118265175
LOC118265224	7.57	uncharacterized protein LOC118265224
LOC118265359	-2.06	uncharacterized protein LOC118265359
LOC118265390	3.73	uncharacterized protein LOC118265390
LOC118265396	-4.67	uncharacterized protein LOC118265396 isoform X1
LOC118265410	-5.06	uncharacterized protein LOC118265410 isoform X1

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118265434	6.27	uncharacterized protein LOC118265434
LOC118265463	3.47	uncharacterized protein LOC118265463 isoform X1
LOC118265464	4.58	uncharacterized protein LOC118265464
LOC118265465	3.12	uncharacterized protein LOC118265465 isoform X1
LOC118265569	4.21	uncharacterized protein LOC118265569 isoform X1
LOC118265618	-2.00	uncharacterized protein LOC118265618
LOC118265716	-3.72	uncharacterized protein LOC118265716
LOC118265717	-4.80	uncharacterized protein LOC118265717
LOC118265721	-2.06	uncharacterized protein LOC118265721 isoform X1
LOC118265788	6.25	uncharacterized protein LOC118265788
LOC118265789	6.78	uncharacterized protein LOC118265789
LOC118265863	10.20	uncharacterized protein LOC118265863
LOC118265966	-2.42	uncharacterized protein LOC118265966
LOC118265992	-2.21	uncharacterized protein LOC118265992
LOC118265994	-2.64	uncharacterized protein LOC118265994
LOC118266040	5.11	uncharacterized protein LOC118266040
LOC118266063	-2.37	uncharacterized protein LOC118266063
LOC118266193	5.02	uncharacterized protein LOC118266193
LOC118266210	-2.92	uncharacterized protein LOC118266210
LOC118266246	-4.61	uncharacterized protein LOC118266246
LOC118266249	-3.92	uncharacterized protein LOC118266249
LOC118266269	6.57	uncharacterized protein LOC118266269
LOC118266287	-3.82	uncharacterized protein LOC118266287 isoform X1
LOC118266301	4.65	uncharacterized protein LOC118266301
LOC118266310	4.63	uncharacterized protein LOC118266310
LOC118266319	6.52	uncharacterized protein LOC118266319
LOC118266335	5.87	uncharacterized protein LOC118266335 isoform X1
LOC118266347	-2.33	uncharacterized protein LOC118266347 isoform X1
LOC118266369	9.35	uncharacterized protein LOC118266369
LOC118266383	9.07	uncharacterized protein LOC118266383 isoform X1
LOC118266385	-3.40	uncharacterized protein LOC118266385
LOC118266434	5.94	uncharacterized protein LOC118266434
LOC118266437	-2.57	uncharacterized protein LOC118266437
LOC118266480	2.81	uncharacterized protein LOC118266480
LOC118266509	3.45	uncharacterized protein LOC118266509
LOC118266606	10.25	uncharacterized protein LOC118266606
LOC118266612	7.36	uncharacterized protein LOC118266612
LOC118266663	-5.52	uncharacterized protein LOC118266663
LOC118266693	2.28	uncharacterized protein LOC118266693
LOC118266802	-3.10	uncharacterized protein LOC118266802
LOC118266845	-4.13	uncharacterized protein LOC118266845
LOC118266910	5.16	uncharacterized protein LOC118266910
LOC118266929	-2.24	uncharacterized protein LOC118266929
LOC118266985	11.32	uncharacterized protein LOC118266985 isoform X1
LOC118267101	10.72	uncharacterized protein LOC118267101
LOC118267218	3.25	uncharacterized protein LOC118267218
LOC118267221	2.22	uncharacterized protein LOC118267221
LOC118267248	2.01	uncharacterized protein LOC118267248 isoform X1
LOC118267296	2.42	uncharacterized protein LOC118267296
LOC118267306	9.60	uncharacterized protein LOC118267306
LOC118267317	3.98	uncharacterized protein LOC118267317
LOC118267326	-3.19	uncharacterized protein LOC118267326
LOC118267364	9.55	uncharacterized protein LOC118267364
LOC118267423	11.18	uncharacterized protein LOC118267423 isoform X1
LOC118267432	9.30	uncharacterized protein LOC118267432
LOC118267445	12.05	uncharacterized protein LOC118267445 isoform X1
LOC118267549	10.21	uncharacterized protein LOC118267549
LOC118267552	2.30	uncharacterized protein LOC118267552
LOC118267565	8.33	uncharacterized protein LOC118267565
LOC118267577	9.79	uncharacterized protein LOC118267577
LOC118267594	-3.05	uncharacterized protein LOC118267594
LOC118267595	-6.42	uncharacterized protein LOC118267595
LOC118267647	5.94	uncharacterized protein LOC118267647
LOC118267664	7.73	uncharacterized protein LOC118267664
LOC118267679	5.72	uncharacterized protein LOC118267679 isoform X1
LOC118267682	4.01	uncharacterized protein LOC118267682
LOC118267711	2.45	uncharacterized protein LOC118267711
LOC118267721	3.82	uncharacterized protein LOC118267721 isoform X1
LOC118267722	2.31	uncharacterized protein LOC118267722
LOC118267733	3.62	uncharacterized protein LOC118267733

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118267748	-2.64	uncharacterized protein LOC118267748 isoform X1
LOC118267779	5.07	uncharacterized protein LOC118267779
LOC118267783	-4.13	uncharacterized protein LOC118267783
LOC118267785	3.86	uncharacterized protein LOC118267785
LOC118267833	6.96	uncharacterized protein LOC118267833
LOC118267858	10.63	uncharacterized protein LOC118267858
LOC118267865	-3.93	uncharacterized protein LOC118267865
LOC118267886	-5.22	uncharacterized protein LOC118267886
LOC118267887	-3.64	uncharacterized protein LOC118267887
LOC118267904	-2.05	uncharacterized protein LOC118267904
LOC118267928	-3.09	uncharacterized protein LOC118267928
LOC118267929	-3.24	uncharacterized protein LOC118267929
LOC118267931	-2.20	uncharacterized protein LOC118267931
LOC118267952	6.92	uncharacterized protein LOC118267952
LOC118267979	-4.40	uncharacterized protein LOC118267979 isoform X1
LOC118267981	-2.49	uncharacterized protein LOC118267981
LOC118267982	-3.68	uncharacterized protein LOC118267982
LOC118267986	-5.27	uncharacterized protein LOC118267986
LOC118267991	-3.06	uncharacterized protein LOC118267991
LOC118268003	9.48	uncharacterized protein LOC118268003
LOC118268133	2.62	uncharacterized protein LOC118268133 isoform X1
LOC118268147	2.01	uncharacterized protein LOC118268147 isoform X1
LOC118268189	-2.30	uncharacterized protein LOC118268189
LOC118268215	3.55	uncharacterized protein LOC118268215
LOC118268327	4.12	uncharacterized protein LOC118268327
LOC118268357	2.62	uncharacterized protein LOC118268357
LOC118268494	-3.19	uncharacterized protein LOC118268494
LOC118268511	5.04	uncharacterized protein LOC118268511
LOC118268519	-2.19	uncharacterized protein LOC118268519 isoform X1
LOC118268555	2.16	uncharacterized protein LOC118268555
LOC118268630	3.26	uncharacterized protein LOC118268630 isoform X1
LOC118268652	2.52	uncharacterized protein LOC118268652
LOC118268672	2.28	uncharacterized protein LOC118268672
LOC118268876	3.75	uncharacterized protein LOC118268876
LOC118268891	3.88	uncharacterized protein LOC118268891
LOC118268943	8.63	uncharacterized protein LOC118268943
LOC118268949	9.24	uncharacterized protein LOC118268949
LOC118269029	4.95	uncharacterized protein LOC118269029
LOC118269033	-2.57	uncharacterized protein LOC118269033
LOC118269044	-2.21	uncharacterized protein LOC118269044
LOC118269048	-2.11	uncharacterized protein LOC118269048
LOC118269096	3.23	uncharacterized protein LOC118269096
LOC118269138	-2.35	uncharacterized protein LOC118269138
LOC118269194	-2.24	uncharacterized protein LOC118269194 isoform X1
LOC118269211	-2.61	uncharacterized protein LOC118269211
LOC118269238	8.57	uncharacterized protein LOC118269238
LOC118269258	-4.27	uncharacterized protein LOC118269258 isoform X1
LOC118269259	-3.89	uncharacterized protein LOC118269259
LOC118269278	2.02	uncharacterized protein LOC118269278
LOC118269329	4.55	uncharacterized protein LOC118269329
LOC118269342	-2.16	uncharacterized protein LOC118269342
LOC118269345	5.32	uncharacterized protein LOC118269345
LOC118269350	-2.69	uncharacterized protein LOC118269350
LOC118269362	2.38	uncharacterized protein LOC118269362 isoform X1
LOC118269363	6.11	uncharacterized protein LOC118269363 isoform X1
LOC118269408	-4.30	uncharacterized protein LOC118269408
LOC118269597	3.49	uncharacterized protein LOC118269597
LOC118269606	-2.35	uncharacterized protein LOC118269606
LOC118269610	2.06	uncharacterized protein LOC118269610
LOC118269612	-2.85	uncharacterized protein LOC118269612
LOC118269652	2.78	uncharacterized protein LOC118269652
LOC118269665	-2.81	uncharacterized protein LOC118269665 isoform X1
LOC118269701	-2.53	uncharacterized protein LOC118269701
LOC118269744	5.20	uncharacterized protein LOC118269744
LOC118269790	6.91	uncharacterized protein LOC118269790
LOC118269793	6.07	uncharacterized protein LOC118269793
LOC118269845	-2.24	uncharacterized protein LOC118269845
LOC118269883	-2.04	uncharacterized protein LOC118269883
LOC118269903	6.99	uncharacterized protein LOC118269903
LOC118269905	4.11	uncharacterized protein LOC118269905
LOC118269909	2.36	uncharacterized protein LOC118269909

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118269934	6.40	uncharacterized protein LOC118269934
LOC118269980	2.21	uncharacterized protein LOC118269980
LOC118269985	3.75	uncharacterized protein LOC118269985
LOC118269994	5.40	uncharacterized protein LOC118269994
LOC118270007	-6.73	uncharacterized protein LOC118270007 isoform X1
LOC118270040	5.69	uncharacterized protein LOC118270040
LOC118270049	2.71	uncharacterized protein LOC118270049
LOC118270054	9.02	uncharacterized protein LOC118270054
LOC118270077	5.51	uncharacterized protein LOC118270077
LOC118270121	7.32	uncharacterized protein LOC118270121
LOC118270141	4.70	uncharacterized protein LOC118270141
LOC118270149	-2.67	uncharacterized protein LOC118270149
LOC118270150	2.20	uncharacterized protein LOC118270150
LOC118270190	-2.36	uncharacterized protein LOC118270190
LOC118270213	3.75	uncharacterized protein LOC118270213
LOC118270224	-4.03	uncharacterized protein LOC118270224
LOC118270293	2.28	uncharacterized protein LOC118270293
LOC118270295	2.69	uncharacterized protein LOC118270295
LOC118270355	2.08	uncharacterized protein LOC118270355
LOC118270399	5.23	uncharacterized protein LOC118270399
LOC118270401	-4.78	uncharacterized protein LOC118270401
LOC118270408	4.67	uncharacterized protein LOC118270408 isoform X1
LOC118270417	3.74	uncharacterized protein LOC118270417 isoform X1
LOC118270432	11.05	uncharacterized protein LOC118270432
LOC118270433	-3.77	uncharacterized protein LOC118270433
LOC118270437	9.80	uncharacterized protein LOC118270437
LOC118270442	4.01	uncharacterized protein LOC118270442 isoform X1
LOC118270447	3.88	uncharacterized protein LOC118270447 isoform X1
LOC118270455	11.35	uncharacterized protein LOC118270455
LOC118270476	3.92	uncharacterized protein LOC118270476
LOC118270487	6.36	uncharacterized protein LOC118270487
LOC118270499	-2.01	uncharacterized protein LOC118270499
LOC118270503	9.70	uncharacterized protein LOC118270503
LOC118270510	11.75	uncharacterized protein LOC118270510
LOC118270511	13.69	uncharacterized protein LOC118270511
LOC118270513	10.23	uncharacterized protein LOC118270513
LOC118270517	11.73	uncharacterized protein LOC118270517
LOC118270525	11.52	uncharacterized protein LOC118270525 isoform X1
LOC118270528	14.28	uncharacterized protein LOC118270528
LOC118270531	4.93	uncharacterized protein LOC118270531
LOC118270538	11.40	uncharacterized protein LOC118270538 isoform X1
LOC118270541	3.57	uncharacterized protein LOC118270541
LOC118270546	13.03	uncharacterized protein LOC118270546
LOC118270551	12.77	uncharacterized protein LOC118270551
LOC118270558	11.67	uncharacterized protein LOC118270558 isoform X1
LOC118270567	10.37	uncharacterized protein LOC118270567
LOC118270591	7.77	uncharacterized protein LOC118270591 isoform X1
LOC118270592	9.68	uncharacterized protein LOC118270592
LOC118270593	4.07	uncharacterized protein LOC118270593
LOC118270596	-2.51	uncharacterized protein LOC118270596
LOC118270622	7.44	uncharacterized protein LOC118270622 isoform X1
LOC118270625	8.19	uncharacterized protein LOC118270625 isoform X1
LOC118270626	4.61	uncharacterized protein LOC118270626 isoform X1
LOC118270655	9.26	uncharacterized protein LOC118270655
LOC118270660	7.77	uncharacterized protein LOC118270660
LOC118270675	10.02	uncharacterized protein LOC118270675
LOC118270676	14.66	uncharacterized protein LOC118270676
LOC118270699	2.91	uncharacterized protein LOC118270699
LOC118270723	2.19	uncharacterized protein LOC118270723
LOC118270727	6.51	uncharacterized protein LOC118270727
LOC118270745	5.70	uncharacterized protein LOC118270745
LOC118270760	11.27	uncharacterized protein LOC118270760
LOC118270762	-9.84	uncharacterized protein LOC118270762
LOC118270770	8.46	uncharacterized protein LOC118270770
LOC118270784	6.98	uncharacterized protein LOC118270784
LOC118270786	12.40	uncharacterized protein LOC118270786
LOC118270787	8.47	uncharacterized protein LOC118270787
LOC118270788	12.17	uncharacterized protein LOC118270788
LOC118270789	8.21	uncharacterized protein LOC118270789
LOC118270805	12.88	uncharacterized protein LOC118270805

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118270819	10.28	uncharacterized protein LOC118270819
LOC118270825	4.15	uncharacterized protein LOC118270825
LOC118270841	8.88	uncharacterized protein LOC118270841
LOC118270842	8.24	uncharacterized protein LOC118270842
LOC118270853	2.30	uncharacterized protein LOC118270853
LOC118270862	-8.03	uncharacterized protein LOC118270862
LOC118270897	-3.91	uncharacterized protein LOC118270897
LOC118270928	-6.25	uncharacterized protein LOC118270928
LOC118270961	6.54	uncharacterized protein LOC118270961
LOC118271003	-2.68	uncharacterized protein LOC118271003
LOC118271015	2.70	uncharacterized protein LOC118271015
LOC118271016	-2.09	uncharacterized protein LOC118271016
LOC118271019	-2.26	uncharacterized protein LOC118271019
LOC118271045	-2.13	uncharacterized protein LOC118271045 isoform X1
LOC118271047	-2.35	uncharacterized protein LOC118271047
LOC118271110	2.53	uncharacterized protein LOC118271110
LOC118271148	-3.48	uncharacterized protein LOC118271148
LOC118271158	2.21	uncharacterized protein LOC118271158
LOC118271193	-2.12	uncharacterized protein LOC118271193
LOC118271210	3.72	uncharacterized protein LOC118271210
LOC118271331	8.39	uncharacterized protein LOC118271331
LOC118271338	2.53	uncharacterized protein LOC118271338
LOC118271353	-4.02	uncharacterized protein LOC118271353
LOC118271360	6.71	uncharacterized protein LOC118271360 isoform X1
LOC118271377	2.61	uncharacterized protein LOC118271377
LOC118271383	2.84	uncharacterized protein LOC118271383
LOC118271384	-3.30	uncharacterized protein LOC118271384
LOC118271396	-2.42	uncharacterized protein LOC118271396
LOC118271405	-3.35	uncharacterized protein LOC118271405
LOC118271409	2.89	uncharacterized protein LOC118271409
LOC118271410	2.35	uncharacterized protein LOC118271410
LOC118271439	2.52	uncharacterized protein LOC118271439
LOC118271444	-3.24	uncharacterized protein LOC118271444
LOC118271453	-2.40	uncharacterized protein LOC118271453
LOC118271469	3.18	uncharacterized protein LOC118271469
LOC118271481	2.84	uncharacterized protein LOC118271481
LOC118271797	3.95	uncharacterized protein LOC118271797
LOC118271800	2.71	uncharacterized protein LOC118271800 isoform X1
LOC118271819	-2.86	uncharacterized protein LOC118271819
LOC118271829	2.06	uncharacterized protein LOC118271829
LOC118271840	2.95	uncharacterized protein LOC118271840
LOC118271903	2.19	uncharacterized protein LOC118271903 isoform X1
LOC118271975	4.29	uncharacterized protein LOC118271975
LOC118271977	-2.69	uncharacterized protein LOC118271977
LOC118271978	-2.29	uncharacterized protein LOC118271978
LOC118272061	5.03	uncharacterized protein LOC118272061
LOC118272138	-4.30	uncharacterized protein LOC118272138
LOC118272139	6.00	uncharacterized protein LOC118272139
LOC118272207	2.63	uncharacterized protein LOC118272207
LOC118272230	2.64	uncharacterized protein LOC118272230 isoform X1
LOC118272249	-2.45	uncharacterized protein LOC118272249
LOC118272279	-2.33	uncharacterized protein LOC118272279 isoform X1
LOC118272346	-3.65	uncharacterized protein LOC118272346
LOC118272368	-4.91	uncharacterized protein LOC118272368
LOC118272384	4.25	uncharacterized protein LOC118272384 isoform X1
LOC118272531	10.46	uncharacterized protein LOC118272531 isoform X1
LOC118272534	-4.86	uncharacterized protein LOC118272534
LOC118272535	-4.58	uncharacterized protein LOC118272535
LOC118272573	2.14	uncharacterized protein LOC118272573
LOC118272626	5.54	uncharacterized protein LOC118272626 isoform X1
LOC118272637	2.54	uncharacterized protein LOC118272637
LOC118272651	3.84	uncharacterized protein LOC118272651 isoform X1
LOC118272702	9.04	uncharacterized protein LOC118272702
LOC118272705	-3.48	uncharacterized protein LOC118272705
LOC118272732	3.62	uncharacterized protein LOC118272732
LOC118272768	2.47	uncharacterized protein LOC118272768
LOC118272800	2.47	uncharacterized protein LOC118272800
LOC118272877	6.87	uncharacterized protein LOC118272877
LOC118272887	-5.74	uncharacterized protein LOC118272887
LOC118272893	-2.87	uncharacterized protein LOC118272893
LOC118272948	-3.13	uncharacterized protein LOC118272948

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118273045	3.40	uncharacterized protein LOC118273045
LOC118273062	7.75	uncharacterized protein LOC118273062
LOC118273134	9.94	uncharacterized protein LOC118273134
LOC118273243	8.72	uncharacterized protein LOC118273243
LOC118273281	-4.24	uncharacterized protein LOC118273281
LOC118273335	2.80	uncharacterized protein LOC118273335
LOC118273355	9.28	uncharacterized protein LOC118273355
LOC118273357	-2.32	uncharacterized protein LOC118273357
LOC118273361	9.85	uncharacterized protein LOC118273361
LOC118273379	2.19	uncharacterized protein LOC118273379
LOC118273394	2.76	uncharacterized protein LOC118273394
LOC118273459	2.10	uncharacterized protein LOC118273459
LOC118273479	4.58	uncharacterized protein LOC118273479
LOC118273604	-2.04	uncharacterized protein LOC118273604
LOC118273695	-2.55	uncharacterized protein LOC118273695
LOC118273711	3.56	uncharacterized protein LOC118273711 isoform X1
LOC118273736	3.44	uncharacterized protein LOC118273736 isoform X1
LOC118273805	-4.59	uncharacterized protein LOC118273805
LOC118273832	-4.66	uncharacterized protein LOC118273832
LOC118273840	9.08	uncharacterized protein LOC118273840
LOC118273859	-5.43	uncharacterized protein LOC118273859
LOC118273870	-4.78	uncharacterized protein LOC118273870
LOC118273888	-2.72	uncharacterized protein LOC118273888 isoform X1
LOC118273905	4.31	uncharacterized protein LOC118273905 isoform X1
LOC118273950	-2.69	uncharacterized protein LOC118273950
LOC118273989	-2.07	uncharacterized protein LOC118273989
LOC118273998	4.42	uncharacterized protein LOC118273998
LOC118274026	7.63	uncharacterized protein LOC118274026
LOC118274027	5.34	uncharacterized protein LOC118274027
LOC118274032	2.88	uncharacterized protein LOC118274032
LOC118274034	6.58	uncharacterized protein LOC118274034
LOC118274037	3.51	uncharacterized protein LOC118274037
LOC118274096	-2.66	uncharacterized protein LOC118274096
LOC118274101	3.96	uncharacterized protein LOC118274101
LOC118274103	2.32	uncharacterized protein LOC118274103
LOC118274110	-4.35	uncharacterized protein LOC118274110
LOC118274129	7.25	uncharacterized protein LOC118274129
LOC118274142	-2.42	uncharacterized protein LOC118274142 isoform X1
LOC118274176	5.92	uncharacterized protein LOC118274176
LOC118274179	-2.59	uncharacterized protein LOC118274179
LOC118274228	7.56	uncharacterized protein LOC118274228
LOC118274319	2.83	uncharacterized protein LOC118274319
LOC118274333	-2.88	uncharacterized protein LOC118274333
LOC118274363	6.46	uncharacterized protein LOC118274363
LOC118274366	3.35	uncharacterized protein LOC118274366
LOC118274367	6.18	uncharacterized protein LOC118274367
LOC118274368	7.74	uncharacterized protein LOC118274368
LOC118274369	6.14	uncharacterized protein LOC118274369
LOC118274372	7.95	uncharacterized protein LOC118274372
LOC118274373	6.34	uncharacterized protein LOC118274373
LOC118274469	-3.29	uncharacterized protein LOC118274469
LOC118274472	-3.25	uncharacterized protein LOC118274472
LOC118274473	3.18	uncharacterized protein LOC118274473
LOC118274479	-2.69	uncharacterized protein LOC118274479 isoform X1
LOC118274502	-3.52	uncharacterized protein LOC118274502
LOC118274532	3.39	uncharacterized protein LOC118274532
LOC118274576	2.49	uncharacterized protein LOC118274576
LOC118274598	3.45	uncharacterized protein LOC118274598
LOC118274600	-3.70	uncharacterized protein LOC118274600
LOC118274662	6.51	uncharacterized protein LOC118274662
LOC118274759	-2.70	uncharacterized protein LOC118274759 isoform X1
LOC118274762	-7.24	uncharacterized protein LOC118274762
LOC118274765	-4.54	uncharacterized protein LOC118274765
LOC118274771	2.81	uncharacterized protein LOC118274771
LOC118274797	2.03	uncharacterized protein LOC118274797
LOC118274808	-2.01	uncharacterized protein LOC118274808
LOC118274810	2.11	uncharacterized protein LOC118274810
LOC118274836	-2.27	uncharacterized protein LOC118274836
LOC118274889	-2.36	uncharacterized protein LOC118274889
LOC118274913	-2.60	uncharacterized protein LOC118274913 isoform X1

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118274922	-2.76	uncharacterized protein LOC118274922
LOC118274937	10.76	uncharacterized protein LOC118274937
LOC118274971	-3.27	uncharacterized protein LOC118274971
LOC118274973	9.59	uncharacterized protein LOC118274973
LOC118274978	6.51	uncharacterized protein LOC118274978
LOC118275001	-2.41	uncharacterized protein LOC118275001
LOC118275058	-2.66	uncharacterized protein LOC118275058 isoform X1
LOC118275072	-3.04	uncharacterized protein LOC118275072
LOC118275096	5.88	uncharacterized protein LOC118275096 isoform X1
LOC118275106	-2.51	uncharacterized protein LOC118275106
LOC118275134	-2.15	uncharacterized protein LOC118275134
LOC118275141	-2.03	uncharacterized protein LOC118275141
LOC118275157	5.04	uncharacterized protein LOC118275157 isoform X1
LOC118275199	-2.94	uncharacterized protein LOC118275199
LOC118275230	3.40	uncharacterized protein LOC118275230
LOC118275232	2.06	uncharacterized protein LOC118275232
LOC118275257	-2.13	uncharacterized protein LOC118275257
LOC118275353	-5.04	uncharacterized protein LOC118275353
LOC118275356	-4.05	uncharacterized protein LOC118275356
LOC118275357	-2.70	uncharacterized protein LOC118275357
LOC118275358	-3.32	uncharacterized protein LOC118275358
LOC118275360	-2.58	uncharacterized protein LOC118275360
LOC118275495	2.42	uncharacterized protein LOC118275495
LOC118275587	-2.45	uncharacterized protein LOC118275587 isoform X1
LOC118275592	2.52	uncharacterized protein LOC118275592
LOC118275630	-2.65	uncharacterized protein LOC118275630
LOC118275703	4.76	uncharacterized protein LOC118275703 isoform X1
LOC118275744	2.29	uncharacterized protein LOC118275744
LOC118275770	-4.56	uncharacterized protein LOC118275770
LOC118275827	-3.01	uncharacterized protein LOC118275827
LOC118275829	2.41	uncharacterized protein LOC118275829
LOC118275928	-4.11	uncharacterized protein LOC118275928
LOC118275983	-3.92	uncharacterized protein LOC118275983
LOC118275992	-2.66	uncharacterized protein LOC118275992
LOC118275998	2.99	uncharacterized protein LOC118275998
LOC118275999	-3.39	uncharacterized protein LOC118275999
LOC118276011	2.08	uncharacterized protein LOC118276011 isoform X1
LOC118276062	2.77	uncharacterized protein LOC118276062 isoform X1
LOC118276175	-5.69	uncharacterized protein LOC118276175
LOC118276237	6.79	uncharacterized protein LOC118276237
LOC118276264	2.35	uncharacterized protein LOC118276264
LOC118276283	-3.46	uncharacterized protein LOC118276283
LOC118276292	3.91	uncharacterized protein LOC118276292
LOC118276310	9.33	uncharacterized protein LOC118276310
LOC118276311	10.06	uncharacterized protein LOC118276311
LOC118276317	-2.12	uncharacterized protein LOC118276317
LOC118276377	9.37	uncharacterized protein LOC118276377
LOC118276382	-2.50	uncharacterized protein LOC118276382
LOC118276383	10.41	uncharacterized protein LOC118276383 isoform X1
LOC118276385	4.60	uncharacterized protein LOC118276385
LOC118276391	-3.86	uncharacterized protein LOC118276391
LOC118276408	5.31	uncharacterized protein LOC118276408
LOC118276412	2.09	uncharacterized protein LOC118276412
LOC118276449	2.16	uncharacterized protein LOC118276449 isoform X1
LOC118276480	-2.06	uncharacterized protein LOC118276480
LOC118276504	2.36	uncharacterized protein LOC118276504
LOC118276510	2.02	uncharacterized protein LOC118276510
LOC118276548	2.03	uncharacterized protein LOC118276548
LOC118276569	-3.05	uncharacterized protein LOC118276569
LOC118276600	2.30	uncharacterized protein LOC118276600 isoform X1
LOC118276719	-4.27	uncharacterized protein LOC118276719
LOC118276750	-2.23	uncharacterized protein LOC118276750
LOC118276776	-3.20	uncharacterized protein LOC118276776 isoform X1
LOC118276790	-2.04	uncharacterized protein LOC118276790
LOC118276799	4.53	uncharacterized protein LOC118276799
LOC118276806	2.65	uncharacterized protein LOC118276806
LOC118276823	-5.47	uncharacterized protein LOC118276823
LOC118276824	2.89	uncharacterized protein LOC118276824
LOC118276871	-3.89	uncharacterized protein LOC118276871
LOC118276938	4.18	uncharacterized protein LOC118276938 isoform X1
LOC118276965	5.53	uncharacterized protein LOC118276965

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118276966	-2.30	uncharacterized protein LOC118276966
LOC118276971	7.58	uncharacterized protein LOC118276971
LOC118277003	-2.05	uncharacterized protein LOC118277003
LOC118277015	4.55	uncharacterized protein LOC118277015 isoform X1
LOC118277123	8.01	uncharacterized protein LOC118277123
LOC118277128	3.06	uncharacterized protein LOC118277128
LOC118277131	8.53	uncharacterized protein LOC118277131
LOC118277141	4.23	uncharacterized protein LOC118277141
LOC118277143	5.25	uncharacterized protein LOC118277143 isoform X1
LOC118277144	4.45	uncharacterized protein LOC118277144
LOC118277145	4.61	uncharacterized protein LOC118277145
LOC118277160	-2.91	uncharacterized protein LOC118277160
LOC118277161	-2.94	uncharacterized protein LOC118277161 isoform X1
LOC118277166	-2.46	uncharacterized protein LOC118277166
LOC118277167	-2.24	uncharacterized protein LOC118277167 isoform X1
LOC118277170	-4.48	uncharacterized protein LOC118277170
LOC118277173	3.94	uncharacterized protein LOC118277173
LOC118277184	-7.10	uncharacterized protein LOC118277184
LOC118277185	-2.81	uncharacterized protein LOC118277185
LOC118277194	-2.05	uncharacterized protein LOC118277194
LOC118277261	-2.69	uncharacterized protein LOC118277261
LOC118277288	-6.32	uncharacterized protein LOC118277288
LOC118277311	-2.14	uncharacterized protein LOC118277311
LOC118277391	-3.24	uncharacterized protein LOC118277391
LOC118277408	-3.06	uncharacterized protein LOC118277408
LOC118277478	9.49	uncharacterized protein LOC118277478 isoform X1
LOC118277507	6.55	uncharacterized protein LOC118277507
LOC118277513	2.13	uncharacterized protein LOC118277513
LOC118277546	4.00	uncharacterized protein LOC118277546 isoform X1
LOC118277637	-3.54	uncharacterized protein LOC118277637
LOC118277731	3.16	uncharacterized protein LOC118277731
LOC118277743	7.64	uncharacterized protein LOC118277743 isoform X1
LOC118277764	-3.64	uncharacterized protein LOC118277764
LOC118277777	4.00	uncharacterized protein LOC118277777
LOC118277812	-3.34	uncharacterized protein LOC118277812
LOC118277813	7.03	uncharacterized protein LOC118277813
LOC118277817	4.17	uncharacterized protein LOC118277817
LOC118277862	5.46	uncharacterized protein LOC118277862 isoform X1
LOC118277910	-4.87	uncharacterized protein LOC118277910
LOC118278009	3.52	uncharacterized protein LOC118278009
LOC118278049	2.87	uncharacterized protein LOC118278049
LOC118278064	-4.91	uncharacterized protein LOC118278064
LOC118278066	-2.11	uncharacterized protein LOC118278066
LOC118278080	5.47	uncharacterized protein LOC118278080
LOC118278128	7.69	uncharacterized protein LOC118278128
LOC118278131	5.98	uncharacterized protein LOC118278131
LOC118278139	-2.12	uncharacterized protein LOC118278139
LOC118278196	5.95	uncharacterized protein LOC118278196 isoform X1
LOC118278206	-8.65	uncharacterized protein LOC118278206
LOC118278223	-3.48	uncharacterized protein LOC118278223
LOC118278229	2.62	uncharacterized protein LOC118278229
LOC118278233	7.76	uncharacterized protein LOC118278233 isoform X1
LOC118278259	10.23	uncharacterized protein LOC118278259
LOC118278465	-2.09	uncharacterized protein LOC118278465
LOC118278596	-4.38	uncharacterized protein LOC118278596
LOC118278604	-3.24	uncharacterized protein LOC118278604
LOC118278613	2.52	uncharacterized protein LOC118278613
LOC118278633	3.04	uncharacterized protein LOC118278633
LOC118278644	-4.31	uncharacterized protein LOC118278644
LOC118278688	2.88	uncharacterized protein LOC118278688
LOC118278749	3.43	uncharacterized protein LOC118278749 isoform X1
LOC118278795	2.43	uncharacterized protein LOC118278795
LOC118278944	8.48	uncharacterized protein LOC118278944
LOC118278951	2.54	uncharacterized protein LOC118278951
LOC118278958	2.96	uncharacterized protein LOC118278958
LOC118278961	2.81	uncharacterized protein LOC118278961
LOC118278984	2.07	uncharacterized protein LOC118278984
LOC118279028	-3.68	uncharacterized protein LOC118279028
LOC118279047	2.11	uncharacterized protein LOC118279047 isoform X1
LOC118279065	2.82	uncharacterized protein LOC118279065 isoform X1

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118279089	-9.40	uncharacterized protein LOC118279089
LOC118279146	-8.69	uncharacterized protein LOC118279146
LOC118279165	-2.44	uncharacterized protein LOC118279165
LOC118279188	2.86	uncharacterized protein LOC118279188
LOC118279214	6.37	uncharacterized protein LOC118279214
LOC118279220	-2.46	uncharacterized protein LOC118279220
LOC118279221	11.11	uncharacterized protein LOC118279221
LOC118279281	-3.00	uncharacterized protein LOC118279281
LOC118279282	8.02	uncharacterized protein LOC118279282
LOC118279327	-2.12	uncharacterized protein LOC118279327
LOC118279350	2.29	uncharacterized protein LOC118279350 isoform X1
LOC118279543	-2.31	uncharacterized protein LOC118279543
LOC118279613	2.19	uncharacterized protein LOC118279613
LOC118279617	4.12	uncharacterized protein LOC118279617 isoform X1
LOC118279636	5.67	uncharacterized protein LOC118279636 isoform X1
LOC118279637	4.05	uncharacterized protein LOC118279637 isoform X1
LOC118279797	-2.54	uncharacterized protein LOC118279797 isoform X1
LOC118279817	-3.05	uncharacterized protein LOC118279817 isoform X1
LOC118279833	5.63	uncharacterized protein LOC118279833 isoform X1
LOC118279864	2.93	uncharacterized protein LOC118279864
LOC118279895	3.91	uncharacterized protein LOC118279895
LOC118279918	3.81	uncharacterized protein LOC118279918
LOC118279923	-3.85	uncharacterized protein LOC118279923 isoform X1
LOC118279973	5.96	uncharacterized protein LOC118279973
LOC118279984	4.90	uncharacterized protein LOC118279984 isoform X1
LOC118280028	3.34	uncharacterized protein LOC118280028
LOC118280034	2.34	uncharacterized protein LOC118280034 isoform X1
LOC118280039	9.07	uncharacterized protein LOC118280039
LOC118280057	8.19	uncharacterized protein LOC118280057 isoform X1
LOC118280067	8.27	uncharacterized protein LOC118280067 isoform X1
LOC118280183	3.10	uncharacterized protein LOC118280183
LOC118280218	4.01	uncharacterized protein LOC118280218
LOC118280326	-2.51	uncharacterized protein LOC118280326
LOC118280353	-3.91	uncharacterized protein LOC118280353 isoform X1
LOC118280383	2.03	uncharacterized protein LOC118280383
LOC118280388	2.43	uncharacterized protein LOC118280388
LOC118280446	-3.04	uncharacterized protein LOC118280446
LOC118280450	-2.50	uncharacterized protein LOC118280450 isoform X1
LOC118280475	4.73	uncharacterized protein LOC118280475
LOC118280506	5.31	uncharacterized protein LOC118280506
LOC118280523	-4.36	uncharacterized protein LOC118280523
LOC118280580	4.54	uncharacterized protein LOC118280580
LOC118280648	-2.19	uncharacterized protein LOC118280648
LOC118280649	-2.61	uncharacterized protein LOC118280649
LOC118280693	-2.54	uncharacterized protein LOC118280693
LOC118280768	-4.50	uncharacterized protein LOC118280768
LOC118280833	-2.80	uncharacterized protein LOC118280833
LOC118280856	-3.99	uncharacterized protein LOC118280856
LOC118280904	-2.39	uncharacterized protein LOC118280904
LOC118280912	2.19	uncharacterized protein LOC118280912
LOC118280969	5.19	uncharacterized protein LOC118280969
LOC118280979	3.62	uncharacterized protein LOC118280979
LOC118281023	2.10	uncharacterized protein LOC118281023
LOC118281025	3.48	uncharacterized protein LOC118281025
LOC118281067	2.33	uncharacterized protein LOC118281067
LOC118281068	2.33	uncharacterized protein LOC118281068
LOC118281069	-4.90	uncharacterized protein LOC118281069
LOC118281081	-3.52	uncharacterized protein LOC118281081
LOC118281163	-2.56	uncharacterized protein LOC118281163
LOC118281331	3.90	uncharacterized protein LOC118281331
LOC118281352	3.76	uncharacterized protein LOC118281352
LOC118281376	-2.25	uncharacterized protein LOC118281376
LOC118281385	-3.88	uncharacterized protein LOC118281385
LOC118281390	3.74	uncharacterized protein LOC118281390 isoform X1
LOC118281402	-3.50	uncharacterized protein LOC118281402
LOC118281410	4.38	uncharacterized protein LOC118281410
LOC118281412	-3.48	uncharacterized protein LOC118281412
LOC118281430	-2.21	uncharacterized protein LOC118281430
LOC118281431	-4.40	uncharacterized protein LOC118281431
LOC118281435	3.53	uncharacterized protein LOC118281435
LOC118281436	3.57	uncharacterized protein LOC118281436

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118281485	8.84	uncharacterized protein LOC118281485
LOC118281493	-3.72	uncharacterized protein LOC118281493
LOC118281496	2.74	uncharacterized protein LOC118281496
LOC118281518	-5.28	uncharacterized protein LOC118281518
LOC118281519	4.02	uncharacterized protein LOC118281519 isoform X1
LOC118281567	3.73	uncharacterized protein LOC118281567
LOC118281574	3.77	uncharacterized protein LOC118281574
LOC118281692	6.31	uncharacterized protein LOC118281692
LOC118281695	-3.06	uncharacterized protein LOC118281695
LOC118281755	3.47	uncharacterized protein LOC118281755
LOC118281784	-2.59	uncharacterized protein LOC118281784 isoform X1
LOC118281802	4.00	uncharacterized protein LOC118281802
LOC118281887	2.29	uncharacterized protein LOC118281887
LOC118281888	3.35	uncharacterized protein LOC118281888 isoform X1
LOC118281889	6.57	uncharacterized protein LOC118281889 isoform X1
LOC118281890	7.61	uncharacterized protein LOC118281890 isoform X1
LOC118281903	5.40	uncharacterized protein LOC118281903
LOC118281915	-2.65	uncharacterized protein LOC118281915
LOC118281926	4.89	uncharacterized protein LOC118281926
LOC118281927	-3.31	uncharacterized protein LOC118281927
LOC118281945	-7.97	uncharacterized protein LOC118281945
LOC118282073	2.89	uncharacterized protein LOC118282073
LOC118282214	3.34	uncharacterized protein LOC118282214
LOC118282226	6.05	uncharacterized protein LOC118282226
LOC118282341	-5.46	uncharacterized protein LOC118282341
LOC118282357	9.24	uncharacterized protein LOC118282357
LOC118282380	2.13	uncharacterized protein LOC118282380 isoform X1
LOC118282387	-3.64	uncharacterized protein LOC118282387 isoform X1
LOC118282432	2.62	uncharacterized protein LOC118282432
LOC118262715	-3.05	uncharacterized protein PB18E9.04c-like
LOC118262535	5.92	UPF0605 protein CG18335-like
LOC118273334	2.05	uricase-like
LOC118279986	2.74	U-scoloptoxin(01)-Cw1a-like
LOC118279993	3.01	U-scoloptoxin(01)-Cw1a-like
LOC118263625	6.73	U-scoloptoxin(01)-Cw1a-like
LOC118263556	10.82	U-scoloptoxin(01)-Cw1a-like
LOC118277941	-2.05	UTP--glucose-1-phosphate uridylyltransferase-like isoform X1
LOC118276365	2.17	vacuolar protein sorting-associated protein 13A-like isoform X1
LOC118273013	5.48	vasorin-like isoform X1
LOC118278418	6.07	vegetative cell wall protein gp1-like
LOC118267908	8.83	vegetative cell wall protein gp1-like
LOC118273858	11.74	vegetative cell wall protein gp1-like
LOC118272696	12.49	vegetative cell wall protein gp1-like
LOC118268300	3.50	venom allergen 5.02-like
LOC118268283	4.44	venom allergen 5.02-like
LOC118262636	-2.77	venom carboxylesterase-6-like
LOC118265778	2.06	venom carboxylesterase-6-like
LOC118275668	4.78	venom carboxylesterase-6-like
LOC118273505	3.16	venom dipeptidyl peptidase 4-like isoform X1
LOC118273663	3.22	venom dipeptidyl peptidase 4-like isoform X1
LOC118282209	-3.32	venom peptide CtAPI-like isoform X1
LOC118282292	-2.43	venom peptide CtAPI-like isoform X1
LOC118278956	-5.18	venom protease-like
LOC118278920	-5.44	venom protease-like isoform X1
LOC118274807	-2.10	venom serine carboxypeptidase-like
LOC118269891	-4.41	venom serine protease inhibitor-like
LOC118269911	-2.21	venom serine protease inhibitor-like
LOC118268742	-3.16	vitamin K epoxide reductase complex subunit 1-like protein 1
LOC118261838	4.07	vitamin K-dependent gamma-carboxylase-like
LOC118279270	4.66	vitellin-degrading protease-like
LOC118280769	-5.03	vitellogenin-like
LOC118280767	-4.35	vitellogenin-like
LOC118277091	2.34	von Hippel-Lindau disease tumor suppressor-like
LOC118277089	3.01	von Hippel-Lindau disease tumor suppressor-like
LOC118267673	-2.25	xanthine dehydrogenase 1-like
LOC118267938	-3.74	xanthine dehydrogenase-like
LOC118265469	-2.44	xanthine dehydrogenase-like
LOC118267651	-2.30	xanthine dehydrogenase-like
LOC118267672	-2.28	xanthine dehydrogenase-like
LOC118267793	4.72	xanthine dehydrogenase-like

Appendix B. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between unselected and susceptible strains (continue).

Gene ID	log2FC	Description
LOC118267951	5.18	xanthine dehydrogenase-like
LOC118269899	-2.09	xylulose kinase-like
LOC118264722	4.02	zinc carboxypeptidase A 1-like
LOC118266727	3.08	zinc carboxypeptidase A 1-like isoform X1
LOC118271362	-3.06	zinc finger BED domain-containing protein 1-like
LOC118264449	3.01	zinc finger BED domain-containing protein 4-like
LOC118277415	-3.32	zinc finger BED domain-containing protein 5-like isoform X1
LOC118270911	-3.19	zinc finger BED domain-containing protein 6-like
LOC118264260	-2.31	zinc finger BED domain-containing protein 6-like
LOC118265342	2.02	zinc finger CCHC domain-containing protein 24-like
LOC118270336	2.46	zinc finger MYM-type protein 1-like
LOC118267857	4.81	zinc finger MYM-type protein 5-like
LOC118282327	4.02	zinc finger protein 112-like isoform X1
LOC118278378	2.76	zinc finger protein 37 homolog
LOC118263161	3.69	zinc finger protein 395-like
LOC118276595	3.36	zinc finger protein 62 homolog
LOC118280641	-2.66	zinc finger protein rotund-like isoform X1
LOC118263591	2.11	zinc transporter 1-like
LOC118275735	-2.03	zinc transporter ZIP1-like
LOC118263330	2.12	zinc/cadmium resistance protein-like isoform X1
LOC118264517	-2.56	zinc-type alcohol dehydrogenase-like protein SERP1785
LOC118264683	-2.39	zinc-type alcohol dehydrogenase-like protein SERP1785
LOC118264652	-2.34	zinc-type alcohol dehydrogenase-like protein SERP1785
LOC118262003	2.18	zonadhesin-like
LOC118271594	2.46	zonadhesin-like
LOC118282451	3.24	zonadhesin-like
LOC118264895	6.88	zonadhesin-like
LOC118261970	4.02	zonadhesin-like isoform X1
LOC118275467	4.20	zonadhesin-like isoform X1

Appendix C. List of differentially expressed genes with adjusted p-value < 0.05 and fold change ≥ |2.0| between selected and unselected strains.

Gene ID	log2FC	Description
LOC118267535	-5.10	39S ribosomal protein L33, mitochondrial-like
LOC118268511	-4.94	eclosion hormone
LOC118278458	-3.32	GILT-like protein 2 isoform X1
LOC118267426	-3.07	glutenin, low molecular weight subunit-like
LOC118278459	-2.80	proclotting enzyme-like
LOC118272261	-2.06	transcriptional regulatory protein AlgP-like
LOC118265116	-2.01	uncharacterized protein LOC118265116
LOC118276388	2.26	uncharacterized protein LOC118267748 isoform X1
LOC118270040	2.37	uncharacterized protein LOC118267749
LOC118281942	2.55	uncharacterized protein LOC118268511
LOC118267749	2.66	uncharacterized protein LOC118270040
LOC118269902	2.71	uncharacterized protein LOC118270897
LOC118277166	2.87	uncharacterized protein LOC118276388 isoform X1
LOC118267748	3.01	uncharacterized protein LOC118277166
LOC118269929	3.02	uncharacterized protein LOC118281942
LOC118270897	4.93	uncharacterized LOC118267535

Appendix D. List of exclusively proteins that were differentially abundant (adjusted p-value < 0.05 and fold change ≥ |2.0|) between spinetoram-resistant and susceptible strains when feeding on corn plants.

Protein ID	log2FC	Description
XP_035449441.1	-2.17	39S ribosomal protein L40, mitochondrial-like
XP_035443033.1	4.37	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
XP_035440036.1	2.80	4-hydroxyphenylpyruvate dioxygenase-like
XP_035449311.1	-3.06	5-3 exoribonuclease 2 homolog
XP_035444913.1	-2.90	actin cytoskeleton-regulatory complex protein PAN1-like isoform X2
XP_035435457.1	-3.45	actin-related protein 3
XP_035455710.1	-3.40	aldo-keto reductase AKR2E4-like
XP_035455346.1	3.39	aldo-keto reductase AKR2E4-like isoform X1
XP_035437420.1	2.14	alkaline phosphatase-like isoform X1
XP_035449808.1	-3.62	AMP deaminase 2-like
XP_035440227.1	-3.43	ankyrin repeat and zinc finger domain-containing protein 1-like
XP_035445701.1	-2.63	ankyrin repeat domain-containing protein 39-like
XP_035453116.1	-2.92	annexin B9-like isoform X3
XP_035458706.1	-3.11	ataxin-10-like
XP_035446732.1	4.67	atlastin-like
XP_035457513.1	-2.98	ATP-dependent RNA helicase abstrakt-like
XP_035447324.1	2.02	beta-ureidopropionase-like
XP_035446999.1	2.04	beta-ureidopropionase-like
XP_035459296.1	-4.71	bifunctional 3-phosphoadenosine 5-phosphosulfate synthase-like isoform X2
XP_035443173.1	3.19	calcium-binding and coiled-coil domain-containing protein 1-like
XP_035439707.1	-6.36	calcium-binding protein E63-1-like isoform X5
XP_035456826.1	4.88	carbonyl reductase [NADPH] 3-like
XP_035456980.1	-2.32	catenin delta-2-like
XP_035447608.1	-4.68	centromere-associated protein E-like
XP_035453934.1	-3.33	charged multivesicular body protein 7-like
XP_035444165.1	-2.97	chloride intracellular channel exc-4-like isoform X1
XP_035433539.1	-2.31	chromatin assembly factor 1 subunit B-like
XP_035429493.1	3.35	coiled-coil domain-containing protein 28A-like
XP_035450148.1	-5.48	cuticle protein 16.5-like
XP_035457922.1	-2.10	cuticle protein 19-like
XP_035457852.1	-8.43	cuticle protein 7-like
XP_035452918.1	-3.24	cuticle protein 7-like
XP_035457914.1	-3.01	cuticle protein 7-like
XP_035429011.1	-8.40	cuticle protein 8-like
XP_035457861.1	-3.94	cuticle protein 8-like
XP_035428578.1	-8.05	cuticle protein-like
XP_035447786.1	-2.79	cuticle protein-like
XP_035451126.1	-3.54	cytadherence high molecular weight protein 1-like
XP_035458248.1	-2.69	DNA translocase FtsK-like isoform X2
XP_035437151.1	-3.06	dnaJ homolog subfamily B member 6-like isoform X2
XP_035458598.1	-4.02	dnaJ homolog subfamily C member 17-like
XP_035438881.1	-3.21	dynactin subunit 4-like
XP_035434748.1	-3.75	dystroglycan-like isoform X4
XP_035452935.1	-4.31	dystrophin, isoforms A/C/F/G/H-like
XP_035440700.1	3.56	E3 ubiquitin-protein ligase RNF181-like
XP_035449179.1	-2.69	egl nine homolog 1-like
XP_035433739.1	-5.32	ell-associated factor Eaf-like
XP_035446433.1	-2.34	elongation factor G, mitochondrial-like
XP_035458840.1	2.82	ets DNA-binding protein pokkuri-like
XP_035430643.1	-5.07	extensin-like
XP_035434864.1	-3.92	F-actin-monooxygenase Mical-like isoform X5
XP_035442388.1	-2.76	fibroin heavy chain-like isoform X1
XP_035443377.1	-6.62	fibroin light chain-like
XP_035429886.1	-3.00	formin-binding protein 1-like isoform X4
XP_035455918.1	3.00	G patch domain-containing protein 4-like
XP_035443321.1	-10.25	galactose mutarotase-like
XP_035446358.1	-3.70	glycerophosphocholine phosphodiesterase GPCPD1-like isoform X2
XP_035455047.1	-3.13	glycylpeptide N-tetradecanoyltransferase 2-like
XP_035435586.1	-4.37	hemocyte protein-glutamine gamma-glutamyltransferase-like
XP_035453972.1	-4.03	hemolin-like
XP_035456360.1	3.39	histidine triad nucleotide-binding protein 1-like
XP_035454856.1	-3.19	homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 2 protein
XP_035433147.1	-2.99	hydroxysteroid dehydrogenase-like protein 2 isoform X1
XP_035449133.1	3.53	keratin, type I cytoskeletal 10-like
XP_035452932.1	-2.40	larval cuticle protein A1A-like
XP_035452921.1	-3.23	larval cuticle protein A3A-like
XP_035452917.1	-2.76	larval cuticle protein A3A-like
XP_035436026.1	-3.59	LOW QUALITY PROTEIN: chromodomain-helicase-DNA-binding protein Mi-2 homolog
XP_035433914.1	-3.07	LOW QUALITY PROTEIN: circadian clock-controlled protein daywake-like
XP_035448298.1	-5.11	LOW QUALITY PROTEIN: eukaryotic translation initiation factor 3 subunit C-like

Appendix D. List of exclusively proteins that were differentially abundant (adjusted p-value < 0.05 and fold change ≥ |2.0|) between spinetoram-resistant and susceptible strains when feeding on corn plants (continue).

Protein ID	log2FC	Description
XP_035430085.1	2.49	LOW QUALITY PROTEIN: extracellular sulfatase SULF-1 homolog
XP_035458212.1	2.69	LOW QUALITY PROTEIN: mitotic checkpoint serine/threonine-protein kinase BUB1 beta-like
XP_035436878.1	2.96	LOW QUALITY PROTEIN: MLX-interacting protein-like
XP_035436142.1	-4.26	LOW QUALITY PROTEIN: pre-rRNA 2-O-ribose RNA methyltransferase FTSJ3-like
XP_035432423.1	2.47	LOW QUALITY PROTEIN: protein tweety-like
XP_035445672.1	-3.52	LOW QUALITY PROTEIN: sodium/hydrogen exchanger 9B2-like
XP_035440548.1	-3.23	LOW QUALITY PROTEIN: valacyclovir hydrolase-like
XP_035445865.1	6.67	LOW QUALITY PROTEIN: venom serine carboxypeptidase-like
XP_035432445.1	-4.14	luc7-like protein 3
XP_035450104.1	4.10	lysine-specific demethylase 3A-like
XP_035451403.1	-5.94	mediator of RNA polymerase II transcription subunit 15-like isoform X2
XP_035433313.1	4.48	MIF-like protein mif-2
XP_035447476.1	4.49	mitochondrial import inner membrane translocase subunit TIM50-C-like
XP_035447546.1	-3.85	mortality factor 4-like protein 1
XP_035439923.1	-4.70	mucin-5AC-like
XP_035449913.1	-4.13	mucin-5AC-like isoform X2
XP_035456929.1	-2.48	myb/SANT-like DNA-binding domain-containing protein 3
XP_035451498.1	4.38	N-acetylgalactosamine kinase-like
XP_035430011.1	-3.01	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2-like isoform X1
XP_035436073.1	-3.79	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial-like
XP_035445909.1	-4.59	neuroguidin-like
XP_035440228.1	-2.94	nose resistant to fluoxetine protein 6-like
XP_035435928.1	-5.06	nuclear cap-binding protein subunit 3-like
XP_035444896.1	-4.35	nucleolar GTP-binding protein 2-like
XP_035432187.1	-2.53	nucleolar protein 12-like
XP_035454177.1	-4.88	nucleolar protein dao-5-like
XP_035430028.1	-3.52	parafibromin-like
XP_035430846.1	3.92	peroxisomal (S)-2-hydroxy-acid oxidase GLO3-like
XP_035438842.1	-3.53	PHD finger protein 14-like isoform X2
XP_035455461.1	-2.82	phosphatidylinositol 4-phosphate 5-kinase type-1 alpha-like isoform X19
XP_035447003.1	-2.48	phosphatidylinositol 5-phosphate 4-kinase type-2 alpha-like isoform X2
XP_035429825.1	3.02	phytanoyl-CoA dioxygenase domain-containing protein 1-like
XP_035458095.1	-3.88	pre-mRNA-processing factor 40 homolog A-like
XP_035451757.1	-6.79	probable salivary secreted peptide
XP_035446386.1	3.97	programmed cell death protein 10-like
XP_035447204.1	3.29	proteasome subunit beta type-3-like
XP_035445716.1	-3.07	protein Dr1-like
XP_035431390.1	-3.51	protein MAK16 homolog B-like
XP_035447938.1	4.07	protein NipSnap-like
XP_035441868.1	-3.28	protein O-GlcNAcase-like
XP_035436269.1	-2.09	protein phosphatase 1 regulatory subunit 12B-like isoform X13
XP_035450184.1	-4.13	protein SON-like isoform X2
XP_035429239.1	-5.68	protein takeout-like
XP_035448948.1	-3.91	protein takeout-like
XP_035430688.1	-2.77	protein takeout-like
XP_035430700.1	3.55	protein takeout-like
XP_035431942.1	-5.10	protein yellow-like
XP_035459271.1	-4.31	proteoglycan 4-like
XP_035432176.1	-4.35	pupal cuticle protein 20-like isoform X2
XP_035435185.1	-3.75	pupal cuticle protein 36a-like
XP_035445363.1	3.14	purine nucleoside phosphorylase-like isoform X2
XP_035448765.1	4.30	putative cystathionine gamma-lyase 2
XP_035452835.1	2.25	putative hydroxypyruvate isomerase
XP_035448145.1	3.83	putative uncharacterized protein DDB_G0277255
XP_035440741.1	3.50	ras-related protein Rap1-like
XP_035447999.1	-2.25	rho GTPase-activating protein 15-like isoform X4
XP_035435692.1	3.69	RING finger and CHY zinc finger domain-containing protein 1-like isoform X2
XP_035442557.1	-6.66	RNA polymerase II degradation factor 1-like
XP_035442880.1	-4.29	RNA polymerase II-associated factor 1 homolog
XP_035451610.1	3.20	RNA-binding protein fusilli-like isoform X1
XP_035446624.1	-2.34	sentrin-specific protease 1-like isoform X2
XP_035453264.1	-2.62	septin-interacting protein 1-like isoform X1
XP_035450982.1	4.83	sperm surface protein Sp17-like
XP_035431469.1	-3.73	splicing factor YJU2-like
XP_035448177.1	-4.43	squamous cell carcinoma antigen recognized by T-cells 3-like isoform X2
XP_035448015.1	-4.63	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1-A-like isoform X1
XP_035440881.1	-3.21	testin-like
XP_035450905.1	-2.70	thyroid receptor-interacting protein 11-like isoform X1

Appendix D. List of exclusively proteins that were differentially abundant (adjusted p-value < 0.05 and fold change ≥ |2.0|) between spinetoram-resistant and susceptible strains when feeding on corn plants (continue).

Protein ID	log2FC	Description
XP_035440711.1	-3.17	transcription elongation factor B polypeptide 3-like
XP_035440191.1	-3.46	translocation protein SEC62-like isoform X4
XP_035445013.1	-5.34	translocon-associated protein subunit alpha-like
XP_035455012.1	-2.51	tudor domain-containing protein 7-like
XP_035456596.1	-5.01	twitchin-like isoform X12
XP_035454179.1	-3.00	U4/U6 small nuclear ribonucleoprotein Prp4-like
XP_035445243.1	3.05	ubiquitin domain-containing protein UBFD1-like
XP_035457820.1	-2.99	uncharacterized protein K02A2.6-like
XP_035428849.1	2.79	uncharacterized protein LOC118261916
XP_035430249.1	-2.63	uncharacterized protein LOC118262761
XP_035430926.1	8.19	uncharacterized protein LOC118263190
XP_035431976.1	-3.63	uncharacterized protein LOC118263875 isoform X2
XP_035435478.1	-3.84	uncharacterized protein LOC118266190
XP_035435561.1	-4.33	uncharacterized protein LOC118266269
XP_035436573.1	4.06	uncharacterized protein LOC118266985 isoform X1
XP_035437665.1	-3.80	uncharacterized protein LOC118267664
XP_035438519.1	2.59	uncharacterized protein LOC118268231
XP_035441177.1	-3.77	uncharacterized protein LOC118269909
XP_035441195.1	3.56	uncharacterized protein LOC118269918
XP_035442009.1	3.19	uncharacterized protein LOC118270513
XP_035442116.1	-4.98	uncharacterized protein LOC118270592
XP_035442379.1	-3.06	uncharacterized protein LOC118270727
XP_035445047.1	-3.55	uncharacterized protein LOC118272569
XP_035447488.1	-4.41	uncharacterized protein LOC118274169
XP_035449380.1	-2.87	uncharacterized protein LOC118275500
XP_035450437.1	4.82	uncharacterized protein LOC118276288 isoform X2
XP_035453897.1	3.24	uncharacterized protein LOC118278688
XP_035454165.1	-6.07	uncharacterized protein LOC118278866
XP_035457958.1	-3.79	uncharacterized protein LOC118281485
XP_035458074.1	-3.75	uncharacterized protein LOC118281574
XP_035458556.1	-3.16	uncharacterized protein LOC118281890 isoform X3
XP_035458640.1	-3.10	uncharacterized protein LOC118281927
XP_035459044.1	4.64	uncharacterized protein LOC118282193
XP_035459294.1	-4.84	uncharacterized protein LOC118282357
XP_035457035.1	4.76	vitellogenin-like
XP_035441137.1	-6.80	WD repeat-containing protein 44-like isoform X5
XP_035443544.1	-3.22	wiskott-Aldrich syndrome protein family member 3-like
XP_035444433.1	2.64	X-ray repair cross-complementing protein 5-like
XP_035443575.1	-6.06	zonadhesin-like
XP_035459453.1	-3.05	zonadhesin-like

Appendix E. List of exclusively proteins that were differentially abundant (adjusted p-value < 0.05 and fold change ≥ |2.0|) between spinetoram-resistant and susceptible strains when feeding on soybean plants (continue).

Protein ID	log2FC	Description
XP_035433226.1	3.84	28S ribosomal protein S23, mitochondrial-like
XP_035453704.1	-3.12	39S ribosomal protein L53, mitochondrial-like isoform X1
XP_035448561.1	-5.57	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
XP_035448839.1	2.44	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
XP_035444238.1	-2.01	60S ribosomal protein L11
XP_035440706.1	-6.95	60S ribosomal protein L15
XP_035440008.1	-2.15	60S ribosomal protein L27-like
XP_035456310.1	-2.86	acetyl-CoA carboxylase-like isoform X4
XP_035455949.1	-2.42	actin-like protein 6A
XP_035445659.1	2.01	activating signal cointegrator 1 complex subunit 1-like isoform X3
XP_035435266.1	-5.03	acyl-CoA-binding domain-containing protein 6-like
XP_035445339.1	-4.07	adenylate cyclase type 2-like isoform X5
XP_035439135.1	4.57	ADP-ribosylation factor GTPase-activating protein 1-like isoform X1
XP_035455743.1	-4.42	aldo-keto reductase AKR2E4-like isoform X2
XP_035455845.1	3.58	aldo-keto reductase AKR2E4-like isoform X2
XP_035434511.1	-2.27	alpha-aminoadipic semialdehyde synthase, mitochondrial-like
XP_035434310.1	-4.04	aminoacylase-1-like
XP_035448262.1	-3.78	apolipoprotein D-like
XP_035458232.1	-2.86	ATPase family protein 2 homolog
XP_035451835.1	2.31	ATPase inhibitor mai-2, mitochondrial-like isoform X2
XP_035437168.1	-3.07	ATP-binding cassette sub-family F member 3-like
XP_035447435.1	-2.87	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial isoform X4
XP_035449405.1	-3.17	ATP-dependent Clp protease proteolytic subunit-like
XP_035436472.1	3.24	ATP-dependent RNA helicase DHX8-like
XP_035444803.1	-5.97	ATP-dependent RNA helicase p62-like
XP_035455367.1	3.85	ATP-dependent zinc metalloprotease YME1L-like
XP_035458158.1	-3.07	beta-1,3-glucan-binding protein-like
XP_035449199.1	-2.45	bifunctional glutamate/proline--tRNA ligase-like isoform X7
XP_035441251.1	2.46	cadherin-87A-like
XP_035458924.1	-4.98	calcium/calmodulin-dependent protein kinase type 1-like
XP_035435613.1	-3.52	cAMP-dependent protein kinase type II regulatory subunit-like isoform X2
XP_035444150.1	-2.67	carboxypeptidase B-like
XP_035436391.1	5.17	caspase Dronc-like isoform X1
XP_035437068.1	6.38	caspase-1
XP_035452238.1	2.48	CCAAT/enhancer-binding protein gamma-like
XP_035441293.1	3.44	CDK5RAP3-like protein
XP_035434677.1	-2.99	ceramide transfer protein-like isoform X2
XP_035430315.1	2.62	choline-phosphate cytidylyltransferase A-like isoform X2
XP_035456978.1	3.37	collagen alpha-1(I) chain-like isoform X3
XP_035437462.1	-3.07	collagenase-like
XP_035437463.1	-2.05	collagenase-like
XP_035442391.1	4.53	complexin-like isoform X2
XP_035444899.1	2.94	craniofacial development protein 1-like
XP_035431045.1	2.74	CREB-binding protein-like isoform X9
XP_035455805.1	3.09	cuticle protein 1-like
XP_035451574.1	-5.03	cystathionine gamma-lyase-like
XP_035438849.1	-3.34	cytochrome b5-related protein-like
XP_035438821.1	-3.12	dipeptidase 1-like isoform X2
XP_035437737.1	-2.88	diphthine--ammonia ligase-like
XP_035439181.1	3.95	disintegrin and metalloproteinase domain-containing protein 10-like
XP_035440972.1	2.61	DNA polymerase delta subunit 3-like
XP_035449937.1	-3.20	DNA-directed RNA polymerase II subunit RPB3-like
XP_035438479.1	4.25	dnaJ homolog subfamily C member 8-like
XP_035452441.1	4.39	dual specificity protein phosphatase 23-like
XP_035452713.1	-4.83	E3 ubiquitin-protein ligase KCMF1-like isoform X2
XP_035433606.1	4.27	embryonic polarity protein dorsal-like isoform X3
XP_035451847.1	-3.75	ER degradation-enhancing alpha-mannosidase-like protein 3
XP_035444718.1	4.03	esterase FE4-like
XP_035453643.1	4.56	eukaryotic translation initiation factor 3 subunit E
XP_035443967.1	-3.06	FAS-associated factor 2-like
XP_035437568.1	-3.25	fatty acid synthase-like
XP_035448825.1	-2.49	gamma-glutamylcyclotransferase-like
XP_035450013.1	3.79	gamma-interferon-inducible lysosomal thiol reductase-like
XP_035447842.1	2.77	GAS2-like protein pickled eggs
XP_035456133.1	-2.29	GATA zinc finger domain-containing protein 14-like isoform X3
XP_035432660.1	-6.22	glucose dehydrogenase [FAD, quinone]-like
XP_035439627.1	-3.29	glutathione hydrolase 1 proenzyme-like isoform X2
XP_035443637.1	3.16	glutathione S-transferase 2-like
XP_035455986.1	2.54	GTPase-activating protein CdGAPr-like isoform X4

Appendix E. List of exclusively proteins that were differentially abundant (adjusted p-value < 0.05 and fold change ≥ |2.0|) between spinetoram-resistant and susceptible strains when feeding on soybean plants (continue).

Protein ID	log2FC	Description
XP_035449533.1	2.44	helicase SKI2W-like
XP_035430718.1	3.90	homeobox protein extradenticle-like isoform X5
XP_035441872.1	4.33	hyphancin-3E-like
XP_035441769.1	2.19	ileal sodium/bile acid cotransporter-like isoform X1
XP_035438337.1	2.66	importin subunit alpha-7-like
XP_035430363.1	2.30	importin-5-like
XP_035437264.1	3.50	inositol-trisphosphate 3-kinase A-like isoform X1
XP_035445715.1	-3.48	insulin-like growth factor-binding protein complex acid labile subunit
XP_035458953.1	2.27	integrator complex subunit 12-like
XP_035437289.1	3.75	interferon regulatory factor 2-binding protein 1-like isoform X2
XP_035438244.1	2.95	interleukin-1 receptor-associated kinase 4-like
XP_035435283.1	3.28	iroquois-class homeodomain protein IRX-2-like isoform X2
XP_035433199.1	-3.41	JNK-interacting protein 3-like isoform X5
XP_035440470.1	2.15	larval cuticle protein LCP-17-like
XP_035440720.1	2.92	leucine-rich repeat protein soc-2 homolog
XP_035431914.1	-2.73	leucine--tRNA ligase, cytoplasmic-like
XP_035446993.1	-5.31	lon protease homolog, mitochondrial-like isoform X4
XP_035444962.1	-2.55	low affinity immunoglobulin epsilon Fc receptor-like isoform X2
XP_035458620.1	-2.51	LOW QUALITY PROTEIN: 28S ribosomal protein S2, mitochondrial-like
XP_035443706.1	5.28	LOW QUALITY PROTEIN: anther-specific proline-rich protein APG-like
XP_035449007.1	-3.68	LOW QUALITY PROTEIN: ATP-dependent RNA helicase Ddx1-like
XP_035449692.1	-2.81	LOW QUALITY PROTEIN: bromodomain adjacent to zinc finger domain protein 1A-like
XP_035436134.1	-4.80	LOW QUALITY PROTEIN: CAD protein-like
XP_035446661.1	-3.02	LOW QUALITY PROTEIN: carnitine O-acetyltransferase-like
XP_035449647.1	-5.91	LOW QUALITY PROTEIN: diphthine methyl ester synthase-like
XP_035444311.1	2.51	LOW QUALITY PROTEIN: fatty acyl-CoA hydrolase precursor, medium chain-like, partial
XP_035446621.1	-2.54	LOW QUALITY PROTEIN: long-chain-fatty-acid--CoA ligase 4-like
XP_035436398.1	-5.29	LOW QUALITY PROTEIN: methylosome protein 50-like
XP_035449185.1	4.96	LOW QUALITY PROTEIN: muscle M-line assembly protein unc-89-like
XP_035436160.1	-4.02	LOW QUALITY PROTEIN: NIF3-like protein 1
XP_035437164.1	4.30	LOW QUALITY PROTEIN: nucleosome-remodeling factor subunit NURF301-like
XP_035443645.1	-2.41	LOW QUALITY PROTEIN: poly(U)-specific endoribonuclease homolog
XP_035451250.1	2.73	LOW QUALITY PROTEIN: ribosomal protein S6 kinase alpha-4-like
XP_035438050.1	-5.82	LOW QUALITY PROTEIN: ribosome biogenesis protein BOP1 homolog
XP_035445626.1	4.32	LOW QUALITY PROTEIN: serine/threonine-protein kinase 24-like, partial
XP_035450055.1	4.39	LOW QUALITY PROTEIN: serine/threonine-protein phosphatase 6 regulatory subunit 3-A-like
XP_035458437.1	4.25	LOW QUALITY PROTEIN: uncharacterized protein C19orf47-like
XP_035442295.1	3.83	LOW QUALITY PROTEIN: uncharacterized protein LOC118270667
XP_035450127.1	-5.02	LOW QUALITY PROTEIN: uncharacterized protein LOC118276079
XP_035457045.1	4.92	LOW QUALITY PROTEIN: uncharacterized protein LOC118280777
XP_035433839.1	-3.23	LOW QUALITY PROTEIN: zinc-type alcohol dehydrogenase-like protein C1773.06c
XP_035433980.1	2.80	lysozyme-like
XP_035430214.1	5.62	maternal protein pumilio-like isoform X5
XP_035436834.1	-3.54	mediator of RNA polymerase II transcription subunit 19-like
XP_035452223.1	3.05	mediator of RNA polymerase II transcription subunit 25-like isoform X2
XP_035430196.1	-3.76	mitochondrial import inner membrane translocase subunit TIM14-like
XP_035457523.1	3.99	monocarboxylate transporter 12-like isoform X1
XP_035437606.1	-5.48	mucin-2-like isoform X11
XP_035457361.1	3.40	multiple epidermal growth factor-like domains protein 10
XP_035448048.1	3.23	myotubularin-related protein 4-like isoform X2
XP_035449472.1	-3.26	NAD-dependent protein deacetylase sirtuin-2-like
XP_035458512.1	-4.05	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial-like
XP_035440639.1	-4.22	NADP-dependent malic enzyme-like isoform X6
XP_035449986.1	2.70	N-alpha-acetyltransferase 40-like
XP_035430652.1	3.48	nascent polypeptide-associated complex subunit alpha, muscle-specific form-like isoform X6
XP_035432948.1	-2.67	nibrin-like
XP_035432879.1	-3.95	nuclear autoantigenic sperm protein-like
XP_035449227.1	-3.88	nuclear export mediator factor NEMF homolog
XP_035432937.1	2.88	nudC domain-containing protein 3-like
XP_035447661.1	3.16	omega-amidase NIT2-like isoform X2
XP_035449343.1	3.14	optic atrophy 3 protein homolog
XP_035452419.1	3.42	PAN2-PAN3 deadenylation complex subunit PAN3-like isoform X2
XP_035430058.1	3.37	PAX3- and PAX7-binding protein 1-like
XP_035458186.1	3.62	PDZ and LIM domain protein 7-like isoform X3
XP_035435129.1	-4.08	peptidyl-prolyl cis-trans isomerase FKBP8-like
XP_035430256.1	2.59	peptidyl-prolyl cis-trans isomerase-like 3
XP_035450643.1	4.04	PHD and RING finger domain-containing protein 1-like isoform X2
XP_035454713.1	3.93	phenoloxidase-activating factor 2-like
XP_035458629.1	2.99	phytanoyl-CoA dioxygenase, peroxisomal-like
XP_035452696.1	-3.16	PIN2/TERF1-interacting telomerase inhibitor 1-like

Appendix E. List of exclusively proteins that were differentially abundant (adjusted p-value < 0.05 and fold change ≥ |2.0|) between spinetoram-resistant and susceptible strains when feeding on soybean plants (continue).

Protein ID	log2FC	Description
XP_035445968.1	3.00	PITH domain-containing protein GA19395-like
XP_035450733.1	-3.64	platelet binding protein GspB-like
XP_035428764.1	-3.52	poly [ADP-ribose] polymerase-like
XP_035455635.1	-3.79	polyhomeotic-like protein 3 isoform X3
XP_035449356.1	-3.75	pre-mRNA-processing factor 39-like isoform X2
XP_035429204.1	-3.48	pre-rRNA-processing protein TSR1 homolog
XP_035441923.1	-3.93	probable small nuclear ribonucleoprotein Sm D2
XP_035451306.1	-4.04	procollagen-lysine,2-oxoglutarate 5-dioxygenase-like isoform X3
XP_035458938.1	-3.06	prolyl 4-hydroxylase subunit alpha-2-like
XP_035450899.1	-5.79	prostamide/prostaglandin F synthase-like isoform X3
XP_035451609.1	-2.91	protein DEK-like isoform X2
XP_035450308.1	3.60	protein FRG1 homolog
XP_035456993.1	-2.11	protein lethal(2)essential for life-like
XP_035446011.1	-2.48	protein phosphatase 1L-like
XP_035450170.1	-2.92	protein sarah-like
XP_035442451.1	2.83	protein Skeletor, isoforms B/C-like isoform X5
XP_035442448.1	-3.93	protein Skeletor, isoforms D/E-like isoform X2
XP_035439220.1	2.93	protein suppressor of sable-like isoform X2
XP_035456582.1	-3.58	protein transport protein Sec24C-like isoform X1
XP_035445607.1	-3.10	protein transport protein Sec61 subunit beta-like
XP_035436932.1	2.50	protein white-like
XP_035450378.1	2.57	proteoglycan 4-like
XP_035443910.1	3.90	putative neuropeptide precursor protein isoform X2
XP_035432542.1	-3.37	pyridoxal-dependent decarboxylase domain-containing protein 1-like
XP_035445314.1	-4.13	pyrimidodiazepine synthase-like
XP_035440511.1	3.40	rac GTPase-activating protein 1-like
XP_035435087.1	3.08	ran-binding protein 9-like isoform X2
XP_035434555.1	-4.87	ras-related protein Rab-2A
XP_035430802.1	-2.95	ras-related protein Rab-7a
XP_035445082.1	-4.21	regulation of nuclear pre-mRNA domain-containing protein 1B-like
XP_035437408.1	3.51	ribokinase-like isoform X1
XP_035436212.1	-2.38	ribosomal protein S6 kinase beta-1-like
XP_035456288.1	-3.22	ribosomal RNA processing protein 1 homolog
XP_035439856.1	2.92	rRNA N6-adenosine-methyltransferase ZCCHC4-like
XP_035436847.1	2.49	RWD domain-containing protein 4-like
XP_035439189.1	-3.08	S-adenosylmethionine synthase-like isoform X1
XP_035439506.1	-4.11	sarcolemmal membrane-associated protein-like isoform X1
XP_035444493.1	2.97	sarcoplasmic calcium-binding protein 1-like isoform X2
XP_035448024.1	-5.08	septin-1-like isoform X2
XP_035440087.1	-3.20	serine protease persephone-like
XP_035453708.1	3.07	serine protease snake-like
XP_035457096.1	3.64	serine protease snake-like
XP_035429974.1	3.60	serine/arginine repetitive matrix protein 1-like isoform X3
XP_035450977.1	3.10	serine/threonine-protein kinase MARK2-like isoform X12
XP_035458599.1	2.29	serine/threonine-protein kinase PAK mbt-like
XP_035445464.1	-10.10	serine/threonine-protein kinase SMG1-like
XP_035436826.1	2.03	serine-rich adhesin for platelets-like isoform X3
XP_035457306.1	3.15	silk gland factor 3-like
XP_035434884.1	2.31	SNAPIN protein homolog
XP_035440744.1	-3.54	splicing factor 3A subunit 3-like
XP_035439463.1	4.73	SUZ domain-containing protein 1-like
XP_035458410.1	-2.76	target of rapamycin complex subunit lst8-like isoform X2
XP_035453463.1	-4.76	tensin homolog
XP_035432520.1	3.58	testis-expressed protein 2-like isoform X3
XP_035429172.1	-2.95	transcription elongation factor 1 homolog
XP_035453725.1	2.86	transcription elongation regulator 1-like isoform X2
XP_035449955.1	-2.69	transcription factor IIIB 90 kDa subunit-like
XP_035452618.1	4.72	transcription initiation factor TFIID subunit 3-like
XP_035449036.1	-5.44	translocating chain-associated membrane protein 1-like
XP_035438022.1	-3.66	transmembrane protease serine 9-like
XP_035434823.1	3.73	transmembrane protein 214-like
XP_035445161.1	-3.64	tripeptidyl-peptidase 2-like isoform X2
XP_035452374.1	-3.69	tRNA (cytosine(34)-C(5))-methyltransferase-like
XP_035447644.1	-2.58	trypsin II-P29-like
XP_035448285.1	-4.75	trypsin, alkaline C-like
XP_035436868.1	2.93	U4/U6 small nuclear ribonucleoprotein Prp31-like
XP_035453722.1	3.45	U4/U6 small nuclear ribonucleoprotein Prp3-like
XP_035449344.1	-4.16	unc-112-related protein-like
XP_035434029.1	-3.55	uncharacterized protein KIAA1143 homolog

Appendix E. List of exclusively proteins that were differentially abundant (adjusted p-value < 0.05 and fold change ≥ |2.0|) between spinetoram-resistant and susceptible strains when feeding on soybean plants (continue).

Protein ID	log2FC	Description
XP_035428570.1	4.53	uncharacterized protein LOC118261727
XP_035432708.1	-5.30	uncharacterized protein LOC118264337
XP_035432876.1	5.21	uncharacterized protein LOC118264469
XP_035432992.1	4.37	uncharacterized protein LOC118264555 isoform X6
XP_035433119.1	4.25	uncharacterized protein LOC118264646
XP_035433471.1	-3.43	uncharacterized protein LOC118264919
XP_035435069.1	-2.97	uncharacterized protein LOC118265899
XP_035435301.1	2.88	uncharacterized protein LOC118266058
XP_035435468.1	2.06	uncharacterized protein LOC118266178
XP_035436571.1	-2.20	uncharacterized protein LOC118266982
XP_035437143.1	2.86	uncharacterized protein LOC118267320 isoform X3
XP_035437419.1	2.48	uncharacterized protein LOC118267497 isoform X2
XP_035437585.1	-2.21	uncharacterized protein LOC118267618
XP_035443136.1	-4.22	uncharacterized protein LOC118271237
XP_035443362.1	-3.34	uncharacterized protein LOC118271384
XP_035443454.1	3.28	uncharacterized protein LOC118271470
XP_035443997.1	2.73	uncharacterized protein LOC118271859
XP_035445224.1	-2.44	uncharacterized protein LOC118272691
XP_035445572.1	2.95	uncharacterized protein LOC118272939
XP_035448607.1	2.55	uncharacterized protein LOC118274922
XP_035448902.1	2.90	uncharacterized protein LOC118275141
XP_035450033.1	4.51	uncharacterized protein LOC118276011 isoform X4
XP_035450531.1	-2.45	uncharacterized protein LOC118276362 isoform X1
XP_035451128.1	2.79	uncharacterized protein LOC118276730
XP_035451776.1	2.28	uncharacterized protein LOC118277169
XP_035453896.1	4.10	uncharacterized protein LOC118278687 isoform X2
XP_035454764.1	3.38	uncharacterized protein LOC118279243
XP_035454840.1	-4.48	uncharacterized protein LOC118279291
XP_035455613.1	3.20	uncharacterized protein LOC118279880 isoform X2
XP_035456816.1	2.96	uncharacterized protein LOC118280646 isoform X2
XP_035457277.1	3.53	uncharacterized protein LOC118280965
XP_035457409.1	4.19	uncharacterized protein LOC118281067
XP_035457507.1	3.04	uncharacterized protein LOC118281130
XP_035458548.1	-2.99	uncharacterized protein LOC118281887
XP_035459375.1	4.18	uncharacterized protein LOC118282411 isoform X4
XP_035459382.1	2.30	uncharacterized protein LOC118282415
XP_035446806.1	-4.38	vacuolar protein-sorting-associated protein 25-like isoform X2
XP_035434615.1	-5.36	variant surface antigen E-like isoform X34
XP_035458687.1	-2.46	vesicle-associated membrane protein 7-like
XP_035430431.1	3.05	vesicle-trafficking protein SEC22b-like
XP_035434090.1	2.50	WASH complex subunit 3-like
XP_035433510.1	-3.07	WD repeat-containing protein 26-like
XP_035445380.1	3.25	WW domain-binding protein 11-like
XP_035458104.1	2.89	WW domain-binding protein 4-like
XP_035449161.1	3.83	zinc finger C2HC domain-containing protein 1C-like isoform X4
XP_035436190.1	3.31	zinc finger protein 91-like isoform X1

Appendix F. List of exclusively proteins that were differentially abundant (adjusted p-value < 0.05 and fold change ≥ |2.0|) between spinetoram-resistant and susceptible strains when feeding on cotton plants.

Protein ID	log2FC	Description
XP_035434958.1	4.12	1-acylglycerol-3-phosphate O-acyltransferase ABHD5-like isoform X5
XP_035447832.1	2.24	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial-like
XP_035449488.1	-3.98	39S ribosomal protein L37, mitochondrial-like
XP_035434304.1	4.29	3-oxoacyl-[acyl-carrier-protein] reductase FabG-like
XP_035434879.1	2.96	5-formyltetrahydrofolate cyclo-ligase-like
XP_035452365.1	2.53	5-oxoprolinase-like
XP_035432059.1	-3.09	60S ribosomal protein L39
XP_035457479.1	-2.11	60S ribosomal protein L4-like
XP_035434143.1	-2.37	acidic leucine-rich nuclear phosphoprotein 32 family member B-like
XP_035434780.1	4.06	aldehyde dehydrogenase, dimeric NADP-preferring-like isoform X9
XP_035451690.1	3.91	alpha-crystallin A chain-like
XP_035435867.1	4.30	alpha-N-acetylgalactosaminidase-like
XP_035450328.1	2.94	aminoacylase-1-like
XP_035434116.1	4.34	aminoacylase-1-like
XP_035439861.1	2.67	annexin B10-like isoform X5
XP_035448157.1	3.97	AP-1 complex subunit beta-1-like
XP_035431292.1	4.23	apoptosis inhibitor 5-like
XP_035436805.1	2.59	ARF GTPase-activating protein GIT2-like isoform X1
XP_035450514.1	2.22	ATP synthase subunit s, mitochondrial-like
XP_035446899.1	-4.26	ATP-dependent RNA helicase dbp2-like isoform X5
XP_035430057.1	2.99	ATP-dependent translocase ABCB1-like
XP_035438282.1	3.28	calcium-binding mitochondrial carrier protein Aralar1-like isoform X6
XP_035448911.1	3.80	carboxypeptidase B-like
XP_035443466.1	2.37	carboxypeptidase B-like isoform X3
XP_035447232.1	-2.59	casein kinase I-like isoform X8
XP_035437058.1	3.89	cdc42 homolog
XP_035438975.1	7.59	centrosomal protein of 290 kDa-like
XP_035435723.1	2.93	ceramide-1-phosphate transfer protein-like
XP_035447712.1	-2.75	chondroitin proteoglycan 2-like
XP_035447516.1	2.59	chondroitin proteoglycan 2-like
XP_035443782.1	3.57	COP9 signalosome complex subunit 4-like
XP_035446290.1	-2.72	COP9 signalosome complex subunit 9-like
XP_035431305.1	2.83	CRAL-TRIO domain-containing protein C3H8.02-like
XP_035429013.1	5.15	cuticle protein 8-like
XP_035447417.1	6.48	cuticle protein 8-like
XP_035447418.1	3.51	cuticle protein-like
XP_035431059.1	5.05	cysteine--tRNA ligase, cytoplasmic-like
XP_035435139.1	5.50	D-aspartate oxidase-like
XP_035438915.1	-4.63	delta(7)-sterol 5(6)-desaturase erg32-like isoform X2
XP_035433093.1	2.85	D-erythronate dehydrogenase-like
XP_035430466.1	2.58	diamine acetyltransferase 2-like
XP_035459429.1	2.35	dipeptidyl peptidase 3-like
XP_035433203.1	-3.24	DNA-directed RNA polymerase I subunit RPA43-like
XP_035458433.1	4.29	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2-like
XP_035440945.1	-4.58	double-stranded RNA-binding protein Staufen homolog 2-like isoform X5
XP_035446390.1	2.67	dTTP/UTP pyrophosphatase-like
XP_035430830.1	2.23	dynamin-like isoform X9
XP_035447293.1	-6.79	dynein heavy chain, cytoplasmic-like isoform X5
XP_035447293.1	-6.79	dynein heavy chain, cytoplasmic-like isoform X5
XP_035452051.1	2.87	dysbindin-like
XP_035452936.1	-3.82	dystrophin, isoforms A/C/F/G/H-like, partial
XP_035430048.1	-2.34	ecotropic viral integration site 5 ortholog-like isoform X5
XP_035446900.1	2.88	ecto-NOX disulfide-thiol exchanger 2-like
XP_035459283.1	4.15	endocuticle structural glycoprotein SgAbd-8-like
XP_035434291.1	2.55	endoplasmic reticulum lectin 1-like isoform X3
XP_035437062.1	3.51	endoplasmic reticulum resident protein 44-like isoform X2
XP_035435406.1	2.64	esterase E4-like
XP_035435407.1	5.50	esterase E4-like
XP_035431132.1	-2.79	eukaryotic translation initiation factor 5B-like
XP_035455557.1	4.92	failed axon connections-like
XP_035456968.1	-3.20	flocculation protein FLO11-like isoform X3
XP_035457324.1	2.91	gametocyte-specific factor 1-like
XP_035441062.1	2.42	GDP-L-fucose synthase-like
XP_035459351.1	4.33	glucose-induced degradation protein 8-A homolog isoform X2
XP_035452115.1	2.32	glutamate--cysteine ligase regulatory subunit-like
XP_035450519.1	2.87	Golgi phosphoprotein 3 homolog sauron-like
XP_035453757.1	-3.18	H/ACA ribonucleoprotein complex subunit 4-like isoform X2
XP_035443398.1	5.64	hemicentin-2-like isoform X3
XP_035448776.1	4.54	hsp70-binding protein 1-like
XP_035446333.1	4.47	inosine triphosphate pyrophosphatase-like

Appendix F. List of exclusively proteins that were differentially abundant (adjusted p-value < 0.05 and fold change ≥ |2.0|) between spinetoram-resistant and susceptible strains when feeding on cotton plants (continue).

Protein ID	log2FC	Description
XP_035448988.1	2.92	inositol oxygenase-like isoform X2
XP_035438862.1	4.43	inositol polyphosphate 1-phosphatase-like
XP_035449418.1	-3.17	insecticyanin-A-like
XP_035449612.1	5.00	isopentenyl-diphosphate Delta-isomerase 1-like
XP_035457230.1	3.66	IST1 homolog
XP_035430692.1	5.75	juvenile hormone esterase-like
XP_035450591.1	3.66	juvenile hormone-binding protein-like
XP_035431061.1	2.38	laminin subunit beta-1-like
XP_035459025.1	2.12	larval cuticle protein 1-like isoform X2
XP_035457293.1	-4.61	larval cuticle protein LCP-17-like
XP_035434330.1	3.94	leucine-rich PPR motif-containing protein, mitochondrial-like
XP_035452271.1	2.77	longitudinals lacking protein-like
XP_035429501.1	-3.78	LOW QUALITY PROTEIN: ATP-binding cassette sub-family F member 1-like
XP_035437213.1	-2.85	LOW QUALITY PROTEIN: echinoderm microtubule-associated protein-like 2
XP_035444121.1	-2.55	LOW QUALITY PROTEIN: general vesicular transport factor p115-like
XP_035444602.1	2.27	LOW QUALITY PROTEIN: glycerol-3-phosphate phosphatase-like
XP_035457750.1	-3.42	LOW QUALITY PROTEIN: guanine nucleotide-binding protein-like 3 homolog
XP_035439524.1	3.44	LOW QUALITY PROTEIN: integrin alpha-PS1-like
XP_035449989.1	-4.11	LOW QUALITY PROTEIN: monocarboxylate transporter 3-like
XP_035437567.1	-2.79	LOW QUALITY PROTEIN: mucin-5AC-like
XP_035431859.1	2.11	LOW QUALITY PROTEIN: N-acetylglucosamine-6-phosphate deacetylase-like
XP_035446347.1	-3.04	LOW QUALITY PROTEIN: nuclear pore complex protein Nup93-like
XP_035444448.1	2.20	LOW QUALITY PROTEIN: ornithine aminotransferase, mitochondrial-like
XP_035447398.1	-2.25	LOW QUALITY PROTEIN: poly(U)-binding-splicing factor half pint-like
XP_035451678.1	-3.56	LOW QUALITY PROTEIN: probable ATP-dependent RNA helicase DDX27
XP_035451178.1	-12.14	LOW QUALITY PROTEIN: RNA polymerase-associated protein Rtf1-like
XP_035429502.1	5.38	LOW QUALITY PROTEIN: spectrin alpha chain-like
XP_035431856.1	-2.23	LOW QUALITY PROTEIN: uncharacterized oxidoreductase YrbE-like
XP_035430031.1	-4.29	LOW QUALITY PROTEIN: uncharacterized protein LOC118262620
XP_035441018.1	-3.22	LOW QUALITY PROTEIN: uncharacterized protein LOC118269805
XP_035440258.1	2.59	LOW QUALITY PROTEIN: valine--tRNA ligase-like
XP_035445911.1	4.85	lysine--tRNA ligase-like isoform X2
XP_035443613.1	2.80	lysozyme-like
XP_035445266.1	-2.04	maternal protein tudor-like isoform X1
XP_035434346.1	2.43	medium-chain acyl-CoA ligase ACSF2, mitochondrial-like
XP_035455600.1	3.03	methionine--tRNA ligase, cytoplasmic-like isoform X2
XP_035438249.1	5.89	MICOS complex subunit MIC13 homolog QIL1-like
XP_035458402.1	7.04	mitochondrial import receptor subunit TOM22 homolog
XP_035441004.1	2.85	mitochondrial transcription rescue factor 1-like
XP_035429418.1	2.90	mitochondrial-processing peptidase subunit alpha-like
XP_035450155.1	4.44	mucin-2-like
XP_035447540.1	3.43	myogenesis-regulating glycosidase-like
XP_035438425.1	-4.24	myosin heavy chain 95F-like isoform X2
XP_035439708.1	-2.68	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6-like
XP_035429449.1	-3.61	neurocalcin homolog
XP_035432401.1	4.25	nuclear distribution protein nudE-like 1 isoform X2
XP_035443306.1	6.44	nuclear pore complex protein Nup58-like
XP_035437317.1	-4.30	nuclear valosin-containing protein-like
XP_035458180.1	-2.83	nucleolar protein dao-5-like isoform X2
XP_035446068.1	3.58	pancreatic lipase-related protein 2-like
XP_035452076.1	3.61	pancreatic triacylglycerol lipase-like
XP_035439051.1	-3.45	peptidoglycan recognition protein-like
XP_035446424.1	3.24	peptidyl-alpha-hydroxyglycine alpha-amidating lyase 1-like isoform X3
XP_035429854.1	3.11	peptidyl-prolyl cis-trans isomerase-like
XP_035441218.1	-2.96	phenylalanine--tRNA ligase alpha subunit-like
XP_035450475.1	4.66	phosphoglycolate phosphatase 2-like
XP_035455008.1	3.57	plectin-like isoform X2
XP_035436663.1	4.21	pre-mRNA-processing factor 19-like
XP_035429216.1	3.37	pre-mRNA-splicing factor ISY1 homolog
XP_035443948.1	3.41	pre-mRNA-splicing regulator female-lethal(2)D-like
XP_035446795.1	4.26	probable alpha-aspartyl dipeptidase
XP_035439764.1	-4.46	probable ATP-dependent RNA helicase DDX56
XP_035432312.1	-3.70	probable isoaspartyl peptidase/L-asparaginase CG7860 isoform X3
XP_035432212.1	3.57	probable low-specificity L-threonine aldolase 2
XP_035436872.1	7.17	probable nuclear transport factor 2 isoform X1
XP_035442341.1	-2.94	probable peroxisomal acyl-coenzyme A oxidase 1 isoform X2
XP_035430323.1	3.84	probable pseudouridine-5-phosphatase
XP_035432381.1	2.81	prostaglandin reductase 1-like
XP_035443336.1	2.42	protein arginine methyltransferase NDUFAF7 homolog, mitochondrial-like
XP_035455523.1	3.89	protein bcn92-like

Appendix F. List of exclusively proteins that were differentially abundant (adjusted p-value < 0.05 and fold change ≥ |2.0|) between spinetoram-resistant and susceptible strains when feeding on cotton plants (continue).

Protein ID	log2FC	Description
XP_035448514.1	-2.90	protein D2-like isoform X1
XP_035438703.1	-3.77	protein FAM76A-like isoform X1
XP_035432557.1	-3.72	protein furry-like isoform X9
XP_035452047.1	-2.37	protein NDUFAF4 homolog
XP_035441620.1	-2.79	protein polybromo-1-like isoform X11
XP_035441606.1	3.01	protein Skeletor, isoforms B/C-like isoform X4
XP_035435450.1	-2.95	protein twisted gastrulation-like
XP_035446786.1	5.70	protein unzipped-like
XP_035434060.1	3.50	protein-L-isoaspartate(D-aspartate) O-methyltransferase-like isoform X3
XP_035457205.1	-2.67	proteoglycan 4-like
XP_035431907.1	-2.80	proton channel OtopLc-like
XP_035439367.1	6.24	ragulator complex protein LAMTOR4 homolog
XP_035434770.1	2.19	ras-like GTP-binding protein Rho1 isoform X2
XP_035434470.1	3.82	retinoid-inducible serine carboxypeptidase-like
XP_035450617.1	3.15	ribosome biogenesis protein NSA2 homolog
XP_035458392.1	2.15	ribosome biogenesis regulatory protein homolog
XP_035440505.1	-2.68	RING finger protein nhl-1-like isoform X2
XP_035436287.1	-2.78	RNA binding protein fox-1 homolog 3-like
XP_035451304.1	3.54	rRNA 2-O-methyltransferase fibrillarin-like
XP_035451591.1	-4.70	ryanodine receptor-like
XP_035455843.1	7.71	serine protease filzig-like
XP_035450843.1	2.28	serine/threonine-protein kinase Genghis Khan-like
XP_035447936.1	-3.15	serine/threonine-protein kinase Tao-like isoform X4
XP_035458828.1	-3.23	serine/threonine-protein phosphatase 4 regulatory subunit 3-like isoform X2
XP_035449166.1	2.96	serine/threonine-protein phosphatase 5-like
XP_035454768.1	3.65	SHC-transforming protein 1-like
XP_035452024.1	-2.76	SOSS complex subunit B homolog
XP_035453560.1	-4.07	spectrin beta chain, non-erythrocytic 1-like isoform X3
XP_035455733.1	3.99	steroidogenic acute regulatory protein-like
XP_035452235.1	4.50	sulfite oxidase, mitochondrial-like
XP_035450635.1	-4.66	syntaxin-binding protein 5-like isoform X3
XP_035432185.1	3.83	TATA-binding protein-associated factor 172-like isoform X2
XP_035456026.1	-2.58	tau-tubulin kinase homolog Asator-like isoform X1
XP_035448121.1	-3.47	TBC1 domain family member 22B-like
XP_035436199.1	-2.96	TBC1 domain family member 9-like isoform X2
XP_035436151.1	-3.98	telomerase-binding protein EST1A-like isoform X4
XP_035431726.1	4.94	tenascin-like isoform X23
XP_035440499.1	4.74	tetratricopeptide repeat protein 36 homolog isoform X2
XP_035440547.1	-6.86	thioredoxin domain-containing protein 5 homolog
XP_035439340.1	-3.99	THO complex subunit 4-like
XP_035458386.1	-3.13	thymidylate kinase-like
XP_035443505.1	2.94	TNF receptor-associated factor 1-like
XP_035453974.1	3.55	transferrin-like
XP_035450403.1	4.61	transferrin-like
XP_035440264.1	-4.08	transformer-2 protein homolog beta-like isoform X5
XP_035435085.1	4.29	translin-associated factor X-interacting protein 1-like isoform X2
XP_035434353.1	-3.77	transmembrane protein 87A-like
XP_035434278.1	-4.32	transport and Golgi organization protein 1-like isoform X4
XP_035436475.1	3.27	troponin C, isoallergen Bla g 6.0101-like
XP_035448861.1	-4.50	trypsin 5G1-like
XP_035449347.1	4.36	tryptophan--tRNA ligase, cytoplasmic-like
XP_035453568.1	2.53	tumor protein D53 homolog isoform X2
XP_035457283.1	8.55	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1
XP_035448881.1	2.36	uncharacterized oxidoreductase MexAM1_META1p0182-like isoform X2
XP_035433506.1	4.56	uncharacterized oxidoreductase MT0954-like
XP_035428810.1	-4.41	uncharacterized protein LOC118261894
XP_035429509.1	4.35	uncharacterized protein LOC118262356
XP_035431005.1	-4.12	uncharacterized protein LOC118263260
XP_035433230.1	2.30	uncharacterized protein LOC118264730
XP_035439147.1	2.72	uncharacterized protein LOC118268676
XP_035441083.1	-2.09	uncharacterized protein LOC118269854
XP_035441504.1	2.53	uncharacterized protein LOC118270149
XP_035443376.1	5.61	uncharacterized protein LOC118271396
XP_035445725.1	-6.09	uncharacterized protein LOC118273069 isoform X2
XP_035446381.1	-2.85	uncharacterized protein LOC118273487 isoform X2
XP_035447411.1	3.26	uncharacterized protein LOC118274120 isoform X3
XP_035448877.1	-3.19	uncharacterized protein LOC118275120
XP_035449167.1	7.18	uncharacterized protein LOC118275355
XP_035451749.1	-3.25	uncharacterized protein LOC118277149

Appendix F. List of exclusively proteins that were differentially abundant (adjusted p-value < 0.05 and fold change ≥ |2.0|) between spinetoram-resistant and susceptible strains when feeding on cotton plants (continue).

Protein ID	log2FC	Description
XP_035452091.1	-3.31	uncharacterized protein LOC118277410 isoform X2
XP_035454918.1	-2.96	uncharacterized protein LOC118279352 isoform X2
XP_035456149.1	5.03	uncharacterized protein LOC118280292
XP_035458475.1	-4.26	uncharacterized protein LOC118281827
XP_035458709.1	4.99	UPF0587 protein GA18326-like
XP_035451592.1	-4.36	vacuolar protein sorting-associated protein 26B-like
XP_035440974.1	2.55	venom peptide BmKAPI-like
XP_035456259.1	-2.68	WASH complex subunit 2A-like
XP_035451521.1	-3.52	WD repeat-containing protein 43-like
XP_035439799.1	-3.86	WD repeat-containing protein 47-like isoform X1
XP_035447217.1	3.63	WD repeat-containing protein 61-like
XP_035444218.1	-4.13	zinc finger CCHC domain-containing protein 9-like
XP_035458209.1	2.36	zinc finger protein 830-like
XP_035448312.1	-2.85	zinc finger protein OZF-like
XP_035447300.1	-3.34	zinc transporter 2-like isoform X4
XP_035432939.1	2.83	zinc-type alcohol dehydrogenase-like protein SERP1785

Appendix G. List of proteins that were common in the comparasion between spinetoram-resistant and susceptible strains in the three host plants (adjusted p-value < 0.05 and fold change ≥ |2.0|).

Protein ID	Expression	Description
XP_035445238.1	Up-regulated	beta-1,3-glucan-binding protein-like
XP_035441964.1	Up-regulated	cationic trypsin-like
XP_035446919.1	Up-regulated	cuticle protein 65-like
XP_035448876.1	Up-regulated	fructose-bisphosphate aldolase-like
XP_035448189.1	Up-regulated	glucose dehydrogenase [FAD, quinone]-like
XP_035430062.1	Up-regulated	glycerophosphodiester phosphodiesterase, periplasmic-like
XP_035444495.1	Up-regulated	glyoxylate reductase/hydroxypyruvate reductase-like
XP_035449042.1	Down-regulated	LOW QUALITY PROTEIN: metastasis-associated protein MTA3-like
XP_035448037.1	Up-regulated	luciferin 4-monooxygenase-like
XP_035448492.1	Down-regulated	protein D2-like
XP_035455240.1	Down-regulated	pupal cuticle protein PCP52-like
XP_035444340.1	Up-regulated	serine protease inhibitor dipetalogastin-like
XP_035456059.1	Up-regulated	SID1 transmembrane family member 1-like
XP_035441655.1	Up-regulated	uncharacterized protein LOC118270264
XP_035445917.1	Down-regulated	uncharacterized protein LOC118273189
XP_035451452.1	Down-regulated	uncharacterized protein LOC118276932
XP_035451767.1	Down-regulated	uncharacterized protein LOC118277162

Appendix H. List of metabolites of spinetoram-resistant and susceptible strains identified by GC-MS analysis.

ID	Common name	Class
38436-mainlib	1,2,3-Butanetriol	Alcohols and polyols
119455-mainlib	1,4-Butanediol	Alcohols and polyols
9617-replib	Inositol 6-phosphate	Alcohols and polyols
9368-replib	myo-Inositol	Alcohols and polyols
38429-mainlib	Lactic acid	Alpha hydroxy acids and derivatives
39628-mainlib	5-Hydroxynorvaline	Amines
66783-mainlib	Ethylamine	Amines
143937-mainlib	Putrescine	Amines
143916-mainlib	Acetyl-Lysine	Amino acids, peptides, and analogues
86273-mainlib	Alanine	Amino acids, peptides, and analogues
39144-mainlib	Aminoisobutyric acid	Amino acids, peptides, and analogues
9234-replib	Asparagine	Amino acids, peptides, and analogues
39055-mainlib	Aspartic acid	Amino acids, peptides, and analogues
171347-mainlib	Cystathionine	Amino acids, peptides, and analogues
24429-replib	Glycine	Amino acids, peptides, and analogues
127203-mainlib	Histidine	Amino acids, peptides, and analogues
39641-mainlib	Homocysteine	Amino acids, peptides, and analogues
171358-mainlib	Homoserine	Amino acids, peptides, and analogues
130529-mainlib	Isoleucine	Amino acids, peptides, and analogues
22746-replib	Leucine	Amino acids, peptides, and analogues
50781-mainlib	Leucine	Amino acids, peptides, and analogues
39000-mainlib	L-Glutamine	Amino acids, peptides, and analogues
39149-mainlib	Lysine	Amino acids, peptides, and analogues
115343-mainlib	Ornithine	Amino acids, peptides, and analogues
90975-mainlib	Phenylalanine	Amino acids, peptides, and analogues
9291-replib	Proline	Amino acids, peptides, and analogues
129206-mainlib	Pyroglutamic acid	Amino acids, peptides, and analogues
86488-mainlib	Serine	Amino acids, peptides, and analogues
39048-mainlib	Thioproline	Amino acids, peptides, and analogues
38412-mainlib	Threonine	Amino acids, peptides, and analogues
27422-replib	Tyrosine	Amino acids, peptides, and analogues
36240-mainlib	Valine	Amino acids, peptides, and analogues
9296-replib	Valine	Amino acids, peptides, and analogues
143908-mainlib	γ-Aminobutyric acid	Amino acids, peptides, and analogues
182910-mainlib	Glutamic acid	Amino acids, peptides, and analogues
69276-mainlib	Methionine	Amino acids, peptides, and analogues
147068-mainlib	Tyrosine	Amino acids, peptides, and analogues
86262-mainlib	Adrenaline	Benzenoids
180081-mainlib	2,5-Dimethoxymandelic acid	Benzenoids
205768-mainlib	3-Hydroxyanthranilic acid	Benzenoids
39433-mainlib	Benzenebutanoic acid	Benzenoids
9382-replib	Malic acid	Beta hydroxy acids and derivatives
9299-replib	Erythronic acid	Carbohydrates and carbohydrate conjugates
9402-replib	Gluconic acid	Carbohydrates and carbohydrate conjugates
39947-mainlib	Gluconic acid phosphate	Carbohydrates and carbohydrate conjugates
164552-mainlib	Glucopyranose	Carbohydrates and carbohydrate conjugates
39404-mainlib	Mannose 6-phosphate	Carbohydrates and carbohydrate conjugates
39358-mainlib	Methyl galactoside	Carbohydrates and carbohydrate conjugates
39381-mainlib	Rhamnose	Carbohydrates and carbohydrate conjugates
9203-replib	Ribitol	Carbohydrates and carbohydrate conjugates
40058-mainlib	Ribulose	Carbohydrates and carbohydrate conjugates
170819-mainlib	Talofuranose	Carbohydrates and carbohydrate conjugates
39379-mainlib	Talopyranose	Carbohydrates and carbohydrate conjugates
38204-mainlib	Xylulose	Carbohydrates and carbohydrate conjugates
38869-mainlib	Mercaptoacetic acid	Carboxylic acids
38695-mainlib	Ethanedioic acid	Dicarboxylic acids and derivatives
182607-mainlib	Fumaric acid/Maleic acid	Dicarboxylic acids and derivatives
119446-mainlib	Glutaric acid	Dicarboxylic acids and derivatives
119441-mainlib	Succinic acid	Dicarboxylic acids and derivatives
9118-replib	Hexadecanoic acid	Fatty acids and conjugates
21411-replib	Itaconic acid	Fatty acids and conjugates
38806-mainlib	Methylmaleic acid	Fatty acids and conjugates
38757-mainlib	Mevalonic acid	Fatty acids and conjugates
9244-replib	Octadecanoic acid	Fatty acids and conjugates
9264-replib	Butyric acid	Fatty acids and conjugates
119414-mainlib	Erythrono-1,4-lactone	Gamma butyrolactones
38939-mainlib	Oxoglutaric acid	Gamma-keto acids and derivatives
40201-mainlib	Glycerol-3-phosphate	Glycerophosphates
39560-mainlib	Coumaric acid	Hydroxycinnamic acids and derivatives
26576-replib	Tryptophan	Indolyl carboxylic acids and derivatives
9961-replib	Linoleic acid	Lineolic acids and derivatives

Appendix H. List of metabolites of spinetoram-resistant and susceptible strains identified by GC-MS analysis (continue)

ID	Common name	Class
39649-mainlib	Adenosine	Nucleosides
39093-mainlib	Adenosine monophosphate	Nucleosides
39534-mainlib	Inosine	Nucleosides
39557-mainlib	2-methyl-Propanetriol	Others
127817-mainlib	Cyclopentene-3-carboxylic acid, 1-(trimethylsilyl)oxy-, methyl ester	Others
38865-mainlib	d-Erythrotetrofuranose	Others
26097-mainlib	S-[2-[N,N-Dimethylamino]ethyl]N,N-dimethylcarbamoyl thiocarbohydroximate	Others
86253-mainlib	Phenylpropanolamine	Phenylpropanes
180906-mainlib	Phosphoric acid, monomethyl ester	Phosphate esters
208122-mainlib	Isoxanthopterin	Pterins and derivatives
40345-mainlib	Uric acid	Purines and purine derivatives
38518-mainlib	2-Hydroxyglutaric acid	Short-chain hydroxy acids and derivatives
37875-mainlib	Aucubin	Terpene glycosides
9376-replib	Aconitic acid	Tricarboxylic acids and derivatives
191513-mainlib	Citric acid	Tricarboxylic acids and derivatives