

**University of São Paulo
“Luiz de Queiroz” College of Agriculture**

**Genetic architecture of root-knot nematode resistance in common
beans**

Talissa de Oliveira Floriani Zimmermann de Souza

Dissertation presented to obtain the degree of Master
in Science. Area: Genetics and Plant Breeding

**Piracicaba
2023**

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DEDICATORY

To my parents Carmelina Floriani and Ademir Floriani

To my husband Alexandre Zimmermann de Souza

My little Amora and Hannah

I love you so much.

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RESUMO

Arquitetura genética da resistência ao nematóide de galhas em feijoeiro comum

O feijão comum (*Phaseolus vulgaris* L.) é uma cultura utilizada para consumo humano direto. O grão contém micronutrientes essenciais e um valioso conteúdo proteico, contribuindo assim para a segurança alimentar nos países em desenvolvimento. No entanto, os ataques do nematóide das galhas (RKN - *Meloidogyne incognita*) representam uma ameaça ao cultivo do feijão comum, causando perdas substanciais de rendimento. Sem dúvida, a resistência das culturas é uma excelente abordagem para suprimir a infecção por nematoides. Para dar continuidade aos nossos estudos anteriores no que tange a arquitetura genética da resposta do feijoeiro ao RKN - raça 3, genótipos contrastantes foram identificados e cruzados. A população segregante (F_2), que consistia em 388 indivíduos, foi genotipada usando GBS (genotipagem por sequenciamento), e uma abordagem personalizada de fenotipagem de alto rendimento foi desenvolvida para adquirir dados de características para um subconjunto de 200 famílias $F_{2,3}$. As características massa de ovos (EM), índice de galhas (GI) e massa seca radicular (RM) foram avaliadas ao longo do tempo em condições de casa de vegetação sobre um delineamento inteiramente casualizados com dez repetições. Foi realizado a construção de um mapa de ligação e mapeamento de QTLs (quantitative trait loci), e o mapeamento funcional das regiões associadas foi utilizado para descoberta de genes candidatos. Um mapa de ligação resultando em 954 SNPs atribuídos a 11 grupos de ligação totalizando 1.687 cM foi usado como base para o Mapeamento de Intervalo Composto (CIM) e Mapeamento de Intervalo Múltiplo (MIM), identificando quatro QTLs principais (Pv03, Pv05, Pv08 e Pv10). O modelo selecionado foi usado para calcular os valores genotípicos dos indivíduos, dentro do enfoque de seleção assistida por marcadores moleculares (MAS), chegando a uma lista de top 10 genótipos para uso em MAS. A correlação entre valores observados e valores preditos foi de 0.72, considerada alta, o resultado mostra a relevância do modelo. Genes candidatos foram identificados em resposta ao GI, com domínios relacionados às cascatas WRKY e MAPK (Mitogen-Activated Protein Kinase). Este trabalho representa um passo significativo na compreensão da arquitetura genética da resistência a RKN no feijoeiro comum. Ele prepara o terreno para a implementação do MAS em uma população segregante para a resistência a patógenos na família do feijão.

Palavras-chave: 1. Mapeamento de QTLs 2. Genes Candidatos 3. *Phaseolus vulgaris* L. 4. *Meloidogyne incognita*

ABSTRACT

Genetic architecture of root-knot nematode resistance in common beans

The common bean (*Phaseolus vulgaris* L.) is a crop used for direct human consumption. The grain covers essential micronutrients and valuable protein content, thus contributing to food security in developing countries. However, attacks by root-knot nematode (RKN - *Meloidogyne incognita*) threaten common bean cultivation, causing substantial yield losses. Undoubtedly, crop resistance is an outstanding approach for suppressing nematode infection. To give continuity to our previous studies for unveiling the genetic architecture of typical bean response to RKN (race 3 of *Meloidogyne incognita*), contrasting genotypes were identified and crossed. The segregating population (F_2), which consisted of 388 individuals, was genotyped using GBS (genotyping-by-sequencing), and a customized high-throughput phenotyping approach was developed to acquire trait data for a subset of 200 $F_{2:3}$ families. The traits egg mass (EM), root-galling index (RG), and root dry mass (RM) were evaluated over time within greenhouse conditions under a completely randomized design with ten replicates. Linkage and quantitative trait loci (QTL) mapping were carried out, and functional mapping of the associated regions was used for candidate genes discovery. A total Linkage map resulting in 954 SNPs assigned to 11 linkage groups totaling 1,687 cM was used as a basis for Composite Interval Mapping (CIM) and Multiple Interval Mapping (MIM), identifying four major QTLs (Pv03, Pv05, Pv08 and Pv10). The selected model was used to calculate the genotypic values of individuals, with the marker-assisted selection (MAS) approach, arriving at a list of the top 10 genotypes for use in MAS. The correlation between observed and predicted values was 0.72, considered high; the result shows the relevance of the model. Candidate genes were identified in response to GI, with domains related to WRKY and MAPK (Mitogen-Activated Protein Kinase) cascades. This work represents a significant step in understanding the genetic architecture of RNK resistance in the common bean. It sets the stage for implementing MAS in a breeding population against pathogen resistance in the bean family.

Keywords: 1. QTL mapping 2. Candidate Genes 3. *Phaseolus vulgaris* L. 4. *Meloidogyne incognita*

1 INTRODUCTION

The common bean (*Phaseolus vulgaris* L., Fabaceae) is a crop of great economic and social importance, representing the most important grain legume for direct human consumption worldwide (BITOCCHI *ET AL.*, 2017). It is the primary source of proteins, fibers, and essential nutrients that are particularly important to people's health in developing countries (AKIBODE and MAREDIA, 2012); (JOSHI and RAO, 2017). Of more significant concern is the fact that more than 800 million people live in hunger worldwide. In 2021, the global production of common bean output reached approximately 27.7 million tons, where Brazil reached out over 2.8 million tons, standing out as the second largest crop producer, where the primary producers are in the Midwest and South regions of the country (FOOD AND AGRICULTURE ORGANIZATION OF THE UNITED NATIONS STATISTICS DIVISION, 2023). Due to the selection process during domestication, cultivated plants acquired a set of new characteristics, which ensured their adaptation to the environments grown and increased their usefulness for farmers and consumers (GEPTS and PAPA, 2003). The common bean crop, originating in Mexico and the southern Andes, went through the process of independent domestication that gave rise to the two gene pools, the Andean pool and the Mesoamerican, which differ from each other morphologically and genetically (KWAK and GEPTS, 2009). The Mesoamerican gene pool has greater genetic diversity compared to the Andean. One of the cultivated types, black and carioca grain beans, with medium to small sizes, are the most consumed in Brazil (BLAIR *ET AL.*, 2013).

In the field, however, the crop faces severe phytosanitary problems due to nematode attacks, reducing yield by compromising its root system and making it more susceptible to biotic and abiotic stresses (GRUNDLER and HOFMANN, 2011). Cyst nematodes (*Heterodera* spp.), lesion nematodes (*Pratylenchus* spp.), and root-knot nematodes (*Meloidogyne* spp.) are the leading causes of production damages, which can reach up to US 173 billion annually (GAMALERO and GLICK, 2020). Root-knot nematodes (RKN) are endoparasites that establish their feeding sites by differentiating the host root cells, resulting in the development of galls (JONES and GOTO, 2011). Regarding common bean cultivation, galls are caused by *M. incognita* and *M. javanica*, which are the most prevalent and destructive species (SINGH and SCHWARTZ, 2011); (SANTOS *ET AL.*, 2012). Galls form because of the abnormal growth activities in response to gall-inducing organisms. Root damage caused by *M. incognita* affects water and nutrient absorption of infected plants, which in response manifests symptoms such as dwarfism and poor development of the vegetative system, compromising the yield (SANTOS *ET AL.*, 2012). Reductions in productivity caused by RKN are distributed worldwide, and the damage caused by them is estimated at around 10% (Whitehead 1998). However, it is not easy to assess the economic impact of nematodes; among them, the damage is less evident than that caused by most insects and pathogens, as they are not always reflections of direct attacks on plant tissues.

Mainly in tropical and subtropical regions, the significance of the damage is due to the pathogen's capacity to suppress the host's defense, high population density, and crop management techniques (e.g., crop rotation and chemical control) (SIKORA *ET AL.*, 2018). These techniques have been employed to reduce pathogen reproduction in the field. However, they are expensive and have had little success. Although nematicides are also an option for controlling RKN, besides the health and environmental risks, the most effective way to prevent the disease is through resistant cultivars (BARBARY *ET AL.*, 2015). There is a consensus that identifying genetic resistance sources through systematic evaluation of the available germplasm is a crucial strategy for a breeding program to reduce the damage caused by RKNs. Even though they seem elusive, some results have been published as regards common bean genotypes' response to RKN and the discovery of putative resistance genes (FERREIRA *ET AL.*, 2010); (BOZBUGA *ET AL.*, 2015); (COSTA *ET AL.*, 2019); (GIORDANI *ET AL.*, 2021);(DIAS *ET AL.*, 2023). The identification of candidate genes was accelerated with the advance of SNPs-based markers; in addition to that, the first

published genetic map in common bean (VALLEJOS *ET AL.*, 1992) opened the frontiers for genetic map construction.

Moreover, the use of QTL mapping to identify resistance genes in response to the RKN is reported in other species, such as soybean (*Glycine max*), cowpea (*Vigna unguiculata*) (SHEARIN *ET AL.*, 2009);(HUYNH *ET AL.*, 2016); (LEAL-BERTIOLI *ET AL.*, 2016); (SANTOS *ET AL.*, 2018); NDEVE *ET AL.* (2019), sweet potato (*Ipomoea batata*) OLOKA *ET AL.* (2021) , and carrot (*Daucus carota*)(PARSONS *ET AL.*, 2015). Among the QTL studies in common beans, the most recent studies are related to abiotic factors such as drought tolerance (DRAMADRI *ET AL.*, 2019), drought stress (VALDISSER *ET AL.*, 2020), and heat stress (VARGAS *ET AL.*, 2021). Regarding resistance to pathogens, especially QTL mapping for nematode resistance in beans, the reference portal is scarce, with most currents related to *Heterodera glycines* (SHI *ET AL.*, 2021) and only one to the RKN (GIORDANI *ET AL.*, 2021). GIORDANI *ET AL.* (2021) carried out a genome-wide association study (GWAS) to look for genomics variants (e.g., SNPs) and identify genotype-phenotype associations by testing for differences in the allele frequencies of SNPs among 175 accessions belonging to a common bean diversity panel. SNP effects were validated via traditional QTL mapping in a BC_2F_4 population, where they reported a major QTL on Pv05 (*Phaseolus vulgaris*, chromosome 05). The same authors identified eight genomics regions on different chromosomes and 216 candidate genes associated with the host response. These included 14 resistance gene analogs (RGAs) and five genes differentially expressed in the previous transcriptome analysis (SANTINI *ET AL.*, 2016).

The efforts created for developing molecular genetic maps by molecular biology techniques have greatly facilitated the advances in understanding complex traits. FISHER (1918) partitioned the genetic variance, and COCKERHAM (1954) enhanced the approach with an orthogonal contrast model; the knowledge developed made it possible to master the genetic basis from nematode disease resistance, mainly from quantitative trait locus. With the increased power from statistical methods and the several versions of the common bean, genome assemblies released (SCHMUTZ *ET AL.*, 2014), the linkage map and multiple QTL mapping together can conceive the genetic architecture of a specific trait (KAO *ET AL.*, 1999); (ZENG *ET AL.*, 1999); (KAO and ZENG, 2002). MAS (Marker-Assisted selection) could select the most resistant genotypes for further population construction based on the breeding values of each one, speeding the development of resistant cultivars of common beans. Traits related to the RKN disease are challenging to manage; they are time-consuming and expensive. MAS could help breeders accelerate the process of creating resistant cultivars. Effective MAS can be found in soybean cyst nematode resistance (CREGAN *ET AL.*, 1999); (YOUNG, 1999) during successful identification and transference of the resistance gene *rhg1* (MARCELINO-GUIMARÃES *ET AL.*, 2007) and in common beans with markers associated with the common bean bacterial blight (YU *ET AL.*, 2000). Therefore, research is needed to enhance expected bean improvement to the RKN resistance.

The objective of the present work was to advance the understanding of the genetic the architecture of traits involved in the typical bean response to RKN and perform QTL mapping to estimate their location and effects. In addition, we intend to progress in identifying causative genes and indicating possible individuals as a basis for the next generations through MAS. To do this, an F₂ progeny derived from two contrasting accessions (one moderately resistant and one susceptible) was genotyped using GBS (genotyping by sequencing), a linkage map was built, a customized high-throughput phenotyping approach was used for acquiring trait data for a subset of F_{2:3} families, a robust model for mapping multiple QTLs was constructed, a candidate gene search was developed, and genotypic values from individuals were predicted based on the QTL model selection to keep the results as a basis for a breeding program in common beans.

2 CONCLUSIONS

In conclusion, the TB population carries the contrast between the parents, which is well suited to the F_2 generation for investigating the architecture of resistance to the RKN. The linkage map construction resulted in 954 SNPs assigned to 11 linkage groups totaling in 1,687 cM. The results from linkage map was used as a basis for Composite Interval Mapping (CIM) and Multiple Interval Mapping (MIM), where not only one, but four major QTLs were identified in the respective chromosomes: Pv03, Pv05, Pv08 and Pv10. The selected model was used to calculate the genetic values of individuals, with the marker-assisted selection (MAS). A list of top 10 genotypes for use in MAS, as the most resistant genotypes were created. The correlation between observed and predicted values from the MAS was 0.72, considered high; showing the relevance of the model. The identified Candidate genes in response to GI, with domains related to WRKY and MAPK (Mitogen-Activated Protein Kinase) cascades represents the essential role in signaling cascades in response to the attack of RKN. The work presented here is one of those multiple efforts focusing on improving a common bean cultivar-resistant to the RKN; the power of genomic, bioinformatic, and statistical genetics. These approaches are essential for common bean breeders since they allow the use of QTL information to increase the efficiency of breeding programs.

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