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**ANÁLISES DA EXPRESSÃO DE GENES DO SISTEMA DE SECREÇÃO
NA INTERAÇÃO *Methylobacterium mesophilicum* SR 1.6/6 COM A
PLANTA HOSPEDEIRA**

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RESUMO

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O gênero *Methylobacterium* é composto por bactérias de coloração rósea, metilotróficas (PPFMs) e que podem colonizar endofiticamente a planta. Algumas espécies deste gênero são capazes de promover o crescimento, aumentar a atividade fotossintética da planta hospedeira e reduzir o ataque de patógenos. A linhagem de *M. mesophilicum* SR1.6/6 é uma bactéria isolada de ramos de citros e devido a sua estratégia de interação com a planta hospedeira e com fitopatógenos, tem sido foco de vários trabalhos. Os mecanismos de interação da bactéria com a planta hospedeira ainda não foram elucidados, porém análises transcritômicas e proteômicas mostram que durante a interação com a planta hospedeira ocorre indução de genes relacionados ao estresse e metabolismo, mas a expressão de genes que codificam proteínas associadas o transporte de moléculas envolvidas com interações bióticas e abióticas no ambiente ainda são pouco conhecidos. Portanto, o objetivo do presente trabalho foi avaliar o efeito dos exsudatos da planta hospedeira sobre o crescimento de *M. mesophilicum* SR1.6/6 e avaliar a expressão de 25 genes envolvidos no transporte. Os compostos secretados pela planta hospedeira (milho e citros) foram avaliados por cromatografia líquida acoplada a espectrometria de massas, enquanto a expressão de genes anotados como pertencentes aos sistemas de secreção tipo I, II, V e bomba de efluxo multidrogas (MDR) foram avaliados no primeiro estágio da colonização da planta hospedeira por *M. mesophilicum*, onde a bactéria deve reconhecer os exsudatos secretados pela planta e posteriormente durante a colonização da raiz da planta hospedeira, com formação de biofilme. Foi observado que as plantas avaliadas secretam moléculas semelhantes, mas em concentrações diferentes. Estes compostos foram principalmente açúcares, ácidos orgânicos, outras moléculas orgânicas, aminoácidos e lipídios, os quais induziram um maior crescimento da planta hospedeira. Foi observado também que a expressão dos genes avaliados é regulada pela presença da planta hospedeira e/ou de seus exsudatos. Foi observado que os genes relacionados ao sistema de secreção tipo II, o complexo SEC e as bombas de efluxo de multidrogas são induzidos durante a interação com as plantas hospedeiras, enquanto genes do sistema de secreção dependente de TAT foram reprimidos. Estes resultados sugerem que durante a interação *M. mesophilicum*-planta, os exsudatos da planta promovem o crescimento desta bactéria endofítica, a qual regula diferencialmente a expressão de genes responsáveis pelo transporte de moléculas.

Palavras-chave: Bactéria metilotrófica. Exsudatos. Expressão gênica. PCR em tempo real. Interação planta-micro-organismo.

ABSTRACT

SALGUERO LONDOÑO, J. K. **Gene expression analysis of secretion system during interaction of *Methylobacterium mesophilicum* SR 1.6/6 with the host plant.** 2015. 113 p. Master thesis (Microbiology) – Instituto de Ciências Biomédicas, Universidade de São Paulo, São Paulo, 2015.

Methylobacterium genus is composed by pink-pigmented facultative methylotrophic bacteria that are able to promote plant growth, increase photosynthetic activity of the host plant and reduce the incidence of pathogens. The *M. mesophilicum* strain SR1.6/6 is a bacterium isolated from citrus and due the interaction with the host plant has been the focus of several studies. The mechanisms of interaction of the bacterium with the host plant have not yet been elucidated, some transcriptomic and proteomic studies show the hyper-regulation of genes related to stress in the plant interaction. Therefore, this project evaluated the expression of some genes related to the codification of protein secretion system that could be involved in *M. mesophilicum*-corn (*Zea miz*) and citros (*Citrus sinensis*) interaction during the colonization of this bacterium through the recognition of root exudates compounds released by the host plant. In this work, we evaluated the bacterial cells adhered to the roots forming biofilm and bacterial cells in suspension (planktonic-celled cells interacting only with root exudates) compared to control (bacterial cells without plant). For expression analysis, genes that encode protein from secretion system (type I, II, V and VI), multidrug efflux pumps and ABC transporters related to proteins transporters were evaluated by qPCR. Then, the *M. mesophilicum* SR1.6/6 genome was reevaluated and genes related to transport systems (type I, II and V protein secretion system, multidrug efflux pumps and related ABC transportes, general secretory pathway SEC dependent and twin arginine translocase system (TAT)) which allow the export, extrusion and translocation of effector molecules during interaction with the host plant. The exsudates released by the host (mayze and citrus) roots, identified by gas chromatography mass spectrometry (GC-MS), are composed mainly by sugars, organic acids, organic compounds, aminoacids and lipids. Analysis of the gene expression showed that during interaction with corn and *citrus* type II secretion system, SEC complex and multidrug efflux pumps were up-regulated while TAT pathway was down-regulated, suggesting a differential activation of secretory machinery for translocation of protein during the interaction between *M. mesophilicum* SR1.6/6 and the host plant.

Keywords: Methylothetic bacteria. Root exsudates. Gene expression. qPCR. Plant-bacteria interaction.

INTRODUÇÃO

O gênero *Methylobacterium* é composto por bactérias de coloração rósea, metilotróficas (PPFMs) capazes de se estabelecer em diferentes nichos na planta hospedeira. Em associação com a planta, algumas espécies deste gênero são capazes de promover o crescimento vegetal, aumentar a atividade fotossintética e reduzir o ataque de patógenos ao hospedeiro. *Methylobacterium* spp. podem estar envolvidas na formação de nódulos e fixação de nitrogênio em fabáceas (leguminosas), além de produzir os reguladores vegetais auxina e citocinina e induzir resistência sistêmica. Este gênero tem despertado grande interesse científico pelo fato de possuir potencial para síntese de produtos biotecnológicos de alto valor agregado como o polihidroxiacetato (PHA) e polihidroxiacrilato (PAA). *M. mesophilicum* SR1.6/6 foi isolada de ramos de citros e devido à interação com diversas plantas hospedeiras e possivelmente *Xylella fastidiosa*, tem sido foco de vários estudos nas áreas de genômica, proteômica e transcritômica.

A compreensão dos mecanismos moleculares envolvidos na interação planta-*Methylobacterium* se torna uma estratégia cada vez mais relevante no panorama da agricultura atual, visto que a compreensão dos processos envolvidos na colonização da planta hospedeira pelo endófito permite estabelecer os mecanismos de respostas da planta, incluindo alterações fisiológicas associadas ao aumento da produtividade agrícola. Entre estes mecanismos, cabe ressaltar a secreção de proteínas ou moléculas requeridas para o reconhecimento, adesão e invasão dos tecidos do hospedeiro por parte da bactéria endofítica. Sabe-se que o estabelecimento da interação entre a planta hospedeira e micro-organismos do solo inicia quando os exsudados da planta são reconhecidos por esta microbiota, a qual leva a ativação de genes que codificam proteínas importantes durante a interação, incluindo proteínas envolvidas com transporte e secreção de moléculas.

Neste contexto, o presente projeto visa avaliar a influência dos exsudatos de citros (*Citrus sinensis*) e milho (*Zea mays*) no crescimento e expressão de genes associados ao transporte de *M. mesophilicum* SR1.6/6. Para isso, os exsudatos da planta foram avaliados por cromatografia líquida acoplada ao espectrômetro de massa, e o seu efeito sobre o crescimento de *M. mesophilicum* avaliado. Além disso, genes envolvidos com transporte foram reanotados no genoma de *M. mesophilicum* SR1.6/6 e a sua expressão avaliada por PCR quantitativo.

CONCLUSÕES

Os resultados obtidos no presente trabalho permitem concluir que:

- Em cultura *in vitro*, plântulas de milho e citros, por meio do seu sistema radicular, secretam açúcares, aminoácidos, lipídios e outros compostos orgânicos que poderiam ser utilizados por micro-organismos presentes na rizosfera;

- Os exsudados liberados pelas raízes de citros e milho, independentes da presença da plântula, induzem um aumento no crescimento de *M. mesophilicum* SR1.6/6 em condições de laboratório;

- A cultura bacteriana na presença das plântulas de milho e soja alcançam uma maior densidade celular, quando comparado à cultura apenas com os exsudados sem as plântulas;

- *M. mesophilicum* SR1.6/6 apresenta os sistemas de secreção do tipo I, II e Va, além da maquinaria de translocação via SEC ou TAT e bombas de efluxo multidrogas para o transporte, translocação e exportação de moléculas efetoras

- A análise da expressão de genes que codificam proteínas de transporte demonstrou que ocorre regulação diferenciada (indução ou repressão) destes genes durante a interação com a planta;

- Durante a interação física (superfície ou interior dos tecidos vegetal) da bactéria com a planta, ocorre preferencialmente uma indução destes genes de transporte;

- Os resultados indicam que os sistemas de transporte são importantes para o estabelecimento da interação entre *M. mesophilicum* SR1.6/6 e a planta hospedeira.

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