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Transcriptome and Proteome Profiling for Analyzing Fates of Global Gene Expression in Plant-Beneficial Bacilli

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Bacteria that are associated with plant roots and exert beneficial effects on plant development are referred to as plant-growth-promoting rhizobacteria (PGPR) [1]. In many cases, their plant-growth-promoting activity is linked with their ability to suppress soil-borne plant pathogens. Besides production of antimicrobial and nematocidal compounds, also stimulation of plant-induced systemic resistance (ISR) and subtle pathogen-biocontrol interactions contribute to their suppressive effects [2]. In course of the last twenty years or so, PGPR have been successfully applied to a wide range of agricultural species to enhance their yield and to avoid harvest damages caused by plant pathogens in a environmentally friendly way. Plant-associated Bacilli are preferred in this context due to their ability to produce heat-resistant and durable endospores ensuring a long shelf life of the respective bioformulation [3]. In order to improve the beneficial action of those bioformulations on plant development it is highly important to understand the interactions of the applied bacterium and their host plant on the molecular level. In recent years, transcriptome-and proteome-analysis have been proven as efficient in enlarging our knowledge base in this topic. The first global study about gene expression in *Bacillus* using DNA-microarrays and 2-D protein gel electrophoresis was performed in 2001 using the laboratory model strain *B. subtilis* 168 [4]. The same model bacterium was used to analyze the global gene response against salicylic acid, an important plant signal compound. Proteome and transcriptome analysis indicated that protein destruction due to salicylic acid led to induction of detoxifying phenolic acid decarboxylases [5]. A DNA microarray supported transcriptome analysis of *B. subtilis* OKB105, a derivative of *B. subtilis* 168 with a restored ability to synthesize surfactin and other nonribosomal secondary metabolites, revealed that 176 genes were differentially expressed after exposing the *Bacillus* cells to rice seedlings. Most of them are likely to be involved in plant-bacteria interactions [6]. In recent years; several studies were performed with plant-associated *B. amyloliquefaciens* FZB42, a plant growth promoting bacterium with industrial importance [3]. A first transcriptome analysis about gene expression in response to maize root exudates revealed that majority of the genes possibly involved in plant plant-bacterium interactions was up-regulated when FZB42 was exposed to root exudates [7]. Extracellular proteome maps of FZB42 generated during the late exponential and stationary phase suggested that *B. amyloliquefaciens* protects plants against disease by eliciting innate immunity. Interestingly, the protein with the highest fold change in the presence of maize root exudates was acetoacetate synthase, an enzyme involved in the synthesis of the volatile acetoin, known as an inducer of systemic resistance against plant pathogens and as trigger of plant growth [8]. The effect of root exudates collected from maize plants grown under nitrogen (N), phosphate (P), iron (Fe) and potassium (K) deficiencies on the transcriptome of FZB42 was evaluated. Exudates from N-deprived maize triggered a general stress response in FZB42 in the exponential growth phase, which was evidenced by the suppression of numerous genes involved in protein synthesis. Global transcriptional changes in FZB42 elicited by nutrient deficient maize exudates were significantly correlated with concentrations of the amino acids aspartate, valine and glutamate in root exudates [9]. Plants colonized by root-colonizing *Bacilli* are affected in their gene expression pattern. Transcript profiling of *Brassica* seedlings primed with *B. amyloliquefaciens* revealed that a systemic gene expression in leaves was provoked by the bacterium [10]. Similar to FZB42, the environmental *B. subtilis* FB 17 acts as a beneficial rhizobacterium. When exposed to *Arabidopsis* roots it affects gene expression in the host plant. Genes up-regulated include auxin-regulated genes as well as genes involved in metabolism, stress response, and plant defense [11]. Taken together, value of global gene expression studies on the transcript and protein level for a deeper understanding of interactions between beneficial Bacilli and their host plants has been impressively verified. It is to expect that in future, analysis of the primary transcriptome by the differential RNA-seq (dRNA-seq) approach [12] will become crucial for analysing the global gene response of plant-associated Bacilli during colonizing plant roots.

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