

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

Rainer Borriss*

Section Phytomedicine, Albrecht Daniel Thaer - Institute of Agricultural and Horticultural Sciences, Faculty of Life Sciences, Humboldt University, Berlin, Lentzeallee 55-57, 14195, Berlin, Germany

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 an 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.

References

1. Kloepper JW, Leong J, Teintze M, Schroth MN (1980) Enhancing plant growth by siderophores produced by plant growth-promoting rhizobacteria. *Nature* 286: 885-886.
2. Haas D, Defago G (2005) Biological control of soil-borne pathogens by fluorescent *Pseudomonas*. *Nat Rev Microbiol* 3: 307-319
3. Borriss R (2011) Use of plant-associated *Bacillus* strains as biofertilizers and biocontrol agents in agriculture. In: Maheshwari DK (ed.) *Bacteria in Agrobiology: Plant Growth Responses*. Springer Heidelberg pp. 41-76.
4. Yoshida K, Kobayashi K, Miwa Y, Kang CM, Matsunaga M, et al. (2001) Combined transcriptome and proteome analysis as a powerful approach to study genes under glucose repression in *Bacillus subtilis*. *Nucleic Acids Res* 29: 683-692.
5. Duy NV, Mäder U, Tran NP, Cavin JF, Tam le T, et al. (2007) The proteome and transcriptome analysis of *Bacillus subtilis* in response to salicylic acid. *Proteomics* 7: 698-710.
6. Shanshan X, Wu H, Chen L, Zang H, Yongli Xie Y, et al. (2015) Transcriptome profiling of *Bacillus subtilis* OKB105 in response to rice seedlings. *BMC Microbiology* 15: 21
7. Fan B, Carvalhais LC, Becker A, Fedoseyenko D, Von Wirén N, et al. (2012) Transcriptomic profiling of *Bacillus amyloliquefaciens* FZB42 in response to maize root exudates. *BMC Microbiol* 12: 116.
8. Kierul K, Voigt B, Albrecht D, Chen XH, Carvalhais LC, et al. (2015) Influence of root exudates on the extracellular proteome of the plant-growth-promoting bacterium *Bacillus amyloliquefaciens* FZB42. *Microbiology* 161: 131-47.
9. Carvalhais LC, Dennis PG, Fan B, Fedoseyenko D, Kierul K, et al. (2013) Linking plant nutritional status to plant-microbe interactions. *PLoS One* 8: e68555.
10. Sarosh BR, Danielsson J, Meijer J (2009) Transcript profiling of oilseed rape

*Corresponding author: Rainer Borriss, Section Phytomedicine, Albrecht Daniel Thaer - Institute of Agricultural and Horticultural Sciences, Faculty of Life Sciences, Humboldt University, Berlin, Lentzeallee 55-57, 14195 Berlin, Germany, Tel: +49 30 2093 46444; E-mail: rainer.borriss@rz.hu-berlin.de

Received May 05, 2015; Accepted May 16, 2015; Published May 19, 2015

Citation: Borriss R (2015) Transcriptome and Proteome Profiling for Analyzing Fates of Global Gene Expression in Plant-Beneficial Bacilli. *Transcriptomics* 3: e110. doi:10.4172/2329-8936.1000e110

Copyright: © 2015 Borriss R. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

(*Brassica napus*) primed for biocontrol differentiate genes involved in microbial interactions with beneficial *Bacillus amyloliquefaciens* from pathogenic *Botrytis cinerea*. *Plant Mol Biol* 70: 31-45.

11. Lakshmanan V, Castaneda R, Rudrappa T, Bais HP (2013) Root transcriptome analysis of *Arabidopsis thaliana* exposed to beneficial *Bacillus subtilis* FB17

rhizobacteria revealed genes for bacterial recruitment and plant defense independent of malate efflux. *Planta* 238: 657-68.

12. Sharma CM, Hoffmann S, Darfeuille F, Reignier J, Findeiss S, et al. (2010) The primary transcriptome of the major human pathogen *Helicobacter pylori*. *Nature* 464: 250-255.

Citation: Borriss R (2015) Transcriptome and Proteome Profiling for Analyzing Fates of Global Gene Expression in Plant-Beneficial Bacilli. *Transcriptomics* 3: e110. doi:[10.4172/2329-8936.1000e110](https://doi.org/10.4172/2329-8936.1000e110)

OMICS International: Open Access Publication Benefits & Features

Unique features:

- Increased global visibility of articles through worldwide distribution and indexing
- Showcasing recent research output in a timely and updated manner
- Special issues on the current trends of scientific research

Special features:

- 700+ Open Access Journals
- 50,000+ editorial team
- Rapid review process
- Quality and quick editorial, review and publication processing
- Indexing at major indexing services
- Sharing Option: Social Networking Enabled
- Authors, Reviewers and Editors rewarded with online Scientific Credits
- Better discount for your subsequent articles

Submit your manuscript at: <http://www.omicsonline.org/submission/>