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Endophytic plant growth promoting bacteria may have significant impact on both the plant physiology and the composition of the plant microbiome. Many different bacterial species proved to induce these plant growth-promoting effects on a variety of plant species. However, regulatory pathways of beneficial effects are still questionable. We described the strain *Enterobacter radicincitans* sp. nov. (DSM 16656) as a new species of the genus *Enterobacter*, inducing growth promotion of root and shoot along with increased yield, by inoculation of various crop and model plant species. Genome sequencing of *E. radicincitans* was performed to unravel underlying molecular mechanisms of observed beneficial effects in host plants. The complete *nif* operon is present and the genome sequence indicates phytohormone production with genes for indole-3-acetaldehyde synthesis and an auxin efflux carrier. Current efforts aim at comparing protein patterns of plant leaves and roots in response to bacterial colonisation. We have selected genetically different *Arabidopsis thaliana* accessions that show the same growth promotion upon inoculation with *E. radicincitans*. These lines are now under investigation in order to identify specific proteomic responses to the endophyte.

P005

Analysis of the liver proteome in response to a genetic divergence in feed efficiency in growing pigs

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The functionality of the liver, a highly specialized organ with a wide range of functions including detoxification, protein synthesis and energy metabolism, may be altered by selection of growing animals for feed efficiency. In this study, three groups of pigs originating from a divergent selection experiment on residual feed intake (RFI) were used. To gain insight on the main pathways represented in the pig liver, an Isotope-Coded Protein Label (ICPL) triplex technology followed by GeLC-MS-MS on a nanoLC-ESI-ion trap mass spectrometer was first applied to porcine hepatic proteins. Then, a comparative quantification ($n = 4$ pigs per group) was performed by two-dimensional gel electrophoresis (2-DE) followed by a MALDI-TOF/TOF analysis.

A total of 246 non-redundant proteins participating to fatty acid catabolism, nitrogen compound biosynthetic process, generation of precursor metabolites and energy, glucose metabolic process, urea cycle, amino-acids metabolisms, anti-apoptosis, or anti-oxidant activity were identified using the ICPL triplex method. Only 19% of these proteins can be quantified, due to the low representation of lysine residues or the presence of modified lysine. After 2-DE, 30 identified proteins had a differential abundance between less and more efficient pigs. Members of the peroxiredoxin family and the superoxide dismutase (SOD)-1 responsible for destroying free superoxide radicals notably had a greater abundance in the most efficient pigs. When the less efficient pigs were feed-restricted, an increased abundance of the peroxiredoxins and glutathione-S transferase involved in detoxification was observed. Together, selection for feed efficiency may have modified the redox state of the animals.

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P006

Functional analysis of the chloroplast antioxidant enzymes in *Arabidopsis thaliana* accessions

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