

Transcriptome and proteome analysis provides insights in metabolic key features of ‘*Candidatus Phytoplasma mali*’

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'*Candidatus Phytoplasma mali*' is the causative agent of apple proliferation, which is one of the most economically important phytoplasma diseases in Europe. Infection results in low fruit quality and reduced productivity of trees. Knowledge on expression of '*Ca. P. mali*' focussed on a few selected genes so far. Here, we provide first insights in the transcriptome and proteome of '*Ca. P. mali*'.

Nicotiana occidentalis plants infected by '*Ca. P. mali*' strain AT (showing chlorosis, small leaf formation and decline) were used for RNA and protein extraction from leaf midribs. Obtained RNA was treated by rRNA-depletion, DNase digest and obtained RNA used as template for RNA-Seq (Illumina) resulting in above 17 million reads. RNA-Seq data were mapped on the bacterial genome using CLC Genomics Workbench.

Protein content was separated via SDS-Page and divided into 16 sections followed by tryptic digest. Samples were analysed by LC-MS/MS and assigned to the deduced protein content of '*Ca. P. mali*' using MaxQuant software package.

Transcripts of around 130 predicted genes were identified by RNA-Seq and around 100 proteins by mass spectrometry. A non-redundant set of around 200 expressed genes of '*Ca. P. mali*' was identified. Expressed genes were analysed according to their assignment to categories in the protein database of Clusters of Orthologous Groups, their cellular location and their impact on bacterial metabolism. This analysis provides new insights into the metabolism of phytoplasmas.