

ACARI MICROBIOTA AND PREDICTION OF METABOLIC PATHWAYS

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Tetranychoida mites are important pest of several crops because of their feeding habits or transmission of pathogens. Microbiota studies of mites are bringing new understanding of mite-microbial interactions as part of the wide range of strategies adopted by these arthropods to colonize and succeed in complex environments. Here we present initial data on fungi microbial diversity associated with four different strains of phytophagous mite vector *Brevipalpus*. The study of arthropod bacteriomes by means of Next Generation Sequencing (NGS) is opening opportunities for the development of unique pest management approaches. Emerging studies on the mite mycobiome certainly will also improve our understanding of the balance of microbial communities, providing new insights to better manage pest populations. Taxa belonging to the skin-specialist genus *Malassezia* were predominant among NGS identified Operational Taxonomic Units in *Brevipalpus*. In Tetranychoida mites, the presence of the endosymbiont bacterium *Cardinium* represents a starting point for pest management research because of its effects in the mites' reproduction, and metabolic traits yet to be discovered, that could be potential new targets. In this study, we used our previously published sequencing data on the 16S Ribosomal RNA from the microbiome bacteria in *Brevipalpus yothersi*, *Raoiella indica*, and *Oligonychus* sp.. With these sequences and the pipeline PICRUSt, we predicted the content of genes with metabolic function in the bacteriome of the mites. Our results indicate that the bacteriomes of *B. yothersi* and *Oligonychus* sp. (which harbor *Cardinium*) contain significantly more genes involved in the metabolism of indole-alkaloids, glutamine, and biotin when compared with *R. indica* (no *Cardinium*). The genes for metabolism of biotin and nicotinate are also more abundant in adult *B. yothersi* and *Oligonychus* sp. than in their eggs. This is associated with lower abundance of *Cardinium* in the eggs. The metabolic specialization of *Cardinium*-dominated bacteriomes could also lead to lack of resistance to β -lactam antibiotics and DDT. While these results are predictive, they highlight the necessity of testing these variations in laboratory.

Keywords: False-spider mite, Acari metabolism, *Cardinium*, antibiotic resistance, amino acid metabolism.

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