
Metagenomics of insect-symbiont interactions

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Abstract

Prolonged associations between microbes and eukaryotic hosts are widespread. This is particularly true for insects which are engaged in multiple forms of interactions with microorganisms. Many arthropods have established intimate and mutualistic partnerships with obligate symbionts which generally supplement the host's diet in key nutrients. Although not essential for their host's reproduction and survival, facultative symbionts are also very common in insects and may have profound impacts on host ecology, physiology and behavior. Until recently, the exploration of insect symbiont diversity was limited by the use of taxon-specific detection techniques or DNA-limiting, time consuming and low throughput methods. The development of new sequencing techniques and bioinformatic tools now permits to assess without *a priori* the diversity and structure of insect microbial communities to better understand the influence of microbes on their host populations and vice versa. Here, we present scientific and methodological advances on aphid-symbiont interactions based on metagenomic approaches. In particular, we showed how resequencing data from individual or pooled host genomes can be used to characterize associated microbial communities at different levels of diversity and to highlight the evolutionary dynamics of symbiotic partnerships.

Keywords: symbiosis, microbes, aphids, metagenomics, diversity

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