

## Symbiosis: Insect-Microorganism Interaction and the Need of Life to Two

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Insect-associated microbiota plays an important role both in beneficial interactions and in pathological interactions [1-3]. Recent genomic studies confirm that insects do not have the complete metabolic repertoire that makes it possible to extract the nutrients of food with maximum efficiency, and depend greatly on the associated microbiota [4-6].

The insects have very uniform nutritional needs, however, they have a very diversified diet [7]. Within the Insecta class we can find specific predators, herbivores and scavengers specialists who use nectar, pollen, plant sap, fungi, skin and blood [7,8]. The ability of insects to adopt certain nutritional lifestyles is not only due to it but to a symbiotic relationship between the insect and microorganisms associated with different biosynthetic and degrading capacities [7,9].

Hansen e Moran (2014) Described endosymbiont bacteria that play an important role in the synthesis of essential nutrients for the insect, such as the use of nitrogenous residues by termites, cockroaches and hemiptera as a consequence of the metabolism of *Bacteroides* and *Citrobacter*. Some bacteria are efficient in fixing atmospheric nitrogen, and the insect-associated microorganisms that have this capacity allow the host a diet with nitrogen supply, as in *Ceratitidis capitata* (fruit fly) in association with intestinal enterobacteria [10-11].

The symbiotic interaction between sap-sucking insects and microorganisms has become indispensable because of the limited metabolism of some insects, in particular because of their inability to synthesize amino acids [7]. Experimental evidence indicates that *Buchnera aphidicola* synthesizes essential amino acids and provides these amino acids for the pea aphid (*Acyrtosiphon pisum*). These results were confirmed by complete annotation of the genome of *B. aphidicola*, revealing that this bacterium has the genetic ability to synthesize these nutrients [8].

Shi, *et al.* (2010) described the production and availability of B-complex vitamins by endosymbiont bacteria. The genome of *Wigglesworthia*, a bacterium endosymbionts of *Glossina brevipalpis*, showed the presence of genes encoding the synthesis of pantothenate (vitamin B<sub>5</sub>), biotin (vitamin B<sub>7</sub>), thiamine (vitamin B<sub>1</sub>), riboflavin (vitamin B<sub>2</sub>), pyridoxine B<sub>6</sub>), nicotinamide (vitamin B<sub>3</sub>) and folic acid (vitamin B<sub>9</sub>) [12].

Steroids can be made available by endosymbiont fungi, once insects cannot produce steroids due to the lack of the enzyme needed to form the steroid nucleus. In insects, steroids are harnessed as hormone precursors and in cellular structure [7,9].

Many studies have described the synthesis of essential nutrients by microorganisms, however, these symbiotic microorganisms can also act in food processing [7]. The mechanical breakdown of cellulose by chewing insects increases the viability of cellulose by the enzymes. Douglas (2009) evidenced the symbiotic relationship between termites (*Nasutitermes takasagoensis* e *N. walkeri*) and intestinal bacteria with cellulolytic capacity (Douglas, 2009). Analysis of metagenomics data identified cellulase and xylanase genes from members of the gut microbiota of *Nasutitermes* sp. [8].

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The intestinal microorganisms of herbivorous insects may also play detoxifying role of host plant compounds [8]. Studies on soybean caterpillar *Anticarsia gemmatalis* (Lepidoptera: Noctuidae) and other soybean herbivores have shown that survival and growth of caterpillars were better when intestinal bacterial communities were intact, suggesting a beneficial role of the microbiota [13,14]. Studies with *Helicoverpa armigera*, a potent pest of soy, maize and cotton, have shown that in addition to aiding in food efficiency, the diversity of its bacterial community is induced by the host plant [4,15]. Jia, *et al.* (2013) evaluated the impact of temperature change on the microbial community associated with the red palm weevil (*Rhynchophorus ferrugineus*) and concluded that extreme changes caused by different seasons of the year caused a drastic change in the profile of the microbial community of this beetle [9].

Studies on bacterial diversity associated with insects are growing rapidly but still lacking information from some important groups of insects (e.g. leptoferos). Advances in the diversity and identity of the native complex microbial communities of the insect gut have been possible due to recent advances in molecular biology techniques, including Next-Generation Sequencing (NGS). Thus, these studies have contributed to form the concept of Microbiome, in which these microorganisms form a fundamental part of the functional genomic repertoire of the insect due to its influence on the physiology of the host [4].

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