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A review on Metagenomic analysis of insect pests

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Abstract

In order to comprehend microbial ecology, metagenomics research has evolved over the past ten years to clarify the genomes of uncultured bacteria. The relevance of the insect-associated microbial communities from an ecological and monetary standpoint is why they are currently receiving so much attention. The tremendous impact that microorganisms have on their host partner has been studied. This impact can be either direct, facilitating relationships with other species, or indirect, affecting the genetic diversity of the host. Additionally, microorganisms can support insects by protecting them from natural adversaries, counteracting host plant defence systems, influencing reproduction, and enabling them to thrive on diets low in nutrients. With the advent of metagenomic tools, the study of host-microorganism interactions has recently garnered a lot of attention. Insect-microbe connections can also be changed to enhance pest control by lowering pest efficiency or enhancing the effectiveness of pest management strategies.

Keywords: Metagenomics, insect, host-microorganisms interaction, pest

Introduction

The study of metagenomics is summarized as the genomic sequencing of all the microorganisms in a particular biological niche without regard to culture (Handelsman *et al.*, 1998) [4]. In its basic form, metagenomics involves the direct isolation of DNA from a specified environment, followed by the cloning of the whole genomes of the entire microbial population in that habitat (Langer *et al.*, 2006) [7]. The generated DNA library is then examined for interesting functions and sequences.

The most successful group of organisms in terms of diversity and capacity to endure in different ecological niches are insects. According to estimates, gut of an insect has 100 times as many microbial genes as animal genes and 10 times as many bacteria as the insect's total number of cells (Rajagopal, 2009) [10].

Insect genomics began in 2000 with the sequencing of the fruit fly *Drosophila melanogaster* whole genome (Adams *et al.* 2000; Myers *et al.* 2000) [1, 9]. With the completion of more than 30 additional whole genome sequences and more than 2 million ESTs, new genomic research on insect mapping has effectively categorised insects as the most varied group of species on earth (Behura 2006) [2].

Agriculture places a significant emphasis on the research of microbial communities associated with insects, primarily because insects are pests. The potential of the insect gut microbiome has also recently received attention in fields like biotechnology, as some bacteria and fungus represent a reservoir of genes for antibiotic resistance (ARGs). Most research to date has focused on defining the role have been predicated on high-throughput sequencing of the insects' gut microbiomes. Metagenomics and/or the 16S rRNA gene (Munoz *et al.*, 2021) [8]. The following discussion provides a glimpse into the metagenome analyses of some of the most significant insect pests in the world.

Metagenomic analysis of insect pests

1. Diamond backmoth

One of the most damaging insect pests plaguing cruciferous vegetables, including cabbage, broccoli, and cauliflower, all over the world is the diamondback moth, *Plutella xylostella* (L.) (Lepidoptera: Plutellidae). Taxonomic profiling of the metagenome indicated that the *P. xylostella* microbiota was dominated by Proteobacteria followed by Firmicutes. More than 97% of the bacteria in the total DBM microbiota, according to the first research on high-throughput DNA sequencing dominated by Enterobacteriales (Proteobacteria) Lactobacillales (Firmicutes). In comparison to the susceptible strain, the study's lines that were resistant to chlorpyrifos and fipronil had more Lactobacillales, the considerably scarcer taxa

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Pseudomonadales and Xanthomonadales, and fewer Enterobacteriales. This is consistent with the concept that Lactobacillales or other scarcer taxa play a role in giving DBM pesticide resistance (Xia *et al.*, 2013)^[13].

2. Whitefly

One of the polyphagous sucking insect pests, whiteflies, *Bemisia tabaci* (Gennadius), infest more than 900 types of plants and act as a vector for the transmission of more than 200 viral diseases. Based on 16SrDNA next generation sequencing, Shah *et al.*, (2020)^[11] identified 50 known and 7 unknown genera of bacteria belonging to 10 phyla, 20 classes, 30 orders, and 40 families. These bacteria were found in wild adult *B. tabaci* infesting cotton plants in eight major cotton growing districts of southern Punjab, Pakistan. The most prevalent phylum was Proteobacteria, followed by Bacteroidetes, Firmicutes, and Actinobacteria.

Comparative analysis of the endosymbionts discovered in 21 species of the *B. tabaci* complex that have been collected from around the world and two samples of *B. afer* using PacBio sequencing of full-length bacterial 16S rRNA gene amplicons unveils putative bacteria, one of which was Halomonas, first identified in MED *B. tabaci* (Indiragandhi *et al.*, 2010)^[6]. Similar to this, fresh Rickettsia and Arsenophonus secondary endosymbiotic strains were also discovered in association with whitefly samples gathered from various sites (Wang *et al.*, 2019)^[12].

3. Termites

Termites are a serious threat to many types of agricultural products, buildings, especially those made of wood, and human civilization as a whole. The higher termites could digest lignocellulose in various stages of humification with the aid of a variety of symbiotic prokaryotic microbiota hosted in their compartmented digestive tract, which is a rich reservoir of bacteria, archaea, and eukarya-related microorganisms. He *et al.* (2013)^[5] revealed the metagenomic profiling of the hindgut pouches of termites wood feeding termites (*Amitermes wheeleri*) and dung feeding termite (*Nasutitermes corniger*) based on 16S rRNA pyrosequencing and showed that Firmicutes and Spirochaetes were the most prevalent phyla in *A. wheeleri*, in contrast to *N. corniger* where Spirochaetes and Fibrobacteres predominated. Additional functional research showed that the microbiota linked to *A. wheeleri* were involved in hemicellulose breakdown and fixed-nitrogen consumption, whereas those linked to *N. corniger* had glycoside hydrolases targeting celluloses and genes for nitrogen fixation.

Of a similar vein, Grieco *et al.* (2019)^[3] study of the complete gut microbiota in seven species of termites (Termitidae) from four different regions in Brazil using metagenomic analysis showed that the bacteria in termite species that feed on litter belong to the phylum Firmicutes While Proteobacteria-related bacteria were prevalent in the termite species that feed on humus. All four subfamilies of termites that were studied have a similar functional carbohydrate-active enzyme profile that was specialized for the breakdown of cellulose and chitin.

Conclusion

Modern molecular technologies and bioinformatic tools now able to explore and finely investigate the insect microbial communities and their interaction with their hosts represent an alternative way to protect our crops.

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Conflict of Interest: None

References

- Adams MD, Celniker SE, Holt RA, Evans CA, Gocayne JD, Amanatides PG, et al. The genome sequence of *Drosophila melanogaster*. *Science*. 2000;287(5461):2185-95.
- Behura SK. Molecular marker systems in insects: current trends and future avenues. *Molecular ecology*. 2006;15(11):3087-113.
- Grieco MB, Lopes FA, Oliveira LS, Tschoeke DA, Popov CC, Thompson CC, et al. Metagenomic analysis of the whole gut microbiota in Brazilian Termitidae termites *Cornitermes cumulans*, *Cryptotermes strictinusus*, *Syntermes dirus*, *Nasutitermes jaraguai*, *Nasutitermes aquilinus*, *Grigiotermes bequaerti*, and *Odontotermes mirim*. *Current Microbiology*. 2019;76(6):687-97.
- Handelsman J. Metagenomics: application of genomics to uncultured microorganisms. *Microbiology and molecular biology reviews*. 2004;68(4):669-685.
- He S, Ivanova N, Kirton E, Allgaier M, Bergin C, Scheffrahn RH, et al. Comparative metagenomic and metatranscriptomic analysis of hindgut paunch microbiota in wood-and dung-feeding higher termites. *PloS one*. 2013;8(4):61126.
- Indiragandhi P, Yoon C, Yang JO, Cho S, Sa TM, Kim GH. Microbial communities in the developmental stages of B and Q biotypes of sweetpotato whitefly, *Bemisia tabaci* (Hemiptera: Aleyrodidae). *Journal of the Korean Society for Applied Biological Chemistry*. 2010;53(5):605-17.
- Langer M, Gabor EM, Liebeton K, Meurer G, Niehaus F, Schulze R, et al. Metagenomics: An inexhaustible access to nature's diversity. *Biotechnology Journal: Healthcare Nutrition Technology*. 2006;1(7- 8):815-21.
- Munoz-Benavent M, Perez-Cobas AE, Garcia-Ferris C, Moya A, Latorre A. Insects' potential: understanding the functional role of their gut microbiome. *Journal of Pharmaceutical and Biomedical Analysis*. 2021;194:113787.
- Myers EW, Sutton GG, Delcher AL, Dew IM, Fasulo DP, Flanigan MJ, et al. A whole-genome assembly of *Drosophila*. *Science*. 2000;287(5461):2196-204.
- Rajagopal R. Beneficial interactions between insects and gut bacteria. *Indian Journal of Microbiology*. 2009;49:114-119.
- Shah SH, Malik AH, Zhang B, Bao Y, Qazi J. Metagenomic analysis of relative abundance and diversity of bacterial microbiota in *Bemisia tabaci* infesting cotton crop in Pakistan. *Infection, Genetics and Evolution*. 2020;84:104381.
- Wang HL, Lei T, Xia WQ, Cameron SL, Liu YQ, Zhang Z, et al. Insight into the microbial world of *Bemisia tabaci* cryptic species complex and its relationships with its host. *Scientific Reports*. 2019;9(1):1-5.
- Xia X, Zheng D, Zhong H, Qin B, Gurr GM, Vasseur L, et al. DNA sequencing reveals the midgut microbiota of diamondback moth, *Plutella xylostella* (L.) and a possible relationship with insecticide resistance. *PloS one*. 2013;8(7):e68852.