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Exploring Genomic Traits of a Midgut Bacterial Symbiont of the Stinkbug Acrosternum arabicum (Hem., Pentatomidae)

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Abstract: Phytophagous pentatomid insects can negatively impact agricultural productivity and the Acrosternum arabicum (Hem.: Pentatomidae) as a pistachio green stink bug can cause kernel necrosis, falling of fruits and transmit the fungal pathogen Nematospora coryli Peglion. Researches are being conducted to understand its biology and to find management solutions, but its symbiotic relationship with gut symbionts, as one aspect of its biology, is not understood. In this study, the contribution of symbiotic bacteria to A. arabicum was inferred using genomic analyses. The Next Generation Sequencing (NGS) was performed and total DNA was sequenced on an Illumina – HiSeq X 2500 instrument. The sequencing produced 43.17 million read pairs of 150 bp that were assembled using SPAdes 3.10 [1] generating 745,758 contigs. This preliminary assembly was subjected to the Blobology pipeline [2], using Bowtie2 [3] to map the reads to the obtained contigs. GC content, readcoverage, and taxonomic information were visualized by the ggplot2 graphics library [4] in R. The obtained blobplot was then reviewed, and the putative symbiont contigs were selected, and the corresponding reads were extracted. Finally, the putative symbiont reads were assembled using SPAdes 3.10 to obtain the final symbiont assembly. Chromosome and plasmid sequences were annotated using Prokka [5], and annotation was manually curated. The bioinformatic pipeline allowed to obtain a 2.9 Mb draft genome of the A. arabicum symbiont, which resulted to belong to the genus Pantoea. Using an annotation procedure, we found a high number of pseudogenes and multiple genes encoding functions that are potentially host-supportive. The reported findings detail genomic features of the A. arabicum symbiont and illustrate the importance of bacterial symbiont in host fitness.

Keywords: Next generation sequencing; gammaproteobacteria; pentatomid; Pantoea genus

References

- [1] S. Nurk *et al.*, "Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products," *J. Comput. Biol.*, vol. 20, no. 10, pp. 714–737, 2013.
- [2] S. Kumar, M. Jones, G. Koutsovoulos, M. Clarke, and M. Blaxter, "Blobology: exploring raw genome data for contaminants, symbionts and parasites using taxon-annotated GC-coverage plots," *Front. Genet.*, vol. 4, no. November, pp. 1–12, 2013.
- [3] Langmead, "Bowtie2," *Nat. Methods*, vol. 9, no. 4, pp. 357–359, 2013.
- [4] H. Wickham, *Ggplot2: Elegant Graphics for Data Analysis*. New York: Springer, 2009.
- [5] T. Seemann, "Prokka : rapid prokaryotic genome annotation," vol. 30, no. 14, pp. 2068–2069, 2014.