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Microbial Community Composition Reveals Spatial Variation and Distinctive Core Microbiome of the Weaver Ant *Oecophylla smaragdina* in Malaysia

Kah-Ooi Chua¹, Sze-Looi Song², Hoi-Sen Yong¹, Wah-Seng See-Too¹, Wai-Fong Yin¹ & Kok-Gan Chan^{1,3}

The weaver ant *Oecophylla smaragdina* is an aggressive predator of other arthropods and has been employed as a biological control agent against many insect pests in plantations. Despite playing important roles in pest management, information about the microbiota of *O. smaragdina* is limited. In this work, a number of *O. smaragdina* colonies (n = 12) from Malaysia had been studied on their microbiome profile using Illumina 16S rRNA gene amplicon sequencing. We characterized the core microbiota associated with these *O. smaragdina* and investigated variation between colonies from different environments. Across all 12 samples, 97.8% of the sequences were assigned to eight bacterial families and most communities were dominated by families Acetobacteraceae and Lactobacillaceae. Comparison among colonies revealed predominance of Acetobacteraceae in *O. smaragdina* from forest areas but reduced abundance was observed in colonies from urban areas. In addition, our findings also revealed distinctive community composition in *O. smaragdina* showing little taxonomic overlap with previously reported ant microbiota. In summary, our work provides information regarding microbiome of *O. smaragdina* which is essential for establishing healthy colonies. This study also forms the basis for further study on microbiome of *O. smaragdina* from other regions.

The ant family Formicidae has 17 subfamilies, 333 genera and 13,263 valid species described¹. The tropical forests in Malaysia have the greatest species diversity recorded but most of these ant species are poorly known and understudied². Besides being famous for their developed social organization and behaviour of labour division, ants are known for harbouring complex bacterial community in their body^{3,4}. Many studies have reported consistent association of individual bacterial taxa or whole communities with certain species of ants⁵⁻⁷. It is believed that symbiotic relationships of ants and microorganisms play an integral role in their evolutionary success⁸.

The ant-associated bacterial taxa and whole communities contribute to nutrition, reproduction and other physiological functions of the hosts which in their absence, influence the health and fitness of the insects^{7,9-11}. The first insect endosymbiont *Blochmannia* species was discovered in ant genus *Camponotus* (Mayr, 1861)¹². The intracellular bacteria were shown to give nutritional support to the host by providing essential amino acids which enhance the competitive ability of the host¹³. Apart from endosymbionts, there are also bacterial taxa that interact with ants as ectosymbionts. A famous example is the filamentous bacteria of genus *Pseudonocardia* that are acquired by fungus-growing Attine ants on their cuticle^{14,15}. The group of bacteria produce antibiotics to suppress *Escovopsis*, a genus of virulent microfungus that attacks the basidiomycetous fungi cultivated as predominant food source by Attine ants^{4,15}. Over the years, studies on the microbiome of ants revealed a plenitude of knowledge from ant-microbe interaction. However, as compared to the diversity of the ant family, the studies on their microbiome are still limited, especially the ant species from tropical areas.

¹Institute of Biological Sciences, Faculty of Science, University of Malaya, 50603, Kuala Lumpur, Malaysia. ²Institute of Ocean and Earth Sciences, University of Malaya, 50603, Kuala Lumpur, Malaysia. ³International Genome Centre, Jiangsu University, Zhenjiang, China. Correspondence and requests for materials should be addressed to K.-G.C. (email: kokgan@um.edu.my)