A molecular survey of Australian and North American termite genera indicates that co-evolution is the primary force shaping termite gut microbiomes

Nurdyana Abdul Rahman1, Donovan H. Parks1, Dana L. Willner1, Anna L. Engelbrektson1,5, Shana K. Goffredi3, Falk Warnecke2,6, Rudolf H. Scheffrahn4, Philip Hugenholtz1,2

1Australian Centre for Ecogenomics, School of Chemistry and Molecular Biosciences, The University of Queensland, St Lucia, Queensland, Australia
2DOE Joint Genome Institute, Walnut Creek, CA, USA
3Biology Department, Occidental College, Los Angeles, CA, USA
4Fort Lauderdale Research and Education Center, University of Florida, Davie, Florida, USA
5Current affiliation: Energy Biosciences Institute, University of California, Berkeley, CA, USA
6Current affiliation: Jena School for Microbial Communication (JSMC) and Microbial Ecology Group at Friedrich Schiller University Jena, Jena, Germany

INTRODUCTION

• Termites and their microbial gut symbionts are major recyclers of lignocellulosic biomass1
• This important symbiosis is obligate, but relatively open and more complex in comparison to other well-known insect symbioses such as the strict vertical transmission of Buchnera in aphids2
• Unlike most insects, termite gut communities are relatively complex comprising in the order of hundreds of species3
• The relative roles of co-evolution and environmental factors such as diet in shaping the termite gut microbiome are not well understood

METHODS

SUMMARY

• Co-evolution is the primary force shaping the termite gut microbiome indicating that species are successfully and faithfully passed from one generation to the next via trophallaxis or coprophagy.
• Changes in relative abundance can occur on shorter timescales and appear to be an adaptive mechanism for e.g. dietary fluctuations.

RESULTS

• Genus-level diversity of microbial communities
• Bacterial profiles

Figure 1: Heatmap showing microbial taxa (mostly genus and family level) with relative abundance ≥ 0.2% in one or more whole gut samples surveyed in this study.

Figure 3: UPGMA tree of unweighted (presence/absence only) Soergel pairwise distances between bacterial profiles. The values on interior nodes represent jackknife support values ≥ 49.

Figure 4: Subtrees of host and bacterial community phylogenetic comparisons showing secondary effect of diet on community structure of polyphagous termite genera. When the relative abundance of bacterial OTUs is taken into account (weighted Soergel), samples cluster according to diet. The values on interior nodes of the COII trees are FastTree local support values and jackknife support values ≥ 49 on the Soergel UPGMA trees.

REFERENCES


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