

P061*Co-evolution is the primary force shaping termite gut microbial communities***Nurdyana Abdul Rahman**, Dana Willner, Donovan Parks, Rudolf Scheffrahn, Mark Morrison, Philip Hugenholtz

Termites provide an appealing model system to explore the relative effects of co-evolution and environmental factors on symbiotic gut microbiota as, unlike most insects, their gut communities are relatively complex. Lignocellulosic biomass is digested through an obligate symbiosis with specialized gut microbiota comprising bacteria and protists in lower termites and bacteria only in higher termites. Accordingly, transmission of gut microorganisms between termites is more strictly regulated than in mammals via trophallaxis (oral transmission) or coprophagy and co-speciation with the host has been observed in selected members of the gut community. Despite the successful application of culture-independent techniques on termite gut, very little molecular data exist for Australian termite species. Here, we surveyed the gut microbiomes of 42 Australian and 24 North American termite samples, representing 16 genera, using 16S rRNA amplicon pyrosequencing. These data represent the first gut microbial community profiles for three higher (*Tenuirostritermes*, *Drepanotermes*, *Gnathamitermes*) and two lower (*Marginitermes*, *Porotermes*) termite genera. Microbial community profiles were compared between termite genera, diet and geographical locations. Our molecular survey revealed that while all termite genera shared a distinctive core set of microbial phyla (Bacteroidetes, Firmicutes, Spirochaetes, Proteobacteria), each termite genus had a characteristic set of microbial populations consistent with vertical inheritance. Secondly, relative abundance of these populations reflected dietary preferences. Our findings suggest that co-evolution is the primary force shaping gut communities in termites.