

OR209*Community profiling and metagenomics of Australian termite gut microbiota***Philip Hugenholtz, Nurdyana Abdul Rahman**

Culture-independent molecular techniques are increasingly being applied to termite gut communities revealing novel organisms and functionality in this fascinating habitat. Relatively little molecular data exist for the gut microbiota of Australian termites, so we conducted a 16S rRNA-based survey of 42 samples representing five higher and six lower termite genera. We discovered that co-evolution appears to be the primary force shaping the membership of these communities and that the relative abundance of Archaea is higher (and more variable) than previously reported. We also detected sequences closely related to the ciliate *Nyctotherus* in higher termites consistent with early microscopic observations. We are currently recovering population genomes from metagenomic data via differential coverage binning from a subset of these samples in order to determine the metabolic potential of gut populations of interest.