



Linking phylogenomics, genome evolution and ecology to globally distributed and biosecurity relevant bark and ambrosia beetles (Curculionidae: Scolytinae).

James Bickerstaff (CSIRO Australian National Insect Collection); (Tom Walsh, CSIRO Black Mountain Laboratories) Rahul Rhane (CSIRO Parkville & Applied BioSciences); Jiri Hulcr (University of Florida); Andrew Johnson (University of Florida); Anthony Cognato (University of Michigan); Sarah Smith (University of Michigan); Bjarte Jordal (University of Bergen); Hermes Escalona (CSIRO Australian National Insect Collection).

Scolytinae bark beetles are a globally distributed group of hyperdiverse weevils reliant on host plant tissues to complete their life histories. They engage in a rich array of ecological strategies, including polyphagous host tree preferences, sibling inbreeding and symbiotic associations (notably fungal farming). Multiple primary industries are impacted by bark beetles due to their life histories and they are one of the most frequently translocated insect pests globally. Despite this, few taxonomic and genomic resources exist for this group, and our understanding of the systematics of Scolytinae is plagued by a contentious taxonomic history and few specialists working on the group. Recent phylogenetic analyses have either used a handful of molecular markers to reconstruct a subfamily wide phylogeny or used genome wide markers focussing on specific taxon groups. Using whole genome sequencing data, we assembled draft genomes and reconstructed the phylogeny of Scolytinae, spanning 100 taxa with over 3000 single copy orthologue genes. Our findings suggest over a five-fold difference in genome assembly size variation across species, genera and tribes. This talk will explore genome evolution in the Scolytinae grounded in a phylogenomic framework, how this may be linked to ecological strategies and the implications this has for global biosecurity.

James Bickerstaff: james.bickerstaff@csiro.au