

A phylogeographic role in host-specificity testing – a case study of *Acacia auriculiformis* herbivores

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Summary *Acacia auriculiformis* (Mimosaceae), also known as earleaf acacia, is a native Australian tree that has now become a category 1 invasive weed in Florida, USA. This research focused on identifying and prioritizing potential biocontrol agents against this weed. Field surveys were conducted (2016-2019) in its native range in Australia i.e. Far North Queensland and the Northern Territory (FNQ and NT, respectively). Over 1,000 specimens, from various insect groups, were collected from *A. auriculiformis* and related species (the latter distributed mainly in southern Queensland), and identified by COI DNA barcoding. Two insect groups were identified as highly damaging to the target weed: the leaf-tying caterpillars (mainly belonging to the cosmopterigid genus *Macrobathra*) and chrysomelid beetles identified as *Calomela intemerata*. Phylogenetic

relationships within *Macrobathra* species were reconstructed using Bayesian inference. Seven moth lineages were identified from the 102 specimens sequenced across both FNQ and the NT. Haplotype networks were also constructed for the different lineages involved. The molecular analyses identified a deep genetic disjunction within many species across the Gulf of Carpentaria, a well-known biogeographic barrier. These disjunctions match the spatial genetic disjunction previously found in *A. auriculiformis*. Some of the lineages, mainly those ones sourced from GenBank and BOLD, were also collected beyond the native range of the target weed. Our findings suggest that the phylogenomic and phylogeographic approaches are helpful in addressing some of the key questions regarding the field host range of a potential weed biocontrol agent at the native range survey stage of a program.