Molecular Analysis of Host-Specificity in Plant-Feeding Insects: Phylogenetics and Phylogeography of *Fergusonina* Flies on Australian Paperbarks

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Abstract

Molecular phylogenetics has been widely used by evolutionary biologists to explore patterns of host-plant specificity in phytophagous insects. This approach has also been used in biological control research where it can provide critical information during pre-release exploration of the potential utility of an insect against a weed target. Most importantly, molecular phylogenetics can resolve species limits, reveal cryptic species, and assess host-specificity within and among closely related species. Intra-specific phylogeographic analysis can provide additional information on the suitability or lack thereof of particular species for use in biological control. *Melaleuca quinquenervia* (Cav.) S.T.Blake. , the “broad-leaved paperbark,” is an Australian wetland tree that has become an important invasive weed within Florida, including the Everglades. The search for potential biological control agents within Australia, discovered undescribed *Fergusonina* gall flies (Diptera: Fergusoninidae) feeding on *M. quinquenervia* and its relatives. Using molecular phylogenetics, we explored species limits and host-specificity in this group of flies from nine species of Australian paperbarks with the aim of assessing host specificity. In most cases, species delimited by molecular data were monophagous, feeding on a single host species. Further analysis of Australian populations of *Fergusonina turneri* Taylor the species on the invasive paperbark, suggest that pre-release agent selection may also need to consider phylogeographic structure of natural populations of potential agents.