# Genetic analysis confirms the need to split Leptospermum into multiple genera


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## Speaker Bio

Margaret Byrne is recognised as a leading plant geneticist in Australia with over 290 publications. Her research has focused on plant genetics to inform conservation strategies for rare and threatened species, as well as biodiversity conservation at landscape scales in relation to remnant viability, revegetation and adaptation to climate change. Her phylogeographic studies have provided a greater understanding of the evolutionary history of Australian flora, and its influence on current distributions, genetic diversity and location of refugia. Margaret is currently the Executive Director of Biodiversity and Conservation Science at the Western Australian Department of Biodiversity, Conservation and Attractions where she is active in the interface between science and policy in biodiversity conservation and management.

## Presentation

Leptospermum is an ecologically and economically important plant genus that has a long history of confusion with other genera. A previous molecular study determined that the genus needed splitting into multiple genera but more data were required to inform the necessary taxonomic changes and unfortunately, this issue has remained unresolved for the last 20 years. Given that Leptospermum honey is a highly valued, globally recognised product, expansion of the industry beyond L. scoparium requires a robust taxonomic foundation to provide confidence in the source of the product and maximising the quality of honey produced from other Leptospermum species. Our study aimed to resolve the taxonomic issues in Leptospermum by sequencing a large volume of nuclear and chloroplast DNA for a comprehensive genetic analysis of 38 Leptospermum species and 11 related genera. Maximum likelihood and Bayesian analyses produced strongly supported phylogenetic trees that allowed a clear interpretation of evolutionary relationships. These data confirmed extensive divergence within what is currently known as Leptospermum, separating five distinct groups that were more closely related to other genera than they were to each other. This confirms the need to split the genus into multiple genera, and the strong support in our data provide confidence in defining those groups. These results not only have major taxonomic implications in resolving a long-standing issue in a challenging group but will also inform breeding programs, branding strategies and expansive opportunities for the bioactive honey industry.