



## **An investigation of Asteliaceae (Asparagales) systematics based on whole chloroplast genome sequencing.**

Declan P. Blackburn (The University of Melbourne); Harvey K. Orel (The University of Melbourne); Rachael M. Fowler (The University of Melbourne); Kerry A. Ford (Allan Herbarium, Manaaki Whenua – Landcare Research); Joanne L. Birch (The University of Melbourne).

The Asteliaceae (Asparagales) are a relatively small but diverse family comprised of three genera and 36 species with an Austral-Pacific distribution. The largest genus, *Astelia* (30 species), is a perennial, rhizomatous herb, and contains species that are dominant in a diverse array of habitats, e.g. *Astelia alpina* in alpine herb fields in Australia and *Astelia menziesiana* in the understory of montane rainforest in Hawai'i. While subgeneric relationships are well understood, species relationships within three of the four subgenera are not well resolved. In addition, while *A. nervosa* (New Zealand) and *A. menziesiana* (Hawaii) are noted as widespread species complexes, their monophyly has not been tested and accurate circumscription of infraspecific taxa has not been possible based on morphological data or sequence data from a small number of chloroplast and nuclear markers. Field work was conducted throughout New Zealand to document the morphological and habitat diversity of *Astelia nervosa* across its geographic range. The Asteliaceae phylogeny, including 101 in-group taxa, is inferred based on Maximum Likelihood and Bayesian Inference analyses of whole chloroplast genome data. Preliminary results will be presented that are informative of species relationships and provide a framework for understanding the diversity within recognised *Astelia* species complexes.

Declan Blackburn: [dblackburn@student.unimelb.edu.au](mailto:dblackburn@student.unimelb.edu.au)