

PROJECT TITLE

Genomics of sympatric speciation in *Howea* palms

CONSORTIUM

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SUMMARY OF THE REPORT

Sympatric speciation has long been viewed as an area of controversy. However, one convincing example is that of the *Howea* palms, which grow only on the minute Lord Howe Island, Australia, where *Howea forsteriana* diverged from its sister taxa *Howea belmoreana*, the only other species in the genus, 1-3 Myr ago^{1,2}. It is hypothesised that colonisation of calcarenite soils by *H. forsteriana* caused a substrate-induced change in flowering time in the species, leading to reproductive isolation and ecological divergence from *H. belmoreana*¹. Calcareous soils provide significant stresses (e.g. drought, salinity, cadmium) and local adaptation to these stresses may have directly influenced flowering time alteration through pleiotropy².

Using detailed soil chemistry analysis and large amounts of RNA-seq data, 11 candidate 'speciation genes' were identified, which may have contributed to the genetic mechanism of species divergence in *Howea*^{2,3}. The present project aimed to investigate these loci and validate their role in palm speciation with mutant *Arabidopsis thaliana* model plants. Using the superb high-throughput phenotyping facilities at the Finnish National Plant Phenotyping Infrastructure at the University of Helsinki, T-DNA knockout mutants of candidate gene orthologs in *A. thaliana* were subject to abiotic stress assays (drought, salinity, and cadmium as on Lord Howe Island), alongside flowering time assays, and the phenotypic response of knockouts measured using RGB, infrared and chlorophyll fluorescence imaging.

Based on these large-scale experiments, multiple candidate genes have been validated as pleiotropically affecting both flowering time and soil stress response in *A. thaliana*. These genes, therefore, have the potential to have been involved in the *Howea* speciation process. Follow-up work will attempt to rescue the phenotypes of such knockouts, through insertion of the orthologous *Howea* genes into the knockout mutant, in order to confirm conserved function between *Howea* and *A. thaliana* orthologs. The combination of these results would provide concrete evidence for a plausible genetic mechanism of sympatric speciation, and be a significant development in speciation biology.