

Trans-species sex and sullied genes: – the pitfalls of resolving a phylogeny for *Coprosma* (Rubiaceae).

Adrienne Markey

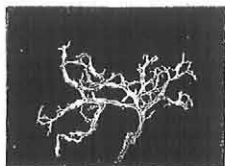
Molecular markers such as proteins or gene sequences have been used to reconstruct the evolutionary relationships of organisms since the mid 1960's. In 1992, Baldwin *et al.* used the ITS region of the ribosomal RNA gene (nrDNA) as a molecular marker, with astounding success, to resolve phylogenetic relationships within the Hawaiian silversword alliance (Asteraceae)¹. This seminal paper initiated a flood of phylogenetic research drawn from across the entire spectrum of eukaryotic organismal diversity. Generally, the ITS and ETS region of nrDNA has been noted for its phylogenetic utility at low taxonomic levels, which has seen its use increase exponentially over the past eight years. However, it has become apparent that reticulate evolution, polyploidy, introgression and ancient hybridisation events pose particular problems for this technique, thereby providing additional insight on current theories on gene and organismal evolution. Using current research into evolution of the genus *Coprosma*, a cautionary tale was presented that outlined the pitfalls and power of phylogenetic inference using sequences from nrDNA.

1: Baldwin, B.G. (1992). Phylogenetic utility of the internal transcribed spacers of nuclear ribosomal DNA in plants: examples from the Compositae. *Molecular Phylogenetics and Evolution* 1: 3-16.

Ecobiomechanics of *Durvillaea*

Deane Harder

This talk was a more detailed update on the ecobiomechanics of the bullkelp. As this term is still quite new, the different aspects and levels of analysis were explained and related to on-going projects. It involves the testing of biomechanical properties of tissue samples as well as a more general structural and morphological analysis of the plant, complemented by the estimation of the hydrodynamic forces actually acting on the kelp.



Ramalina unilateralis

A lichen found on twigs in high light habitats.