ABSTRACTS

Abstracts for both oral and poster presentations are listed alphabetically by the surname of the presenter. Where a presentation or poster has multiple authors the presenter is indicated in **bold** text.

Oral Presentations

Using genotyping by sequencing to resolve evolutionary relationships in a species complex of Australian arid zone grasses (*Triodia*)

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Tuesday 1 December, 10:00–10:15

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The application of next generation sequencing (NGS) technologies to systematics is still an emerging area of research, and systematists are increasingly faced with the challenge of interpreting the massive data sets associated with NGS. Genotyping by sequencing (GBS) is one of a number of NGS approaches based on the digestion of genomic DNA by restriction enzymes, and it can be applied to non-model systems. The *Triodia basedowii* species complex comprises two named taxa, five informally-named taxa and at least two additional taxa awaiting recognition. Morphological overlap between taxa and variability within taxa make identifications challenging, and previous sequencing of ITS was unable to clearly distinguish between some taxa. We applied GBS to samples from the *T. basedowii* complex using a commercial service through ANU. We used STACKS and PyRAD to demultiplex sequences and assemble them into loci for calling single nucleotide polymorphisms (SNPs). As part of this process, we optimised assembly parameters using replicate samples and genetic distances within populations. We analysed concatenated loci using RAxML, and used hierarchical clustering and PCA on distance matrices based on called SNPs. Our preliminary results reveal strong support for previously recognised taxa and distinction between taxa that were indistinguishable using ITS.

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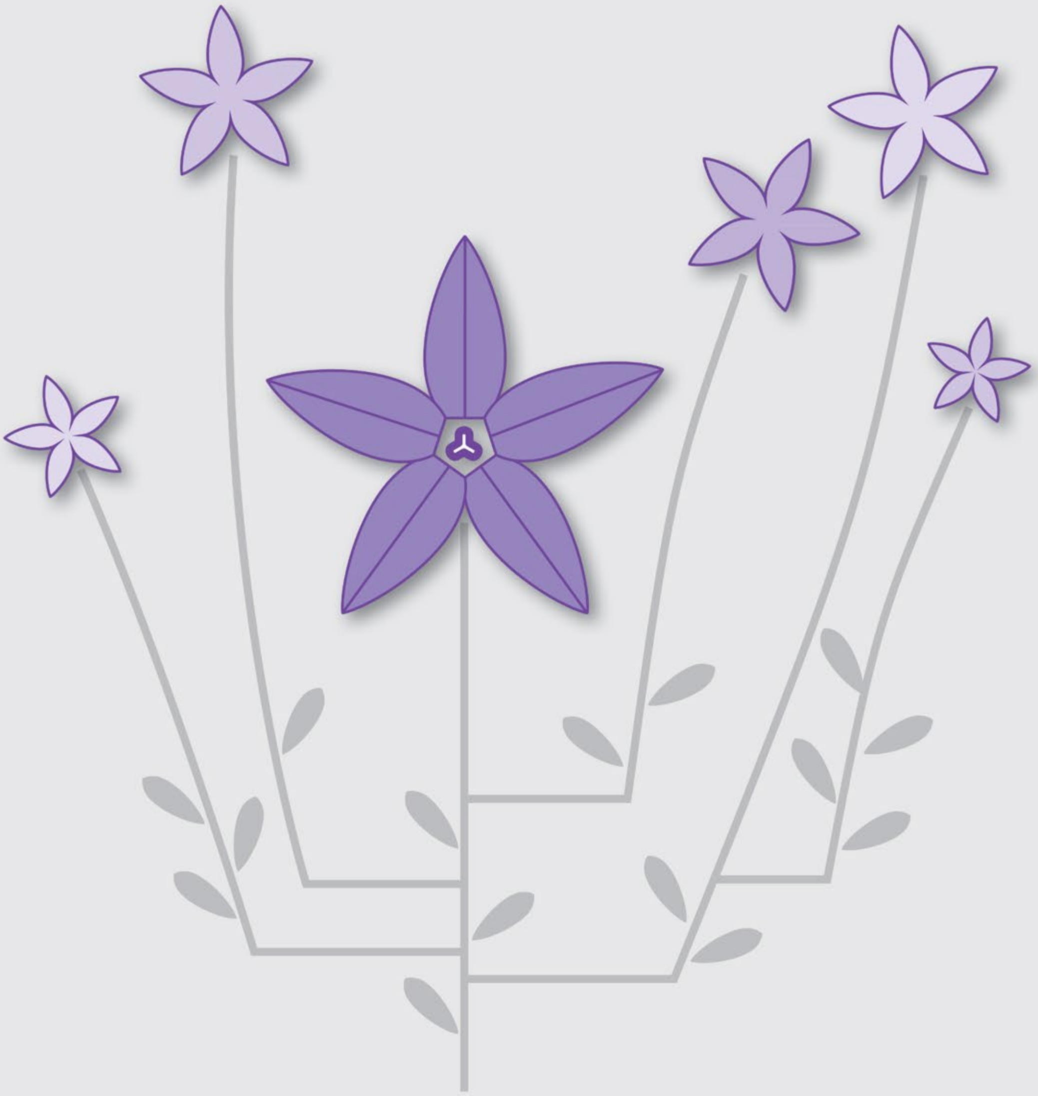

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