

Report on a Hansjörg Eichler Scientific Research Fund Award.

Reassessment of *Baeckea s.l.* using molecular data.

The *Baeckea* "complex" is taxonomically recalcitrant on several levels. In its early history there was considerable disagreement about generic concepts: during the mid 1800s some 20 genera were proposed within *Baeckea s.l.* (Bean 1995), but Bentham (1866) recognised a single genus with six sections. The tribe Baeckeeae, which also included *Astartea* DC., *Hypocalymma* Endl., *Scholtzia* Schauer and *Balaustion* Hook., was established by Schauer (1843), but later reduced to the sub-tribe Baeckeinae within the Leptospermeae (Niedenzu 1898). *Malleostemon* Green has subsequently been added to the complex (Green 1983). Briggs and Johnson (1979) recognised essentially the same group of genera as the *Baeckea* sub-alliance within the Chamelaucium alliance in their initial informal classification of Myrtaceae, but later they (Johnson and Briggs 1984) dropped the sub-alliance, raising questions about the monophyly of both the genus and the sub-alliance.

Since then, *Ochrosperma* Trudgen (Trudgen 1987) has been erected and some of the segregate genera submerged by Bentham (1866) have been re-established [viz. *Rinzia* Schauer (Trudgen 1986), *Triplarina* Raf. (Bean 1995), *Babingtonia* Lindl. (Bean 1997)], or their recognition promoted [*Euryomyrtus* Schauer (Trudgen unpublished)]. While Bean and Trudgen have made progress in resolving the generic status of parts of the complex, there remain many problems at this level. For instance, Trudgen (*pers. comm.*) has questioned the monophyly of *Astartea* and *Malleostemon*, and has mooted several new genera from elsewhere within the complex.

The suprageneric status of the group appears uncertain. Trudgen (1986, 1987) has used the concept of Baeckeinae [essentially the "paraphyletic" *Baeckea* sub-alliance of Johnson and Briggs (1984)], noting that this "heterogeneous assemblage" can be divided into three affinity groups. Both he and Bean (*pers. comm.*) have suggested a group whose affinity may be revealed by the presence of a reniform seed. This includes *Rinzia*, *Ochrosperma*, *Hypocalymma*, *Triplarina*, *Euryomyrtus*, *Balaustion*, some members of *Astartea s.l.* and certain other species of *Baeckea s.l.* (the last two possibly constituting further segregate genera).

The aim of my honours project is to use nucleotide sequence data from selected regions of the chloroplast genome to assist in the resolution of affinities at any of the levels described above. For this reason, the collection of fresh specimens was required, since extracting genomic material from herbarium specimens can be extremely difficult, depending on storage time and treatment prior to storage. The Hansjörg Eichler Award of \$500 enabled me to undertake a two week field trip to the southwest of Western Australia during October 1997 to obtain fresh specimens of a wide representation of the group. The grant substantially covered the absolutely cheapest return airfare on 'the red-eye special' Sydney-Perth-Sydney, which also saved on accommodation.

Once in Perth, I was able to join Drs Elizabeth Brown and Peter Wilson from the Royal Botanic Gardens, Sydney, for part of their collecting trip to Western Australia (for the period 12th Oct. - 26th Oct.). In this time we travelled approximately 3000km in the southwest of the state, roughly bounded in the northeast by Coolgardie and in southeast by Cape Arid. Seventy-three specimens representing all of the above mentioned genera [and also most of those mooted by Trudgen (*pers. comm.*)] were collected for later DNA extraction: a small amount of young leaves stored in zip-lock bags containing silica gel, plus a full voucher specimen for morphological study.

DNA has now been extracted from approximately thirty-three of these specimens, with the aim of having at least two representatives from each of the proposed genera in each data set. Two regions within the chloroplast genome have been targeted for sequencing - the *atpB-rbcL* spacer and the *matK* gene. The spacer data set (approximately 1000 base pairs) is now 90% complete, but the *matK* gene (some 1500 base pairs) has presented some problems with primer specificity and is still only about half completed.

Preliminary parsimony analyses on these partial data sets indicate that both regions have relatively low phylogenetic signal to noise ratios. Despite this, good resolution at the generic level should be obtained through the combination of the two datasets, as was found by O'Brien (1998) in a similar analysis of the *Leptospermum* sub-alliance. I also plan to use the molecular estimate of phylogeny to test a range of morphological characters that have been used to erect genera within the *Baeckea* group.

I wish to record my appreciation of the Hansjörg Eichler Scientific Research Fund Award from the Australian Systematic Botany Society. Without this assistance it would have been very difficult to obtain sufficient material for my project. I would also have been much the poorer for having missed both the experience of collecting in such a rich botanical region and the valuable field training I received from Elizabeth and Peter. I also want to record my thanks to Mr Tony Bean (BRI) and Mr Malcolm Trudgen (PERTH) for the assistance and advice they have so freely given, the Director and staff of PERTH for help with locality data, the Director of NSW for allowing me to hitch a ride with Peter and Elizabeth, and my supervisor, Chris Quinn, for covering my other expenses.

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