



New combinations in Aeridinae (Orchidaceae)

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Abstract

New combinations are made in the genera *Arachnis*, *Brachypeza*, *Dimorphorchis*, *Grosourdyia*, *Phalaenopsis*, *Renanthera*, *Robiquetia*, *Taeniophyllum*, *Thrixspermum*, *Trachoma* and *Trichoglottis*. Two new subgenera are established in *Phalaenopsis* (subgen. *Ornithochilus* and *Hygrochilus*). These changes are proposed to begin aligning the genera recognized in subtribe Aeridinae with results of recent DNA analyses (published elsewhere).

Introduction

Few of the c. 70 subtribes currently recognised in Orchidaceae have caused as many difficulties in generic delimitation as Aeridinae. In the most recent overview, by Senghas (1986–1990), the subtribe comprises 100 genera (excluding the misplaced *Dunstervillea*, now treated in Oncidiinae) with an estimated 1260 species; 25 genera are monotypic. Since then, several small genera have been added, such as *India* A.N.Rao, *Samarorchis* Ormerod, *Eclecticus* P.O'Byrne and *Ophioglossella* Schuit. & Ormerod, while species number has increased to well over 1500. Previously, details of floral morphology have been utilised to distinguish genera in this group of monopodial orchids. Characters such as presence of a column-foot, number of pollinia, slits on pollinia and whether they are porate or entire, spur presence, shape and size of lobes and callosities of the lip, lip motility, length of the rostellum, shape of the stipe and others have been given weight in classification of Aeridinae. Almost every combination of these characters has prompted recognition of new genera without taking homoplasy into account, resulting in an unprecedented proliferation of small (often monospecific) genera without any consideration given to phylogenetic relationships.

DNA-based phylogenetic studies in Aeridinae published so far have either concentrated on particular genera (*Aerides*, Kocyan *et al.* 2008; *Holcoglossum*, Fan *et al.* 2009, Liu 2011; *Phalaenopsis*, Padolina *et al.* 2005, Yukawa *et al.* 2005, Tsai *et al.* 2010; *Vanda*, Gardiner *et al.* 2013) or, when broader in scope, suffered from a relatively limited taxon sampling (Topik *et al.* 2005, Carlsward *et al.* 2006, Kocyan *et al.* 2008). The first author has performed a molecular phylogenetic analysis based on a sampling of 198 species of Aeridinae, utilising DNA sequences of the following regions: plastid *matK*, *trnL-trnL-F* and *trnS-G* and ITS nrDNA; this is presented in and formed the basis of the generic treatment of Aeridinae in the forthcoming *Genera orchidacearum* vol. 6 (Pridgeon *et al.* 2014). This paper makes the new combinations necessitated by this treatment; more detailed discussions of the phylogenetic findings and their taxonomic implications will be published in Pridgeon *et al.* (2014) and elsewhere (A. Kocyan, unpubl.). Among the key insights provided by DNA analyses in this subtribe is that all floral characters previously used for generic delimitation are to a greater or lesser extent subject to homoplasy because these (mostly) floral features are likely to be strongly influenced by pollinator-mediated selection (Topik *et al.* 2005, Kocyan *et al.* 2008, Kocyan unpubl.). Taxa with similar floral morphology may be only distantly related (e.g. *Phalaenopsis* and *Paraphalaenopsis*), whereas others with highly divergent floral characters may be closely related (e.g. *Ascocentrum* and *Vanda* s.s.; Gardiner 2012, Gardiner *et al.* 2013).

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