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SPECIAL ISSUE INTRODUCTION: UNDERSTANDING BIODIVERSITY IN THE MEGADIVERSE GENUS *BEGONIA*

Collaborative research on the genus *Begonia* has accelerated over the past two decades, and it has become clear that with its pantropical distribution and amazing species diversity, it is an ideal model for understanding genome evolution and tropical diversity.

A stable classification is critical to establishing *Begonia* as a model for tropical diversity and genome evolution, and the initial infrageneric classification of Doorenbos *et al.* (1998) has paved the way for more recent DNA-based classifications of the genus (Moonlight *et al.*, 2018; Shui *et al.*, 2019). This work is taken forwards in this special issue by the newly established Begonia Phylogeny Group (2022).

A fundamental challenge in *Begonia* is characterisation of the diversity in the genus. Since the publication of the 2000th species last year, species discovery has continued apace. In this issue, species are described as new to science from Sarawak (Julia *et al.*, 2022), Bhutan (Gyeltshen *et al.*, 2022), Bolivia (Moonlight & Fuentes, 2022), Sulawesi (Ardi & Thomas, 2022), Colombia (Jara-Muñoz *et al.*, 2022; Moonlight & Pérez, 2022), Ecuador (Moonlight & Pérez, 2022) and the Philippines (Ang *et al.*, 2022). Taxonomic effort also requires a synthesis and review of existing species information, and an updated checklist for Bolivia (Moonlight & Fuentes, 2022), a synopsis of the species in northern Sulawesi (Ardi & Thomas, 2022), and nomenclatural clarifications (Rubite *et al.*, 2022) are presented.

It is clear that an explanation of the species richness and diversity of form in *Begonia* will require a genomic explanation, a field of enquiry that is currently expanding rapidly as genetic knowledge accumulates, such as the first genetic map for the genus (Brennan *et al.*, 2012), quantitative trait locus analysis of species-level variation (Twyford *et al.*, 2014), and reference genomes for several species (Griesmann *et al.*, 2018; Li *et al.*, 2022). This has led to a hypothesis of a dynamic genome underlying the evolution of species and morphological diversity in *Begonia* (Dewitte *et al.*, 2011; Li *et al.*, 2022). These resources open up the field of comparative genomics and provide a solid background for further exploration of genetic variation between species and drivers of diversity such as expression analysis (Kidner *et al.*, 2016; Emelianova *et al.*, 2021; Ting *et al.*, 2021). In the special issue, we have further insights in genome size and chromosome number, plastid genome evolution and comparative transcriptomics (Campos-Domínguez *et al.*, 2022; Emelianova & Kidner, 2022; Tseng *et al.*, 2022). We also include details of a new hybrid capture bait set to facilitate collaborative studies of gene evolution and phylogenomics in *Begonia* (Michel *et al.*, 2022).

The authorship of the papers in this special issue spans the globe, representing 21 countries and showing the vibrancy and depth of the current research on *Begonia*. The *Edinburgh Journal of Botany* is an eminently suitable home for this special issue, because

it is published under the Diamond Open Access model and is the institutional journal of the Royal Botanic Garden Edinburgh, which is a globally recognised centre for *Begonia* research.

Mark Hughes & Catherine Kidner
Guest editors

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