

Target sequence data shed new light on the infrafamilial classification of Araceae
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Araceae phylogenomics

ABSTRACT

PREMISE: Recent phylogenetic studies of the Araceae have confirmed the position
of the duckweeds nested within the aroids, and the monophyly of a clade containing
all the unisexual flowered aroids plus the bisexual-flowered *Calla palustris*. The main

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objective of this work was to better resolve the deep phylogenetic relationships among the main lineages within the family, particularly the relationships between the eight currently recognized subfamilies. We also aimed to confirm the phylogenetic position of the enigmatic genus *Calla* in relation to the long-debated evolutionary transition between bisexual and unisexual flowers in the family.

METHODS: Nuclear DNA sequence data were generated for 128 species across 111 genera (78%) of Araceae using target sequence capture and the Angiosperms353 universal probe set.

RESULTS: The phylogenomic data confirmed the monophyly of the eight Araceae subfamilies but the phylogenetic position of subfamily Lasioideae remains uncertain. The genus *Calla* is included in subfamily Aroideae which has also been expanded to include Zamioculcadoideae. The tribe Aglaonemateae is newly defined to include the genera *Aglaonema* and *Boycea*.

CONCLUSIONS: Our results strongly suggest that new research on African genera (*Calloopsis*, *Nephtytis* and *Anubias*) and *Calla* will be important to understand the early evolution of the Aroideae. Also, of particular interest are the phylogenetic positions of the isolated genera *Montrichardia*, *Zantedeschia* and *Anchomanes*, which remain only moderately supported here.

KEY WORDS

Angiosperms353, nuclear phylogenomic tree, Alismatales, Lemnoideae.

INTRODUCTION

The Araceae has a particular significance in the evolution of the monocots, one of the major clades of angiosperms (APG IV). It arises from one of the earliest branching events in Alismatales and is by far the most diverse subclade of the order (Stevens 2001 onwards). It also has a remarkable fossil history, including some of the earliest known records for monocots, stretching back to the early Cretaceous (Friis et al., 2004, 2010; Hesse and Zetter, 2007; Bogner, 2009; Iles et al., 2015; Smith, 2013; Mayo et al., 2013; Hoffman, 2021). A recent review found that the family was particularly diverse during the late Cretaceous and early Paleocene (Stockey et al., 2021). Nauheimer et al. (2012), using a molecular analysis combined with fossil data and computational modelling, concluded that the early evolution of the family was linked to aquatic or sub-aquatic environments and that early diversification within the family, which led to the evolution of subfamilial lineages, took place during the Cretaceous and was associated with the fragmentation of the supercontinent Pangaea.

Araceae comprises 3,667 species assigned to 143 genera (Boyce and Croat, 2011 onwards), of which many are globally important in horticulture and agriculture. They make up one of the most ecologically diverse families of flowering plants, from the smallest known species (*Wolffia globosa* (Roxb.) Hartog & Plas) to the largest unbranched inflorescence (*Amorphophallus titanum* (Becc.) Becc.), and with habits ranging from floating aquatics, geophytes and large arborescent herbs to nomadic vines and epiphytes. The family is cosmopolitan, although it is by far most diverse in the wet tropics, particularly in South and Central America and Southeast Asia.

The large body of work on the molecular systematics of Araceae (e.g. Duvall et al. 1993, Sriboonma et al. 1993, French et al. 1995, Wen et al. 1996, Othman 1997,