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A new *Haniffia* species (Zingiberaceae) and a new generic record from Sarawak, Malaysian Borneo

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Abstract

Background: *Haniffia* Holttum is a genus of three described species of terrestrial gingers hitherto restricted to Peninsular Thailand and various localities in Peninsular Malaysia.

Results: With generic placement confirmed using nrITS, *trn*K and *mat*K plastid sequence data, *Haniffia santubongensis* S.Y. Wong & P.C. Boyce is described as a taxonomically novel species representing a new generic record for Borneo, to where it is endemic to Mount Santubong, Kuching Division, NW Sarawak, Malaysian Borneo. An identification key to all species is given and *H. santubongensis* is illustrated from living plants.

Conclusion: *Haniffia santubongensis* is the fourth species of *Haniffia* so far described, and the first occurring on sandstone.

Keywords: *Haniffia santubongensis*; Mount Santubong; Phylogeny; Taxonomy

Background

Haniffia Holttum is a genus of three described species of terrestrial gingers hitherto restricted to Peninsular Thailand and various localities in Peninsular Malaysia. The three described species are all seemingly locally endemic. The type species, *H. cyanescens* (Ridl.) Holttum, is restricted to Bukit Tanga (Negeri Sembilan, Peninsular Malaysia), with a variety, *H. cyanescens* var. *penangiana* C.K. Lim, occurring on Pulau Pinang and Kedah. The most recently recognized species, *H. flavescens* Y.Y. Sam & Julius (Sam et al. 2009) is known only from Endau Rompin National Park (Johor, Peninsular Malaysia). The sole extra-Malaysian species, *H. albiflora* K. Larsen & Mood, is confirmed only from Nam Tok Chatwarin, Naratiwat, Thailand. A summary of the taxonomic history of *Haniffia* Holttum is presented by Larsen and Mood (2000).

Methods

Plant material

Fresh leaf material of *Haniffia santubongensis* was collected from the type locality, Mount Santubong. The type specimen with the spirit material was deposited to SAR.

DNA extraction, amplification and sequencing

Genomic DNA was extracted using a modified CTAB protocol. ITS, *trn*K intron and *mat*K gene were amplified using the same set of primers as in Leong-Škorničková et al. (2011). PCR products were purified using GenJet PCR purification kit (Thermo Scientific, Vilnius, Lithuania) and sent for sequencing in forward and reverse directions at First BASE Laboratories Sdn. Bhd., Selangor, Malaysia. Sequences were edited, assembled and aligned using MUSCLE (Edgar 2004) as implemented in Geneious Pro v5.6.4 (Biomatters Ltd., Auckland, New Zealand; www.geneious.com; Drummond et al. 2012). Two newly generated sequences were deposited into GenBank under accession numbers KJ452785 (*trn*K/*mat*K) and KJ452784 (ITS), and combined with sequences included in Leong-Škorničková et al. (2011). When the placement of the new sequences was confirmed to fall within the *Kaempferia* Clade, then the final data matrix was reduced to include all the species in the *Kaempferia* Clade with *Cautleya gracilis* (Sm.) Dandy and *Roscoea cautleoides* Gagnep. selected as outgroups. Table 1 shows the list of species included for the final data matrix. The data matrix was deposited into TreeBASE (reviewer access URL: http://purl.org/phylo/treebase/phylows/study/TB2:S15361?x-access-code=f78126f9da891d3c6999dd52dfafdf77&format=html).

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