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Parapolystichum novoguineensis (comb. nov.; Dryopteridaceae) from New Guinea

MICHAEL SUNDUE & WESTON L. TESTO

Department of Plant Biology, Pringle Herbarium, University of Vermont, Burlington, Vermont, USA, 05405.

Email for correspondence: sundue@gmail.com

Recent phylogenetic analyses have recovered *Lastreopsis* sensu Tindale (1965) as paraphyletic with *Coveniella* Tindale, *Megalastrum* Holttum, *Rumohra* Raddi, and *Oenotrichia tripinnata* (F. Muell. ex Benth.) Copel. nested within it (Labiak *et al.* 2014a). Species of *Lastreopsis* sensu Tindale were resolved in two clades now recognized as *Lastreopsis* s.s. and *Parapolystichum*. Accordingly, Labiak *et al.* (2014b) made new combinations for *Conveniella* and *Oenotrichia tripinnata* in *Lastreopsis*, and for 27 species of *Lastreopsis* in *Parapolystichum*. *Lastreopsis* s.s. now comprises 16 species, placed into two subgenera, subg. *Lastreopsis* and subg. *Rhopalotricha* (Labiak *et al.* 2015). *Lastreopsis* and *Parapolystichum* cannot always be distinguished from each other morphologically, therefore Labiak *et al.* (2014) refrained from making combinations for nine species that had not been included in their phylogenetic analysis, treating them as *Incertae Sedis*. We address one of those species here, *Lastreopsis novoguineensis* Holttum, which was described posthumously along with other novelties for the Flora Malesiana (Holttum, 1991). Here, we place *Lastreopsis novoguineensis* within a phylogenetic framework based on Labiak *et al.* (2014a) and resolve its taxonomic status based on these findings.

Plants were collected in Chimbu Province of Papua New Guinea on Mt. Wilhelm in the eastern slopes of the Piunde-Aunde valley at 3200 m (5°48'25.185"S, 145°4'19.7544"E), and deposited at LAE, VT, and in the herbarium of the Binatang Research Station in Madang as Sundue *et al.* 3653 (Fig. 1). Additional images of the specimen are archived online at fernsoftheworld.com. Identification was made through consultation with Tindale (1965) and Holttum (1991) and by comparison with the type, *Nakaike 578* (K-000235793) via the image provided online. Total genomic DNA was extracted from silica-dried leaf material obtained using a modified CTAB protocol (Doyle and Doyle, 1987). Two chloroplast intergenic spacer regions (*rps4-trnS* and *trnL-trnF*) were amplified using PCR in 25 µL reactions comprising 1 µL DNA, 9 µL water, 1.25 µL of both forward and reverse primers, and 12.5 µL Bullseye Red Taq DNA polymerase master mix. The *rps4-trnS* intergenic spacer was amplified using the primers *rps4-3r.f* (Skog *et al.* 2004) and *trnS-R* (Souza-Chies *et al.* 1997) and the *trnL-trnF* spacer was amplified using the primers *e* and *f* of Taberlet *et al.* (1991). For both markers, we used a program beginning with one initial denaturation step of 7 min at 94 °C; followed by 35 cycles of 45s at 94 °C, 45s at 52 °C, 1 min at 72 °C; and a final extension period of 7 min at 72 °C. The resulting PCR products were then visualized on a 1.2% agarose gel stained with ethidium bromide. PCR products were purified using shrimp alkaline phosphatase and both forward and reverse sequences were generated using the amplification primers on an ABI PRISM 3730xl platform at Beckman Coulter Genomics (Danvers, MA, USA). DNA sequences from *Lastreopsis novoguineensis* for both *rps4-trnS* and *trnL-trnF* were visually inspected and assembled using Geneious v.7.0.2 (Biomatters, Ltd.). We assembled a matrix comprising all 112 specimens and the four chloroplast markers (*rbcl*, *trnG-trnR*, *rps4-trnS*, and *trnL-trnF*) used by Labiak *et al.* (2014a; GenBank accession numbers available therein) as well as *rps4-trnS* (GenBank accession number KU295571) and *trnL-trnF* (GenBank accession number KU295570) sequences for *L. novoguineensis*. Each region was aligned using the Geneious MAFFT (Kato *et al.* 2002) plugin and all four regions were concatenated to form a final matrix of 113 sequences and 3187 sites, which was used for phylogenetic analyses. These data, partitioned by marker, were analyzed using both Bayesian Inference (BI) and Maximum Likelihood (ML) approaches, using MrBayes 3.2.2 (Ronquist and Huelsenbeck 2003) and RAxML 8.2.3 (Stamatakis 2006), with the same substitution models employed by Labiak *et al.* (2014a). The BI analysis was run for 5 million generations; 100 bootstrap replicates were run for the ML analysis. All analyses were run using the online Cipres Science Gateway portal.

The results of our phylogenetic analyses (Fig. 2) are congruent with those of Labiak *et al.* (2014a) and find strong support (BI posterior probability = 1.0, ML bootstrap support = 94%) for *Lastreopsis novoguineensis* as nested within a clade of largely Australian *Parapolystichum*, sister to *P. smithianum* + *P. glabellum*. Consequently, we provide a new combination here.



FIGURE 1. *Parapolystichum novoguineense*, Sundue 3653.

Taxonomy

Parapolystichum novoguineense (Holttum) Sundue & Testo, *comb. nov.* (Fig.

Basionym:—*Lastreopsis novoguineensis* Holttum (1991: 557).

Type:—PAPUA NEW GUINEA. Central District: Woitape, Abios, en route from Woitape to Mt. Albert-Edward, 2500 m, 18 Jan. 1974, Nakaike 578 (holotype K-000235793, image seen!).

With the addition of *Parapolystichum novoguineense*, *Parapolystichum* now comprises 28 species. It is distributed in both the New World and Old World tropics, but *P. novoguineense* is the only species known with certainty by us to occur on New Guinea, where it is distributed in montane regions from 1800–3200 m (Holttum 1991, Conn 2006+). The presence of lastreopsid ferns other than *P. novoguineense* in New Guinea is not well known. Tindale did not list any species in her 1965 monograph. Two collections at CANB (*Kalkman 4748, 5081*) from the Southern Highlands of Papua New Guinea have been identified as *P. smithianum*, but we believe those are misidentifications of *P. novoguineense* pre-dating its publication, as that species is most likely an Australian endemic (Tindale 1965, Jones 1988, Labiak *et al.* 2014b). Labiak *et al.* (2014a) stated that two species of *Lastreopsis* s.s. occur on New Guinea, but did not indicate which species they believed were present there. However, only *L. tenera*, which is widespread throughout Malesia, is likely to be present there, but confirmation is needed. *Parapolystichum novoguineense* can be distinguished from both of these species by the clavate yellow glands that are present upon the abaxial lamina. *Parapolystichum glabellum*, the other most closely related species in our phylogenetic results, is known only from New Zealand. It can be distinguished by having dentate segment margins, dark brown indusia, and abaxial laminae that are abundantly provided with 0.2 mm long reddish simple hairs, and scattered 0.2 mm long clavate yellow glands. By comparison, *P. novoguineense* has crenate segment margins, light brown indusia, and abaxial laminae with sparse reddish simple hairs, and abundant clavate yellow glands.

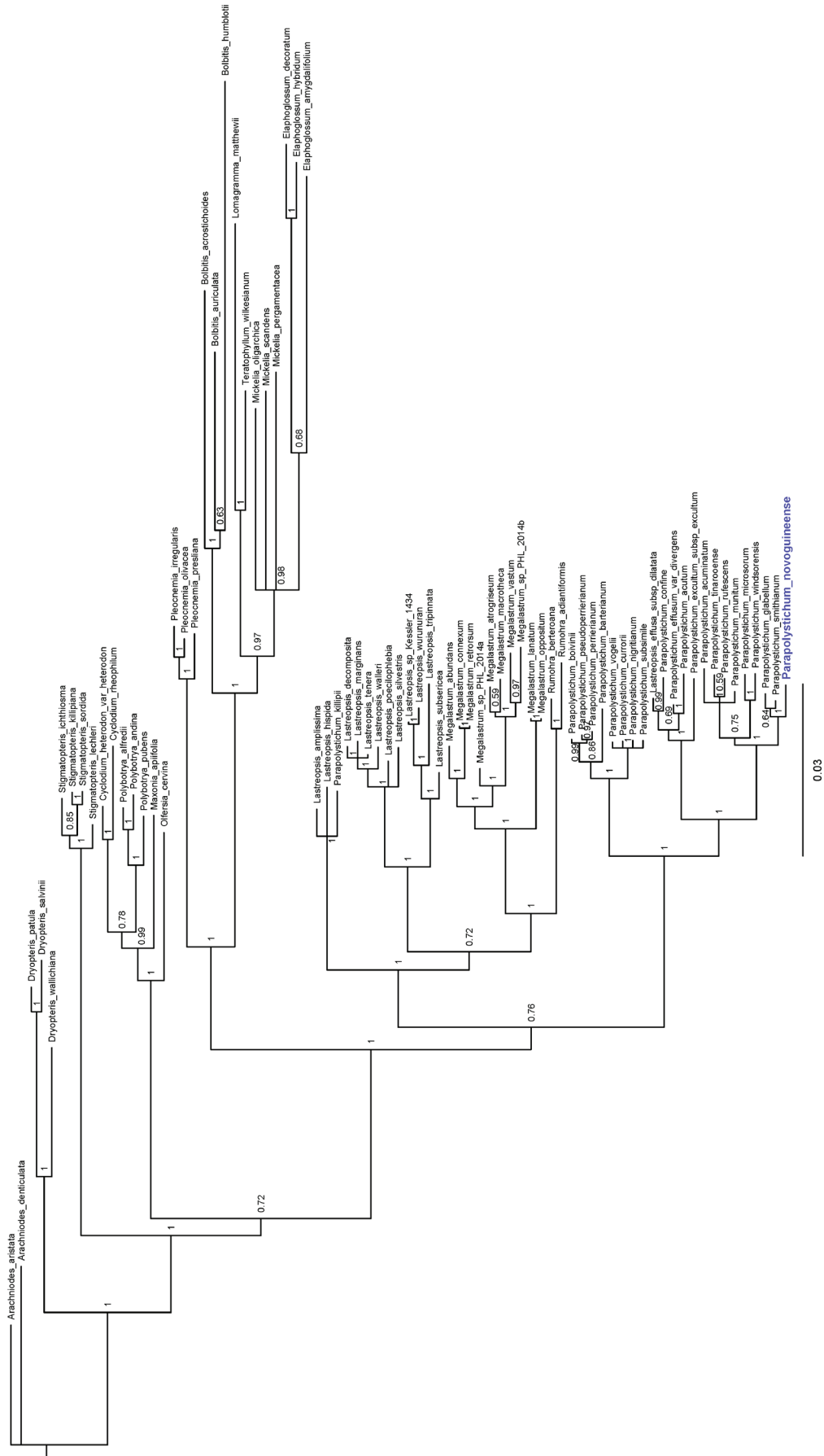


FIGURE 2. Results from Bayesian phylogenetic analyses based on chloroplast sequences. Numbers associated with nodes are posterior probabilities for each branch. The scale bar represents the number of substitutions per site.

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