Kiyotaka Hori\textsuperscript{a,*} and Aung Zaw Moe\textsuperscript{b}: \textit{Hymenasplenium quangnamense} (Aspleniaceae) New to Myanmar

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Summary: \textit{Hymenasplenium quangnamense} Li Bing Zhang, K. W. Xu & Liang Zhang (Aspleniaceae), recently described from Vietnam, is reported from Myanmar for the first time. The reproductive mode was estimated to be apogamous. This report suggests there may be more species of the genus \textit{Hymenasplenium} in Myanmar.

We newly report \textit{Hymenasplenium quangnamense} Li Bing Zhang, K. W. Xu & Liang Zhang (Aspleniaceae) from Pinlong Reserve Forest, Shan State, Myanmar. This species has been recognized to be endemic to Vietnam (Xu et al. 2018a). This species is similar to \textit{H. apogamum} (N. Murak. & Hatan.) Nakaike in having densely scaly rhizomes, robust roots (ca. 1 mm in diam.), and quadrangular or trapeziform pinnae, but the former has often slightly retuse marginal teeth at the base of pinnae, veins terminating below notches, and supramedial to (sub)marginal sori, while the latter has entire marginal teeth at the base of pinnae, veins terminating in marginal teeth, and medial sori (Xu et al. 2018a).

\textit{Hymenasplenium quangnamense} was collected in 2014, during plant inventory research by the Myanmar-Japanese cooperative program for contributing to the flora of Myanmar. Voucher specimens were deposited in the Herbaria of the Kochi Prefectural Makino Botanical Garden (MBK) and the Forest Research Institute (RAF), Myanmar.

Materials and Methods

\textit{Molecular analysis of plastid rbcL gene}

We compared the newly analyzed \textit{rbcL} sequence of \textit{H. quangnamense} from Myanmar (MBK0299600, Fig. 1) with the accessions of GenBank from 23 species of the genus \textit{Hymenasplenium}. For the PCR amplification of DNA, only one sequence representing each allele for each haplotype was applied (aF3-5\textsuperscript{\textprime} -ATGTCAACACAAACGGAGACTAAA GC3-3\textsuperscript{\textprime} and cR3- 5\textsuperscript{\textprime} -GCGGCAGCCAATTCC GGACTCCA-3\textsuperscript{\textprime}, Hori et al. 2018). The sequences were aligned using MUSCLE (Edgar 2004) and phylogenetically analyzed separately by neighbor-joining (NJ), maximum parsimony (MP), and maximum likelihood (ML) analyses (Kimura 2-parameter + G model) by using MEGA version 6 (Tamura et al. 2013).

Results and Discussion

The data matrix for phylogenetic analyses included 1,086 characters, after editing, of which 135 (12\%) were polymorphic and 72 (6\%) were parsimoniously informative. NJ, MP, and ML analyses resulted in phylogenetic trees with similar topology. The ML tree (highest log likelihood = −2671.4736) with BPs of NJ/MP/ML analyses is shown in Fig 2. The \textit{rbcL} sequence of \textit{H. quangnamense} examined in this study (voucher, MBK0299600; accession no, LC427111) composes a monophyletic group with the holotype (Zhang & al. 7884 in Xu et al. 2018a, b, MH065412) supported by high BPs of NJ/MP/ML analyses.
Note: We checked at least five sporangia with normal spores for this specimen to estimate reproductive mode (Manton 1950). We estimated it to be apogamous because the spore number per sporangium was 32.

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References

H. quangnamense は Xu et al. (2018a) がペットナムをタイプ产地として記載した新種であり、今後もミャンマーから未記載のホウピシンガ見つかる可能性がある。なお今回報告する植物は，高知県立牧野植物園およびミャンマー連邦天然資源環境省の研究協定にもとづくミャンマー・シャン州の植物目録作成を目的とした2014年の調査において採集されたものである。

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