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BRYOPHYTE MOLECULAR BARCODING RECORDS. 5

БРИОЛОГИЧЕСКИЕ НАХОДКИ ПО РЕЗУЛЬТАТАМ ДНК-МАРКИРОВАНИЯ. 5

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Abstract

DNA-barcoding revealed/confirmed the range extension of the following bryophytes: *Hygrohypnum stryriacum* (North Ural Mountains, Khanty-Mansi Autonomous District, Asiatic Russia), and *Thuidium kanedae* (Kuril Islands).

Резюме

С помощью ДНК-баркодинга выявлены или подтверждены находки за пределами основного ареала следующих видов мохообразных: *Hygrohypnum stryriacum* (Северный Урал, Ханты-Мансийский АО) и *Thuidium kanedae* (Курильские острова).

KEYWORDS: mosses, new records, molecular markers, nrITS, Russia

INTRODUCTION

This paper continues the series of brief reports of new findings in the course of the bryophyte DNA studies. It presents various finding where the sequencing either confirms species identities, which are ambiguous by various reasons, or disclose their affinities, or support generic placements of certain taxa that have never been investigated for moleculer markers earlier, or have never been barcoded previously, or have been barcoded from other parts of the world. Being obtained in the course of screening rather than special projects of a particular group, such data may remain unsubmitted to DNA databases and stay neglected and not searchable among published materials.

1. ***Thuidium kanedae*** Sakurai

Contributors: V.E. Fedosov, A.V. Fedorova.

Specimens: Russia, Sakhalin Province, Shikotan Island; Shikotan Mt summit area, 43.8694°N – 146.8571°E, alt. ca. 400 m, alpine community, on soil. 29 August 2021, Fedosov s.n. (MW) – isolate ThF73; the same area, vicinity of Dimitrova Bay, 43.80055°N – 146.80769°E, alt. ca. 30 m, on litter covering shaded rocks near waterfall. 27 August 2021, Fedosov s.n. (MW) – isolate ThF76.

DNA: isolate ThF73, Genbank # OL825641, isolate ThF76 OL825642 (nuclear Internal Transcribed Spacer region). Reference: isolate ThF54, Genbank # OL825640, Bryophytes of Asia 539, Japan, Shikoku, 6 June 2015 Orgaz s.n. (MW9075555).

This species was described from Japan and further was also reported from China (Wu *et al.*, 2002) and Russia (Ignatov *et al.*, 2006). However, specimens from Primorsky Territory, which were previously assigned to this species according to results of molecular phylogenetic study, represent other species. At the same time, recently collected specimens from Shikotan Island have identical ITS sequences with Japanese specimen used as reference and morphologically fit the description by Noguchi *et al.* (1991).

2. ***Hygrohypnum styriacum***

Contributors: E.D. Lapshina, M.S. Ignatov, O.I. Kuznetsova.

Specimen: Russia, Khanty-Mansi Autonomous District, Berezovo District, eastern slope of Subpolar Urals, vicinity of Ner-Oika, right bank of Shaitanka Creek, on fine soil over rocks, 64°34'08"N, 59°39'32"E, 460 m a.s.l., Coll. E.D. Lapshina 2.VIII.2013, #13-82 (YSU, dupl. MHA).

DNA: isolate OK2924 Genbank #OL825639 (nuclear Internal Transcribed Spacer region).

Jamieson (1976, 2014) reported this species to be be confined to West Europe and Western North America and Rockies. *Hygrohypnum styriacum* is related to *H. luridum* and the problems of their differentiation are discussed by Jamieson (2014), and also by Czernyadjeva (2012) in her book about Kamchatkan mosses, where some specimens of *H. luridum* were found to be similar

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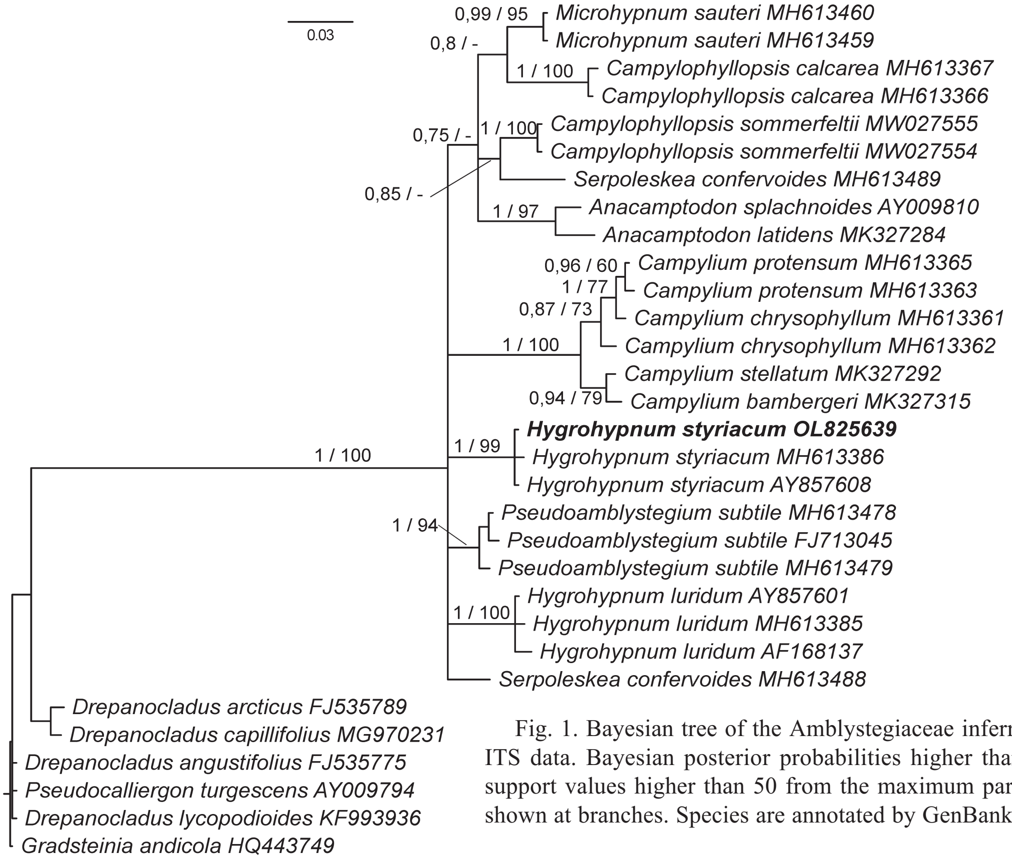

Fig. 1. Bayesian tree of the Amblystegiaceae inferred from the nuclear ITS data. Bayesian posterior probabilities higher than 0.7 and bootstrap support values higher than 50 from the maximum parsimony analysis are shown at branches. Species are annotated by GenBank accession numbers.

to *H. styriacum*. Thus despite a specimen from Asian slope of the Ural Mountains fits *H. styriacum* by morphology, we sequenced it to confirm its first record in Asia. As nuclear ITS was proved to be useful for elucidation of taxonomy in many pleurocarpous groups, including *Hygrohypnum* s.l. (Olivan *et al.*, 2007; Ignatov *et al.*, 2007), we used it, and here provide a phylogenetic tree based on this DNA marker. Accessions most similar by BLAST search in GenBank were taken for comparison. Some accessions of much repeated species where omitted. Dataset was analysied in MrBayes (Ronquist *et al.*, 2012) [GRT model, 5000000 iterations] and Nona (Goloboff, 1994) [bootstrap, 1000 iterations].

Both analyses showed a significant support of the identity of Urals specimen with *H. styriacum* specimens from Austria (MH613386) and Norway (AY857608).

Note, however, that *H. styriacum* and *H. luridum* did not form a clade, unlike e.g. species of *Campylium*. Their placement in one genus might be challenged in the further studies.

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