

BRYOPHYTE MOLECULAR BARCODING RECORDS. 10

БРИОЛОГИЧЕСКИЕ НАХОДКИ ПО РЕЗУЛЬТАТАМ ДНК-МАРКИРОВАНИЯ. 10

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Abstract

DNA-barcoding revealed/confirmed the range extension of the following bryophytes: *Bryoerythrophyllum rubrum* (Krasnoyarsk Territory, Kara Sea Islands), *Hedwigia kuzenevae* (Bashkortostan, South Urals), and *Chionoloma orthodontum* (Ingush Republic, Caucasus).

Резюме

С помощью ДНК-баркодинга выявлены или подтверждены находки за пределами основного ареала следующих видов мохообразных: *Bryoerythrophyllum rubrum* (Красноярский край, Карское море, острова Известий ЦИК), *Hedwigia kuzenevae* (Башкортостан, Южный Урал) и *Chionoloma orthodontum* (Республика Ингушетия, Кавказ).

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

INTRODUCTION

This paper continues the series of brief reports of new findings proved in the course of the bryophyte DNA barcoding 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 molecular markers earlier, or have never been barcoded previously, or have been barcoded from different 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. *Bryoerythrophyllum rubrum* (Jur.ex Geh.) P.C. Chen

Contributors: I.V. Czernyadjeva, M.S. Ignatov, O.I. Kuznetsova

Specimen: Russia, Asian Part, Kara Sea, Archipelago of the Izvestia Islands Central Election Commission, Troynoy Island, Kruglaya Bay, (75°57'24"N – 82°34'29"E), 35 m a.s.l., polygonal gravelly grass-moss tundra, on the bare soil of polygon, 4.IX.2021 coll. Czernyadjeva # 8-21, det. Ignatov (LE, dupl. MHA).

DNA: Isolate OK3965. GenBank accession number: PQ066786, nrITS.

Poorly developed High Arctic plants of many Pottiaceae species, including *Bryoerythrophyllum*, are easy to confuse. Molecular phylogenetic results, however, unequivocally suggest the affinity of the studied plant to *B. rubrum*, especially to the specimen recently collected in the North Ural by Lapshina (coll. number 05/8, GenBank accession number OR466077, cf. Kuznetsova *et al.*, 2023).

In Russia, isolated finds of *B. rubrum* are known in the Caucasus, Republic of Karachaevo-Cherkessia (Fedosov & Ignatova, 2008), Republic of Kabardino-Balkaria (Sofronova *et al.*, 2017), Republic of North Ossetia (Sofronova *et al.*, 2023), Stavropol Territory (Doroshina, 2012), the Taimyr Peninsula, Taimyrsky State Nature Reserve (Fedosov & Ignatova, 2008), New Siberian Islands Archipelago, Stolbovoy Island (Czernyadjeva *et al.*, 2021), and Sakhalin Island (Bakalin *et al.*, 2012).

2. *Hedwigia kuzenevae* Ignatova & Ignatov

Contributors: E.Z. Baisheva, E.A. Ignatova, O.I. Kuznetsova

Specimen: The Republic of Bashkortostan, Abzeli-ovskiy District, 4.2 km north of Murakaevoy village, the

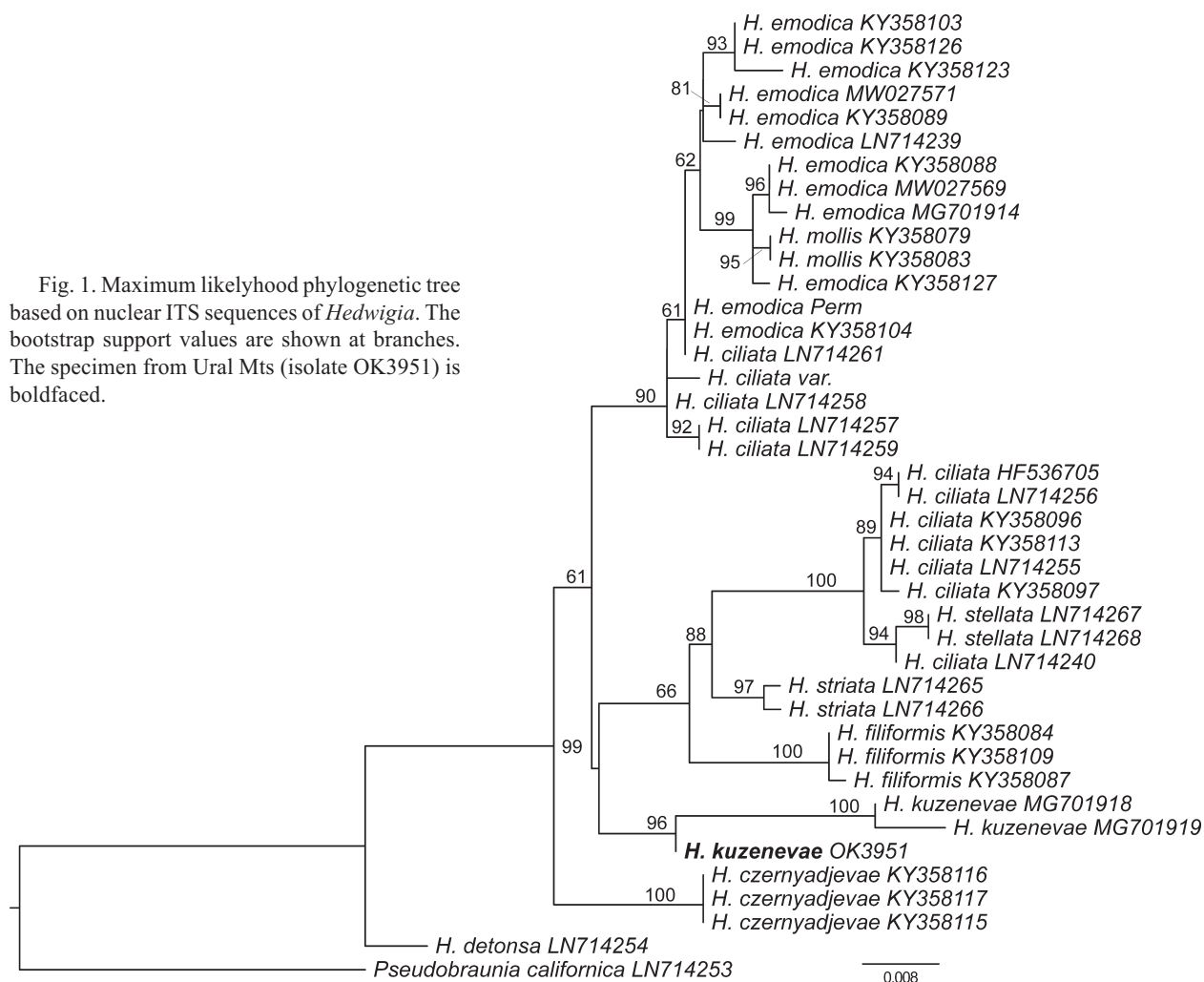
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Kurkak Range (53.807403°N, 58.702047°E), 890 m alt., on rock outcrops, 18.VI.1997. Coll. Baisheva, 167-1997-1, det. Ignatova [Together with *Schistidium papillosum*, *Rhytidium rugosum*, *Dicranum schljakovii*, *Hypnum cupressiforme*.] (UFA, dupl. MHA).

DNA: Isolate OK3951. GenBank accession number: PQ066788, nrITS.

This species was described from East Siberia and Russian Far East (Ignatova *et al.*, 2017), and this record is the first one for Ural Mountains (East faced slope, e.g. Asian part). *Hedwigia kuzenevae* is differentiated from the *H. ciliata* s.str. in the densely papillose hyaline hair points (with more scattered papillae in *H. ciliata*) with long, sharply acute and often curved marginal teeth (vs. short in *H. ciliata*).

The supporting ML phylogenetic tree (Fig. 1) was done at W-IQ-TREE server (Trifinopoulos *et al.*, 2016), with 1000 replications and otherwise default parameter, models selected by this facility (ITS1: HKY+F+G4, 5.8S gene: K2P+I, ITS2: TN+F+G4).

The obtained tree topology principally agrees with previous molecular phylogenetic analyses of the genus *Hedwigia* (Buchbender *et al.*, 2014; Ignatova *et al.*, 2016,

2017; Huang *et al.*, 2024). *Hedwigia kuzenevae* forms a clade sister to the mainly ‘North Atlantic’ clade, which includes *H. ciliata* s.str., *H. stellata*, *H. striata*, and also a more widespread *H. filiformis* (incl. *H. nemoralis*, cf. De Luna, 2022; Huang *et al.*, 2024).

The newly reported specimen from the Urals has all the unique substitutions of Asian specimens of *Hedwigia kuzenevae* in ITS1, whereas the substitutions in ITS2 are partly shared with those common for species of the ‘North Atlantic clade’, which explains its somewhat distant position from the Asian specimens in Fig. 1.

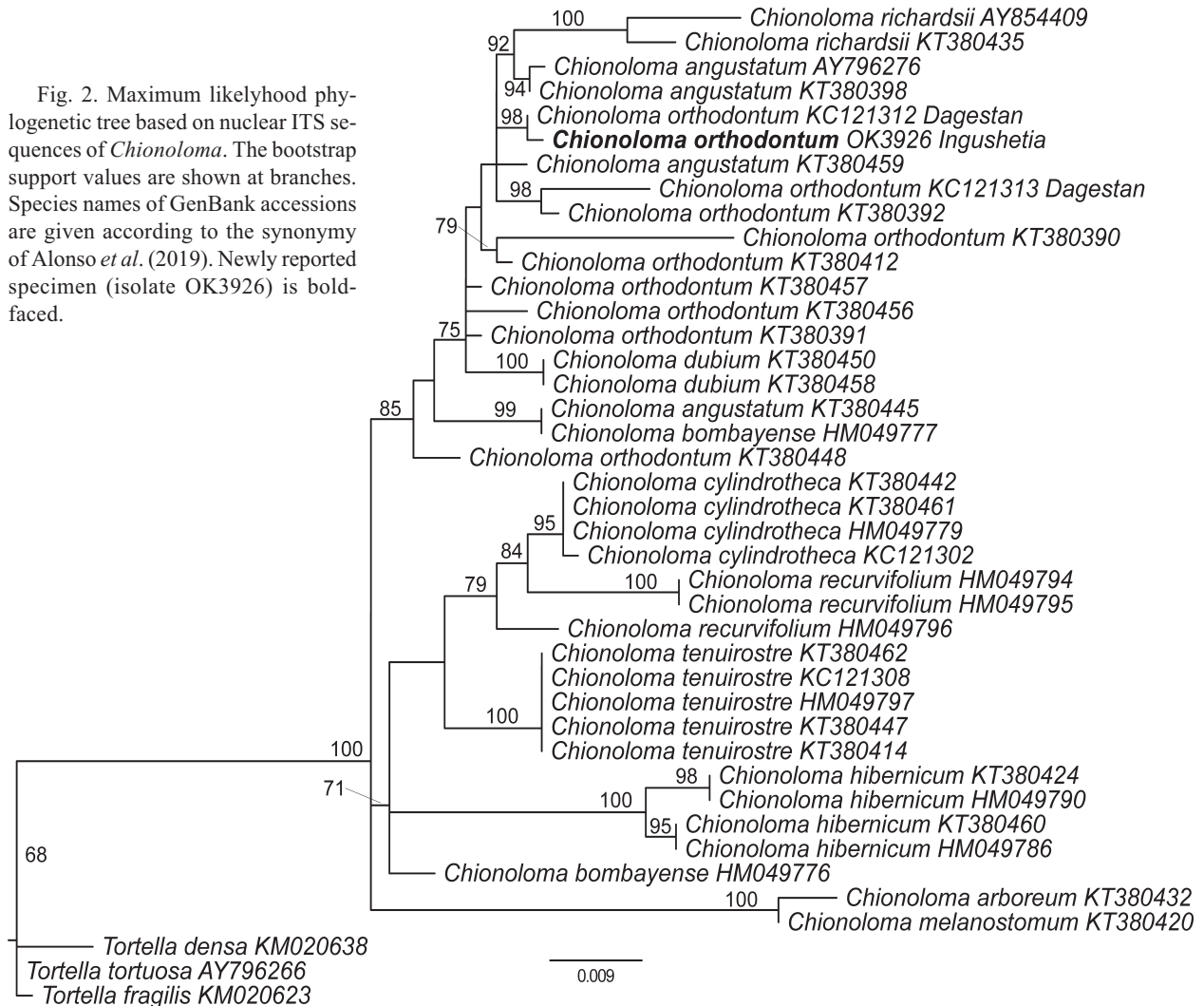
We enriched the dataset with GenBank data to be certain in the stability of *H. kuzenevae*-clade. Doing this, we added *H. ciliata* s.l. and did not check *H. emodica* and *H. mollis* specimens, thus the position of the latter within the genus is approximate, not indicating their conspecificity.

3. *Chionoloma orthodontum* (Müll. Hal.) M. Alonso, M.J. Cano & J.A. Jiménez.

Contributors: A.N. Bersanova, A.V. Fedorova, M.S. Ignatov, E.A. Ignatova

Specimen: Russia, Ingushetia, Erzi Nature Reserve,

Fig. 2. Maximum likelihood phylogenetic tree based on nuclear ITS sequences of *Chionoloma*. The bootstrap support values are shown at branches. Species names of GenBank accessions are given according to the synonymy of Alonso *et al.* (2019). Newly reported specimen (isolate OK3926) is bold-faced.



Niikote, 42°49'58.4"N, 45°01'44.0"E. 1933 m alt., on soil in pine forest. 17 April 2018, coll. M. Ignatov, E. Ignatova, M. Kolesnikova & A. Bersanova 18-433 (MHA9026821).

DNA: Isolate OK3926. GenBank accession number: PQ066787, nrITS.

This species was reported as a new for Russia by Alonso *et al.* (2019) based on the study of one of two specimens found in the Caucasus, Dagestan and reported as *Pseudosymblypharis bombayense* by Ignatova *et al.* (2012). *Chionoloma orthodontum* has a rather widespread pantropical distribution, while the Caucasian population is considerably isolated: its closest localities are in Pakistan and Nepal (Alonso *et al.*, 2019). Ingushetia is the second Caucasian region where this species was found, in a rather similar environment. The species grew of soil in open pine forest at the level of upper forest zone, though in xeric climate of Ingush Republic, the small forested areas at that elevation are commonly intermingled with steppe vegetation.

The Caucasian specimens are resolved in the terminal clade of *Chionoloma* phylogenetic tree (Fig. 2), based

mostly on GenBank data, deposited at least partly before the revision of Alonso *et al.* (2019). Most species names in this clade are consistent with the identification of the Caucasian plants as *Chionoloma orthodontum*. The tree (Fig. 2) was done at W-IQ-TREE server (Trifinopoulos *et al.*, 2016), with 1000 replications and otherwise default parameter, models selected by this facility (ITS1: K2P+G4, 5.8S gene: K2P, ITS2: K2P+G4).

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