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TAXONOMICAL AND CHOROLOGICAL NOTES 2 (20–27)

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Abstract: The second part of the recently launched series includes miscellaneous new records from fungi to vascular plants. New chorological records of five taxa of fungi are provided here: two new for Hungary (*Entoloma tjallingiorum* and *Mycoacia nothofagi*), one (*Hohenbuehelia mastrucata*) new for the Vértes and Börzsöny Mts, additional records and confirmations for two taxa (*Entoloma lampropus* and *Hohenbuehelia atrocoerulea*) are also provided. New chorological records of three vascular plants are provided: one taxon (*Draba muralis*) new for the Tiszántúl region, two (*Rubus armeniacus* and *Najas marina*) new for the North Hungarian Mts.

Key words: Brassicaceae, Entolomataceae, Hungary, Hydrocharitaceae, Meruliaceae, Pleurotaceae, Rosaceae

INTRODUCTION

This paper is the second part of the series launched in *Studia botanica hungarica* focusing on the new chorological records, nomenclature, and taxonomy of plant species from algae to vascular plants and fungi (Barina *et al.* 2015).

MATERIAL AND METHODS

For the fungal specimens the Phire® Plant Direct PCR Kit (Thermo Scientific, USA) was used for the DNA extraction and PCR following the recommendations of the manufacturer.

The ITS region of the nrDNA was amplified with the primer pairs ITS1F/ITS4 (White *et al.* 1990). The amplicons were sequenced at LGC Genomics (Berlin, Germany) with the same primers used in PCR reactions. The chromatograms were checked, assembled and edited with the Pregap4 and Gap4 programs of the Staden package (Staden *et al.* 2000) as well as with the CodonCode Aligner package (CodonCode Corp., Centerville, Massachusetts, USA).

For the dataset of *Entoloma* and *Hohenbuehelia* multiple sequence alignments were done with PRANK (Löytynoja and Goldman 2005) as implemented in its graphical interface (PRANKSTER) under default settings. *Mycoacia* sequences were aligned by MAFFT (online version 7) using the E-INS-i algorithm (Katoh and Toh 2008). After manual adjustments in SeaView (Gouy *et al.* 2010) the phylogenetically informative indels were coded in the three alignments, following the simple indel coding algorithm (Simmons et al. 2001) with the program FastGap 1.2 (Borchsenius 2009).

Bayesian inference (BI) analyses were performed with MrBayes 3.1.2 (Ronquist *et al.* 2012). The nucleotide and indel characters were split into two partitions to which the GTR + G and two-parameter Markov model, respectively, were applied. Four Markov chains were run for 10,000,000 generations, sampling every 1000th generation and with a burn-in of every 3,000 sampled trees. The post burn-in trees were used to compute a 50% majority rule consensus phylogram and posterior probabilities (PP) were calculated.

Maximum Likelihood (ML) analysis was carried out using RAxML (Stamatakis 2014) in raxmlGUI (Silvestro and Michalak 2012). Rapid bootstrap analysis and 1,000 replicates under the GTRGAMMA substitution model were used for the partitioned alignment (ITS + indels). The newly generated sequences were deposited in GenBank (Figs 1–3).

NEW RECORDS WITH ANNOTATIONS

Fungi

(20) ***Entoloma tjallingiorum*** Noordel. (Entolomataceae)

Hungary, Vértes Mts: near Csákberény, Juhdöglő-völgy Forest Reserve, on *Quercus* sp.; leg. V. Papp, 07.10.2010, BP 106905 (PV538), GenBank: KX349905

For comments see *Entoloma lampropus*.

(21) ***Entoloma lampropus*** (Fr.) Hesler

Hungary, Zemplén Mts: Pálháza-Kőkapu, in the valley of the Kemence-patak, in *Alnetum*; leg. B. Dima, 24.09.2006, BP 106906 (DB2529), GenBank: KX349904

Entoloma (Fr.) P. Kumm. s. lato is a cosmopolitan species-rich genus of Agaricales with highly variable sporocarp morphology (Noordeloos and Morozova 2010). The life strategies are equally varied in the genus; most of the species are terrestrial or wood-inhabiting saprotrophs, but some are parasitic or mycorrhizal symbionts (Largent 1994, Noordeloos 1992, 2004, Noordeloos and Gates 2012). Several authors considered that the genus *Entoloma* is polyphyletic, and certain clades and morphological groups have been treated as separate genera (e.g. Aime *et al.* 2010, Baroni *et al.* 2011, Henkel *et al.* 2010, 2014, Largent *et al.* 2011*a*, *b*, 2013*a*, *b*, Ovrebo and Baroni 2007). However, other authors stated that the genus is one species-rich entity with extensive infrageneric classification (e.g. Co-David *et al.* 2009, Morgado *et al.* 2013, Noordeloos 2004, Noordeloos and Gates 2012), hence the different lineages (e.g. *Leptonia* group) are discussed below genus level (subgenera, sections, etc.) (e.g. Morozova *et al.* 2014, Noordeloos 1982). Since the polyphyly of the genus *Entoloma* has not yet been unambiguously proved even with the help of multi-gene phylogenetic analyses, we still treat the species of the *Leptonia* group within the genus.

The type species of the *Entoloma* subgen. *Leptonia* (Fr.) Noordel. emend. O. V. Morozova, Noordel. et Vila (≡ *Leptonia* (Fr.) P. Kumm.) is *Agaricus euchrous* Pers. (≡ *Entoloma euchroum* (Pers.) Donk) (Noordeloos 1981), which is characterised by blue-violaceous colour of the basidiocarp, sweet smell, and lignicolous habitat (Noordeloos 1992). Based on a recent phylogenetic study of the subgenus *Leptonia* in boreal-temperate Eurasia (Morozova *et al.* 2014), the section *Leptonia* forms a well-supported monophyletic clade including only those species, which have weakly angled, almost nodulose spores: *Entoloma chytrophilum* Wölfel, Noordel. et Dähncke, *E. euchroum*, *E. lampropus* (Fr.) Hesler, *E. placidum* (Fr.) Noordel., *E. sublaevisporum* Vila, Noordel. et O. V. Morozova, *E. tjallingiorum* Noordel. s. lato. Three of these species have been recorded from Hungary in the literature, however, only based on morphological identification: *E. lampropus*, *E. euchroum*, and *E. placidum* (e.g. Lukács 2007, Sántha 2003).

The Hungarian specimen (BP 106905) was found as new for Hungary in the Juhdöglő-völgy Forest Reserve (Vértes Mts) and identified as *E. tjallingiorum* based on morphology. In our phylogenetic analyses the ITS sequence of this specimen nested in the subclade of *E. tjallingiorum* var. *tjallingiorum* according to Morozova *et al.* (2014), and it clustered together with the sequence obtained from the type material (KC898412) with strong support (PP = 1.00, BS = 100%)

(Fig. 1). A new occurrence of another member of the sect. *Leptonia*, *E. lampropus* for Hungary, was verified by ITS data too. Our collection from the Zemplén Mts clustered together with the neotype sequence of the species (KC898377) and also gained maximum support in both BI and ML analyses (Fig. 1).

The *Entoloma tjallingiorum* species complex treated in Morozova *et al.* (2014) needs further taxonomical revision based on our phylogenetic analyses, because the recently described variety, *E. tjallingiorum* var. *laricinum* from Kamchatka, Russia

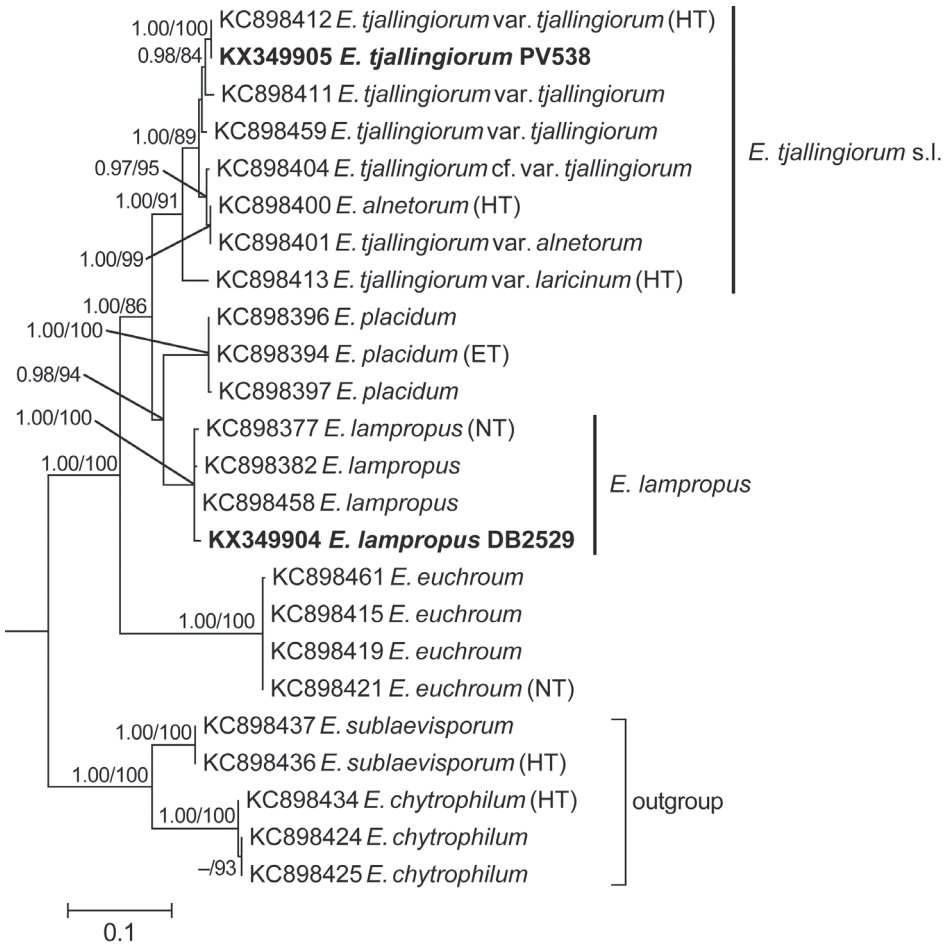

Fig. 1. 50% majority rule consensus phylogram derived from Bayesian inference analysis of nrDNA ITS sequences of *Entoloma* species. *Entoloma sublaevisporum* and *E. chytrophilum* served as outgroup. Numbers at branches represent nodal support (BI posterior probability (PP) and ML bootstrap percentage). Voucher numbers are indicated only at the two newly generated sequences which are marked in boldface. Abbreviations: HT = holotype, ET = epitype, NT = neotype. Scale bar indicates 0.1 expected changes per site per branch.

has a significant genetic distance (only 96% similarity in the ITS region) compared to the two other varieties (var. *tjallingiorum* and var. *alnetorum*).

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(22) ***Hohenbuehelia mastrucata*** (Fr.) Singer (Pleurotaceae)

Hungary, Vértes Mts: near Csákberény, Juhdöglő-völgy Forest Reserve, on *Fagus sylvatica* log; leg. V. Papp, 01.08.2012, BP 106919 (PV712), GenBank: KX349907. – Hungary, Vértes Mts: near Csákberény, Juhdöglő-völgy Forest Reserve, on *Fagus sylvatica* log; leg. V. Papp, 25.10.2013, BP 106920 (PV1019). – Hungary, Börzsöny Mts: near Hont, on decayed hardwood; leg. V. Papp, 08.10.2014, BP 106927.

For comments see *Hohenbuehelia atrocoerulea*.

(23) ***Hohenbuehelia atrocoerulea*** (Fr.) Singer

Hungary, Vértes Mts: near Csákberény, Juhdöglő-völgy Forest Reserve, on *Quercus petraea* log; leg. V. Papp, 24.10.2012, BP 106921 (PV774), GenBank: KX349906. – Hungary, Vértes Mts: near Csákberény, Juhdöglő-völgy Forest Reserve, on *Fagus sylvatica* log; leg. V. Papp, 24.10.2012, BP 106922 (PV776).

Hohenbuehelia Schulzer (anamorphic synonym: *Nematoctonus* Drechsler) is a cosmopolitan saprotrophic and nematode-destroying genus in the family Pleurotaceae Kühner belonging to the suborder Pleurotineae Aime, Dentinger et Gaya (Dentiger *et al.* 2016) in Agaricales Underw. The genus is morphologically characterised by crepidotoid to pleurotoid, rarely omphalinoid basidiocarp and the gelatinous zone beneath the pileipellis, and metuloid pseudocystidia (Koziak *et al.* 2007, Thorn and Barron 1986).

Hohenbuehelia mastrucata was described by Fries (1818) as *Agaricus mastrucatus* and it is characterised by crepidotoid basidiocarp, greyish to sordid white pileus with conical scales, and relatively thick (up to 1.5 mm) gelatinous layer (Elborne 2012). Krieglsteiner (2000) earlier stated that it is a variety of *H. atrocoerulea*, however, our phylogenetic analysis that includes the ITS sequences of both epitypes selected by Consiglio (2016) did not support this morphological concept. The ITS sequence of the Hungarian specimen (BP 106919) found in the Juhdöglő-völgy Forest Reserve (Vértes Mts) nested in the subclade of *H. mastrucata* and clustered together with the ITS sequences obtained from the epitype material (KU355336) and two North American specimens (KP026227, EF409736) with strong support (PP = 1.00, BS = 100%) (Fig. 2). In addition, a new Hungarian occurrence of the more frequent *H. atrocoerulea* (e.g. Dima *et al.* 2010, Lukács 2010) from the Vértes Mts was also verified by ITS data, which clustered together with the epitype (KU355304) and the two other sequences originated from China: GQ142024 (as "*H. reniformis*") and GQ219732 (as undetermined *Hohenbuehelia* species) (Fig. 2).

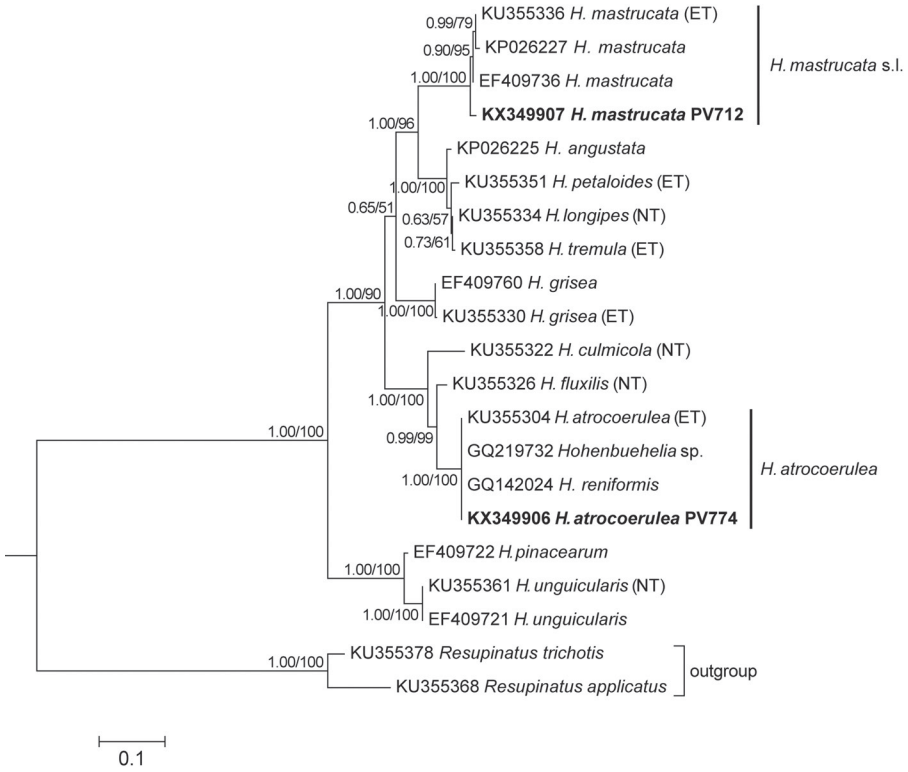

Fig. 2. 50% majority rule consensus phylogram derived from Bayesian inference analysis of nrDNA ITS sequences of *Hohenbuehelia* species. *Resupinatus trichotis* and *R. applicatus* served as outgroup. Numbers at branches represent nodal support (BI posterior probability (PP) and ML bootstrap percentage). Voucher numbers are indicated only at the two newly generated sequences which are marked in boldface. Abbreviations: ET = epitype, NT = neotype. Scale bar indicates 0.1 expected changes per site per branch.

In Hungary *Hohenbuehelia mastrucata* is listed on the unofficial red list of macrofungi (Rimóczi *et al.* 1999) as a critically endangered species. Reference to Hungarian occurrence has been found in the collection of László Hollós (as *Pleurotus mastrucatus*) from the surroundings of Szekszárd (Babos 1984). Later Babos (1989), in her comprehensive work based on the fungal collections of the Hungarian Natural History Museum (BP), mentioned only a single known locality of this species from the Szentendre Island (Central Hungary), on *Populus* log. Nagy and Gorliczai (2007) published a new record (as *H. atrocoerulea* var. *mastrucata*) from Kecskemét-Tőserdő (Southern Great Plain). Herein, new Hungarian records of this taxon are presented from the Juhdöglő-völgy Forest Reserve (Vértes Mts, Central Transdanubia) and the Börzsöny Mts (Northern Hungary).

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(24) ***Mycoacia nothofagi*** (G. Cunn.) Ryvarden (Meruliaceae)

Hungary, Vértes Mts: near Csákberény, Juhdöglő-völgy Forest Reserve, on *Fagus sylvatica* log; leg. V. Papp, 22.07.2011, BP 106923 (PV387). – Hungary, Vértes Mts: near Csákberény, Juhdöglő-völgy Forest Reserve, on *Fagus sylvatica* log; leg. V. Papp, 22.07.2011, BP 106924 (PV549). – Hungary, Vértes Mts: near Csákberény, Juhdöglő-völgy Forest Reserve, on *Fagus sylvatica* log, 47.380483° N, 18.337427° E; leg. V. Papp, 03.08.2011, BP 106925 (PV551), GenBank: KX349908. – Hungary, Vértes Mts: near Csákberény, Juhdöglő-völgy Forest Reserve, on *Fagus sylvatica* log, 47.380283° N, 18.337561° E; leg. V. Papp, 20.10.2012, BP 106926 (PV1031)

The resupinate hidnoid fungus, *Mycoacia nothofagi* (≡ *Phlebia nothofagi* (G. Cunn.) Nakasone) is distinguished by the monomitic hyphal system and the rather thick-walled, densely encrusted hymenial cystidia (Nakasone 1997). The type of this species (as "*Odontia nothofagi* G. Cunn.") was described from New Zealand, where it was grown on *Nothofagus menziesii* (Hook. f.) Oerst. (Cunningham

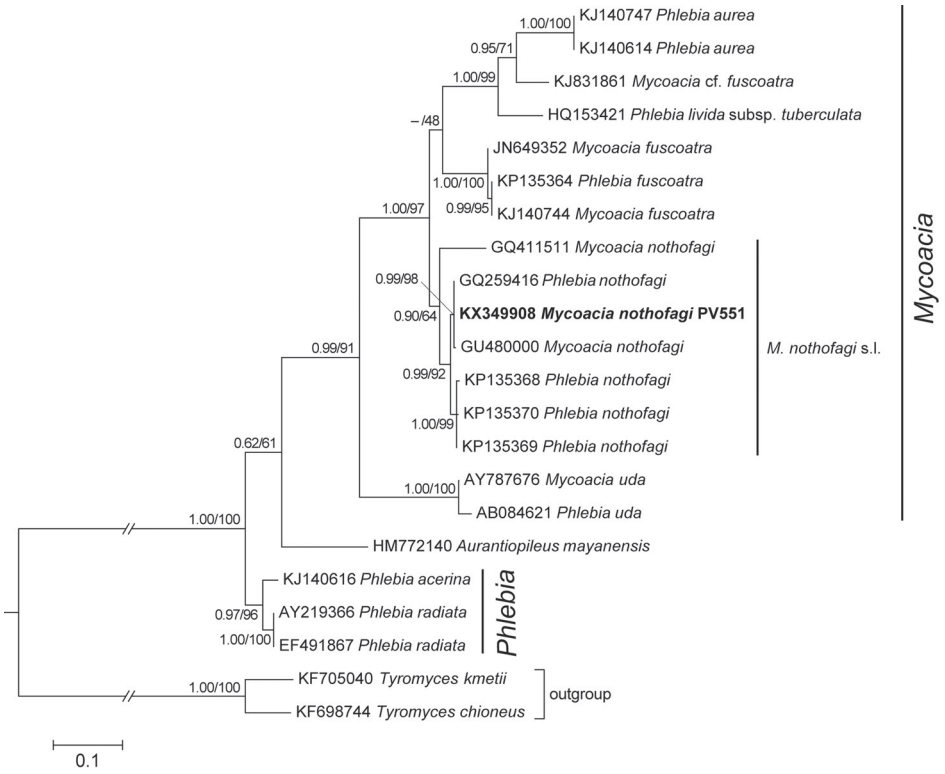

Fig. 3. 50% majority rule consensus phylogram derived from Bayesian inference analysis of nrDNA ITS sequences of *Mycoacia* species. *Tyromyces kmetii* and *T. chioneus* served as outgroup. Numbers at branches represent nodal support (BI posterior probability (PP) and ML bootstrap percentage). Voucher numbers are indicated only at the two newly generated sequences which are marked in boldface. Scale bar indicates 0.1 expected changes per site per branch.

1959). In Europe it was known as an indicator species of natural beech forests (Christensen *et al.* 2004), nevertheless, Bernicchia and Gorjón (2010) mentioned from different substrata (*Populus nigra*, *Ulmus glabra*, *Quercus ilex*, and *Abies alba*). In Europe it is known from Bosnia and Herzegovina, Bulgaria, Czech Republic, Germany, Great Britain, France, Italy, Portugal, Romania, Slovakia, Spain, and Switzerland (Bernicchia and Gorjón 2010, Nakasone 1997). In this study, *Mycoacia nothofagi* is reported as new to Hungary.

The ITS sequence obtained from the Hungarian specimen (BP 106925) identified as *Mycoacia nothofagi* based on morphology nested in the clade of *M. nothofagi* s. lato and it belonged to the subclade formed by exclusively European sequences published by Moreno *et al.* (2011) from Spain (GQ259416) and France (GU480000). The sequences of *M. nothofagi* originating from the USA (KP135368, KP135369, KP135370) and published by Floudas and Hibbett (2015) formed a sister clade of the European sequences with strong support. Furthermore, the ITS sequence (GQ411511) originating from the type locality area (New Zealand) showed significant difference towards the North American and European sequences (only 91% similarity in the ITS region), which can well be enough for species level separation of these subclades (Fig. 3).

If the sequence from New Zealand (GQ411511) published by Fukami *et al.* (2010) was identical with the type material of *M. nothofagi* (PDD7281), the European and North American "*M. nothofagi*" should probably be described as new species. However, to clarify the species limits in the complex, molecular examination of the type specimen of *M. nothofagi* and other samples, in addition to a comprehensive morphological survey, would be required.

V. Papp and B. Dima

Vascular plants

(25) ***Draba muralis*** L. (Brassicaceae)

Hungary, South Tisza Valley: Szentes, on the left side embankment of the river Tisza, in uncharacteristic secondary grasslands, ~46.68465° N, ~20.20916° E, 80 m, (9387.1); leg. A. Takács and T. Nagy, 12.04.2015, DE-Soo-38837.

Draba muralis L. is distributed from the Iberian Peninsula and North Africa (Morocco, Algeria) to the Caucasus Mountains and to the south of Sweden and Finland (Jalas *et al.* 1996) including introductions, e.g. in UK, France, Germany, Austria (Ratcliffe 1960, Jalas *et al.* 1996), and maybe in the northern part of the area (Walters and Akeroyd 1993). In the south of its range *D. muralis* is connected to higher altitudes (Ratcliffe 1960). This annual species generally

occurs on open, stony soils or sands (e.g. Oberdorfer 1949, Ratcliffe 1960, Walters and Akeroyd 1993).

The presence of this taxon in Hungary is well known (Jávorka 1924, Simon 1992, Barina 2009), but the known occurrences are confined to colline regions of Transdanubia and the western part of the North Hungarian Mountains (Börzsöny, Naszály) (Barina 2009, Bartha *et al.* 2015). The first record of *D. muralis* in the Tiszántúl region was discovered in spring, 2015. A few hundreds of individuals grew on the outside (floodless) slope of Tisza's embankment, exposed to NE, in uncharacteristic, secondary mesophile grasslands. Supposedly, this remote occurrence is a result of introduction, since (i) there are no other known localities of *D. muralis* in the Tiszántúl and the Duna–Tisza Interfluve, (ii) the floodplain of Tisza with non-calcareous sediments represents unfavourable habitats for this species, (iii) in addition, it appeared on a construction where tourist traffic is general.

A. Takács and T. Nagy

(26) ***Rubus armeniacus*** Focke (Rosaceae)

Hungary, North Hungarian Mts (Északi-középhegység), Miskolci-Bükkalja micro-region, Miskolc, Kőporos Str., spreading spontaneously in hedges, 48.10595° N, 20.75559° E, 145 m; leg. J. Koscsó, 03.05.2014, det.: G. Király (7890.4); – Rákóczi Str., spontaneous scrub at a garden retaining wall, 48.10035° N, 20.78244° E, 135 m; leg. J. Koscsó, 25.08.2015, det.: G. Király (7890.4). – Miskolc, Tímár Str., shrubbery at a garden fence, 48.07063° N, 20.75798° E, 129 m; leg. G. Király & A. Schmotzer, 18.04.2016 (7990.2).

Rubus armeniacus (*Rubus* ser. *Discolores* (P. J. Müller) Focke) is an invasive alien bramble of Caucasian origin that became widespread in Central and Western Europe in the last century (Kurtto *et al.* 2010, Weber 1995,). The species was first recognised with scattered occurrences mainly W of the Danube River in Hungary by Király *et al.* (2014), whereas it has not been yet recorded in the northeastern part of the country. Here we report on the first occurrences in the North Hungarian Mts (and, at the same time, in the Carpathians) based on some introduced stands found in the vicinity of Miskolc. The species is probably a garden escape in this city that grows both in urban and suburban areas and shows unambiguously an advancing tendency; this behaviour is similar to those observed e.g. in the case of cities of Sopron and Budapest in Hungary. The further expansion of the species is expected in semi-ruderal habitats of the Turkey oak and forest steppe belts in the North Hungarian Mts (e.g. along railways, in black locust woods and abandoned pastures), however, its spreading seems to be rather unlikely in closed natural forest communities of the region.

G. Király and J. Koscsó

(27) ***Najas marina*** L. (Hydrocharitaceae)

Hungary, Hernád Valley: Hernádszurdok, in an abandoned meander (oxbow) between Felső-rét and Malom-szer areas; leg. Á. Malatinszky, 20.07.2013, s.n. (photodocumented) (7593.1).

This species is widespread across Europe, Africa, Asia, the Americas, Australia, and several oceanic islands, in various aquatic habitats from freshwaters till brackish aquatic habitats, including alkaline lakes (Stuckey 1985).

Although this taxon is known from several locations on the Great Hungarian Plain, the Lake Balaton, and Western Transdanubia, no records were found so far in the Northern Hungarian floristical region (Matricum). Its closest localities are found in the interfluve of the Bodrog and Tisza rivers (Bartha *et al.* 2015). Therefore, this record largely extends the species' known area in Hungary.

Á. Malatinszky

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Összefoglaló: Jelen közleményünk a tavaly megkezdett, regionális jelentőségű előfordulásokat és nevezéktani megjegyzéseket tartalmazó sorozat (Barina *et al*. 2015) második része. Ebben a részben két, hazánkra új gombafaj (*Entoloma tjallingiorum* és *Mycoacia nothofagi*) adatát; egy, a Vértes és a Börzsöny területére új gombafajét (*Hohenbuehelia mastrucata*); valamint két további gombafaj (*Entoloma lampropus* és *Hohenbuehelia atrocoerulea*) megerősítését és új adatait közöljük. A Tiszántúl területére újként közöljük a *Draba muralis* előfordulását és az Északi-középhegység területére a *Rubus armeniacus* és *Najas marina* előfordulását. Utóbbiak közül a *Draba muralis* tiszántúli megjelenése behurcolás, míg a *Rubus armeniacus* miskolci megjelenése kivadulás eredménye lehet.

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