A molecular perspective on generic concepts in the *Hypotrachyna* clade
(Parmeliaceae, Ascomycota)

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Abstract

Recently, molecular phylogenetic studies have revolutionized the generic concepts in Parmeliaceae and in lichen forming fungi in general. In the present study, the generic delimitation in the *Hypotrachyna* clade is revised using a molecular phylogeny of nuclear ITS, LSU and mitochondrial SSU rDNA sequences of 88 hypotrachynoid taxa. Morphological and chemical features are also revised in each group. 118 sequences are newly generated for this study. Our phylogenetic analyses show the polyphyly of *Hypotrachyna* as currently circumscribed which falls into four well-supported and one unsupported clade. *Cetrariastrum*, *Everniastrum* and *Parmelinopsis* are nested within *Hypotrachyna* s. lat., *Parmelinopsis* being also polyphyletic and nested in one of the *Hypotrachyna* clades. *Cetrariastrum* is monophyletic but clustered within *Everniastrum*. Two alternative hypotheses tests significantly rejected the monophyly of these three genera. As a consequence, the genera *Cetrariastrum*, *Everniastrum*, and *Parmelinopsis* are reduced to synonymy with *Hypotrachyna*. Furthermore, we here propose an alternative classification to recognize the well-supported clades at subgeneric level and leave the remaining species unclassified within the genus. Five new subgenera are proposed: *Hypotrachyna* subgen. *Cetrariastrum*, *Hypotrachyna* subgen. *Everniastrum*, *Hypotrachyna* subgen. *Parmelinopsis*, and *Hypotrachyna* subgen. *Sinuosae*. Forty-nine new combinations are proposed.

Key words: generic classification, lichens, molecular systematics, parmelioid lichens, taxonomy

Introduction

Traditionally, the generic classification in lichenised fungi is based on morphological, anatomical and chemical characters. In Parmeliaceae, morphology of vegetative thalli have traditionally played an important role in circumscribing genera with a number of generic segregates being described over the last three decades (Culberson & Culberson 1981; Elix 1993b; Elix & Hale 1987; Elix et al. 1986; Hale 1974a, 1974b, 1984, 1986a, 1986b; Krog 1982; Kurokawa 1991; Sipman 1980; Sipman 1986). However, in recent years a number of taxonomic re-evaluations, mainly based on molecular phylogenies, have been proposed (Amo de Paz et al. 2010a; Amo de Paz et al. 2010b; Blanco et al. 2005; Blanco et al. 2004b; Crespo et al. 2010b; Crespo et al. 2007; Divakar et al. 2006; Divakar et al. 2010; Divakar et al. 2012; Thell et al. 2006; Wirtz et al. 2006). These studies revealed that the taxonomic significance of phenotypical characters of the vegetative thallus was overestimated in several groups. As a consequence, some former segregates were synonymized, such as *Rimeliella* Kurokawa (1991: 1) within *Canomaculina* Elix & Hale (1987: 239); nine genera in
Xanthoparmelia; Canomaculina, Concamerella Culberson & Culberson (1981: 307) and Rimelia Hale & Fletcher (1990: 23) within Parmotrema Massalongo (1860: 248) (reviewed by Crespo et al. 2011; Thell et al. 2012). At the same time, molecular data have helped to discover previously unrecognized lineages (genera) within the family Parmeliaceae. Examples include the genera Melanelixia Blanco et al. (2004a: 881), Melanohalea Blanco et al. (2004a: 882) and Montanelia Divakar et al. (2012: 222) as segregates of Melanelia Esslinger (1978: 46) s. lat. (Blanco et al. 2004a; Divakar et al. 2012); Austroparmelia Crespo et al. (2010a: 209) segregated from Parmelina Hale (1974a: 481). Lastly, Remototrachyna Divakar et al. (2010: 584) was segregated from Hypotrachyna Hale (1974b: 340) s. lat. (Divakar et al. 2010). All the aforementioned segregates were based on molecular and morphological data.

A group of tropical parmelioid lichens with predominantly corticolous species, lacking pseudocyphellae, and having a pored epicortex includes the genera Bulbothrix Hale (1974a: 479), Cetrariastrum Sipman (1980: 335), Everniastrum Hale ex Sipman (1986: 237), Hypotrachyna s. lat., Parmelinella Elix & Hale (1987: 241) and Parmelinopsis Elix & Hale (1987: 242). These genera were included in the Hypotrachyna clade in previous molecular studies (Blanco et al. 2006; Crespo et al. 2007; Divakar et al. 2006). However, in more recent studies the genera Bulbothrix, Parmelinella and Remototrachyna were shown to be distantly related to the other genera and placed in the Parmelina clade (Crespo et al. 2010b; Divakar et al. 2010). The genera Cetrariastrum, Everniastrum, Hypotrachyna s. lat., and Parmelinopsis clustered together in the Hypotrachyna clade, which is one of the larger major clades among parmelioid lichens (Parmeliaceae) (Crespo et al. 2010b; Divakar et al. 2010). Within the Hypotrachyna clade, the genus Hypotrachyna is the largest with ca. 188 described species. It includes mainly tropical species growing in moderate to high altitude with a centre of diversity in tropical America (Sipman et al. 2009). Hypotrachyna species are characterized by a pored epicortex, narrow, sublinear to linear elongate lobes, with truncate apices; dichotomously branched rhizines, oval-ellipsoid ascospores and bifusiform conidia (Divakar et al. 2001, 2010; Elix 1993b; Hale 1975). Parmelinopsis (25 species), a pantemperate and pantropical genus is a segregate of the genus Parmelina (Elix & Hale 1987). The genus is readily distinguished by having sublinear, narrow, apically truncate grey lobes, simple cilia, and simple to weakly dichotomously branched rhizines; ellipsoid, relatively large ascospores and cylindrical-bifusiform conidia. Everniastrum (40 species) is characterized by regularly dichotomously branched lobes, apothecia with hollow stipe, relatively large asci and a thin hypothecium (Sipman 1980). Cetrariastrum sensu Sipman (1980) is similar to the former genus, but distinguished by having irregularly branched lobes, apothecia with solid stipe, smaller asci and a thicker hypothecium. Both genera, whose distinction has been disputed (Culberson & Culberson 1981), share common characters, such as long, linear, canaliculate lobes, long marginal cilia and both have a pantropical distribution (Sipman 1986).

The present study aims to clarify the phylogenetic positions of Cetrariastrum, Everniastrum and Parmelinopsis and also test the hypothesis that the morphological characters have evolved independently within the clade as adaptations to ecological conditions. To address these questions, we used three molecular markers ITS, nuclear LSU and mitochondrial SSU rDNA, and analysed these data using Bayesian and maximum likelihood approaches. We sampled specimens from all the continents of their distribution: America, Africa, Asia, Australia and Europe. The morphological features of the species were also revised.

Materials and Methods

Taxon sampling:—Data matrices of 88 samples, representing 58 species of the Hypotrachyna clade (Crespo et al. 2010b) were assembled using sequences of nuclear ITS, LSU and mitochondrial SSU rDNA. Two species of Parmeliopsis were used as outgroup, since this genus has previously been shown to be closely related to this clade (Crespo et al. 2010b). GenBank accession numbers and details of studied material are shown in Table 1. The data sets include 122 sequences from previous publications by our group (Blanco et al. 2004a; Crespo et al. 2007; Divakar et al. 2006; Divakar et al. 2010; Lumbsch et al. 2008), five downloaded from GenBank and 118 newly generated sequences.
**Molecular methods:**—Small samples prepared from freshly collected and frozen specimens were ground with sterile plastic pestles. Total genomic DNA was extracted using the DNeasy Plant Mini Kit (Qiagen, Hilden, Germany) according to the manufacturer’s instructions but with slight modifications (Crespo et al. 2001). Dilutions of 1:10 of the total DNA were used for PCR amplifications of the ITS, nu LSU rDNA and mt SSU rDNA regions. Primers, PCR and cycle sequencing conditions were the same as described previously (Crespo et al. 2007; Divakar et al. 2005). Sequence fragments obtained were assembled with SeqMan 4.03 (DNAStar) and manually adjusted.

**Sequence alignments:**—We used the program MUSCLE (Edgar 2004) to align DNA sequences of 88 specimens (Table 1) for each data set separately. The program Gblocks v0.91b (Castrésana 2000; Talavera & Castrésana 2007) was used to remove regions of alignment uncertainty, using options for a “less stringent” selection on the Gblocks web server (http://molevol.cmima.csic.es/castresana/Gblocks_server.html).

**Phylogenetic analyses:**—The alignments were analyzed using maximum likelihood (ML) and a Bayesian approach (B/MCMC). ML analyses were performed using an online version of the program RaxML v7.0.4 (http://phylobench.vital-it.ch/raxml-bb/; Stamatakis 2006; Stamatakis et al. 2008) for the partitioned combined data set. We used the GTRGAMMA model, which includes a parameter (Γ) for rate heterogeneity among sites and chose not to include a parameter for estimating the proportion of invariable sites (Stamatakis 2006; Stamatakis et al. 2008). The bootstrap analysis was run with 1000 pseudoreplicates.

Bayesian analyses were done using the program MrBAYES 3.1.2 (Huelsenbeck & Ronquist 2001). Models of DNA sequence evolution for each locus were selected with the program jModelTest v0.1 (Posada 2008), using the Akaike information criterion (AIC; Akaike 1974). The concatenated three-loci data set was partitioned as ITS, nuLSU and mtSSU, specifying the best fitting model, allowing unlinked parameter estimation and independent rate variation. No molecular clock was assumed. Four parallel runs were made with 4,000,000 generations starting with a random tree and employing 8 simultaneous chains each. Every 200th tree was saved into a file. The first 4000 trees were deleted as the “burn in” of the chains.

We used AWTY (Nylander et al. 2007) to compare splits frequencies in the different runs and to plot cumulative split frequencies to insure that stationarity was reached. A majority rule consensus tree with average branch lengths was calculated using the sumt option of MrBayes.

We used a ML approach to examine the heterogeneity in phylogenetic signal among the three data partitions (Lutzoni et al. 2004). For the three loci and the concatenated analyses, the set of topologies reaching ≥70% bootstrap under likelihood was estimated. The combined data set topology was then compared for conflict with ≥70% bootstrap intervals of the single gene analyses. If no conflict was evident, it was assumed that the two data sets were congruent and could be combined.

Only clades that received bootstrap support above or equal 70% in ML analysis or posterior probabilities equal or above 0.95 in MrBayes analysis were considered as well supported. Phylogenetic trees were drawn using TREEVIEW (Page 1996).

**Hypothesis testing:**—The results of the phylogenetic analyses were incongruent with the current generic classification in the Hypotrachyna clade. Hence we tested whether our data were sufficient to reject the monophyly of currently accepted genera. For the hypothesis testing two different methods were employed: 1. Shimodaira-Hasegawa (SH) test (Shimodaira & Hasegawa 1999) and 2. expected likelihood weight (ELW) test (Strimmer & Rambaut 2002). The SH and ELW tests were performed using Tree-PUZZLE 5.2 (Schmidt et al. 2002) with the combined data set on a sample of 200 unique trees, the best trees agreeing with the null hypotheses, and the unconstrained ML tree. These trees were inferred in Tree-PUZZLE employing the GTR+I+G nucleotide substitution model.

**Morphological and chemical studies:**—Thallus morphology was studied using a Leica Wild M 8 dissecting microscope for the measurement of lobe shape, size and width. All specimens included in the molecular analysis were studied (see Table 1).

Chemical constituents were studied by thin layer chromatography using standardized methods (Culberson 1972; Culberson & Johnson 1982).
Results and Discussion

Phylogenetic studies:—A total of 34 new nuclear ITS, 43 new LSU rDNA and 41 new mitochondrial SSU rDNA sequences were generated (Table 1). These were aligned with 122 sequences previously published by us and five downloaded from GenBank (Table 1). The aligned matrix contained 453 unambiguously aligned nucleotide position characters in ITS, 835 in nu LSU and 783 in mt SSU. The final alignment of combined data set was 2071 positions in length, with 645 variable characters. The ITS PCR product obtained ranged between 600 to 800 bp. Differences in size were due to the presence or absence of insertions of about 200 bp identified as group I introns (Gutierrez et al. 2007) at the 3’ end of the SSU rDNA. We excluded group I introns and 166 bp of the mtSSU and 47 bp of the ITS alignments from the analysis using GBlocks. GTR+G, TIM1+I+G, and TIM1+I+G are resulted as best fit model of evolution for ITS, nu LSU and mt SSU respectively. Topologies of single-locus analyses did not show conflict and hence combined analyses were performed. Since the topologies of the ML and B/MCMC analyses did not show any supported conflict, only the 50% majority-rule consensus tree of Bayesian tree sampling is shown with nodes in bold that received strong support either in ML or Bayesian analyses (i.e. PP ≥0.95 in B/MCMC analysis and ML bootstrap ≥70%) (Fig. 1). B/MCMC posterior probabilities equal or above 0.95 are indicated above branches, while values below branches are bootstrap support values of ML analysis.

**TABLE 1.** Specimens used in the study, with location, reference collection detail and GenBank accession numbers. Newly obtained sequences for this study are in bold face. Missing data are indicated with dash (—).

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<th>Species</th>
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<th>Voucher Specimens</th>
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TABLE 1 (continued)

"... continued on the next page"
The best tree under likelihood had a likelihood value of \( \ln -15002.199 \). In the B/MCMC analysis, the likelihood parameters in the sample had the following mean (Variance): \( \ln L = -15045.533 (0.356) \), the gamma shape parameter alpha = 0.312 (0.002) and pinvar = 0.496 (0.002).

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### TABLE 1 (continued)

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<th>Species</th>
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The best tree under likelihood had a likelihood value of \( \ln -15002.199 \). In the B/MCMC analysis, the likelihood parameters in the sample had the following mean (Variance): \( \ln L = -15045.533 (0.356) \), the gamma shape parameter alpha = 0.312 (0.002) and pinvar = 0.496 (0.002).

The currently accepted genera *Everniastrum*, *Hypotrachyna* and *Parmelinopsis* are not monophyletic, with *Everniastrum* and *Hypotrachyna* being paraphyletic, and *Parmelinopsis* polyphyletic. *Cetrariastrum* is monophyletic but clustered within *Everniastrum* and this clade is nested within *Hypotrachyna* s.lat. Monophyly of these three genera was rejected by the two alternative hypothesis tests (\( p<0.001 \) in all cases). This clearly indicates that the current generic concept in the *Hypotrachyna* clade does not reflect phylogenetic relationships and this is consistent with previous studies (Blanco *et al*. 2006; Crespo *et al*. 2010b; Crespo *et al*. 2007; Divakar *et al*. 2006; Lumbsch *et al*. 2008).
FIGURE 1. 50% majority-rule consensus tree of the molecular phylogenetic relationships in the Hypotrachyna clade, based on 64000 trees from a B/MCMC tree-sampling procedure of a combined dataset of ITS, nu LSU, and mt SSU sequences. Two species of Parmeliopsis used as outgroup. Posterior probabilities ≥ 0.95 are given above the branches, and values below the branches are ML bootstrap values ≥ 70%. Branches that received strong support in any of the two analyses (RaxML and B/MCMC) are in boldface. Asterisk mark shows the type species of the genus Hypotrachyna. Clades numbered indicate phylogenetic clusters explained in the text.
Several well supported clades can be found within the *Hypotrachyna* clade. Clade 1 is sister to the remaining species of the clade. It includes *H. fissicarpa*, endemic to east and south Africa, and the *H. longiloba* group that includes species with separate, linear lobes, a densely rhizinate lower surface, and containing atranorin and alectoronic, α- and β- collatolic, gyrophoric or anziaic acids. *Hypotrachyna fissicarpa*, however, has short, sublinear, imbricate lobes, a moderately rhizinate lower surface and contains atranorin and protocetraric acid. Species with similar morphology and chemistry can be found in other clades, such as clade 5 (*Hypotrachyna* s. str.), and the unsupported clade (Fig. 1). The sister-group of clade 1 is well-supported and consists of two major groups, only one of them, however, receives strong support. The latter consists of clade 2 and a number of species currently placed in *Hypotrachyna* which form an unsupported sister-group to clade 2. Clade 2 mostly includes species with separate, linear lobes and a densely rhizinate lower surface, similar to species of clade 1. However, taxa in clade 2 contain usnic acid in the cortex, rarely accompanied by atranorin. *Hypotrachyna microblasta* (Vain.) Hale (1975: 47) differs morphologically by having short, sublinear lobes, but agrees with the other species in clade 2 in having a densely rhizinate lower surface and containing usnic acid. The species in the unsupported sister-group of clade 2 are morphologically and chemically similar to *Hypotrachyna* s.str. [clade 5, with type species *H. brasiliiana* (Nyl.) Hale (1974b: 341)], but only distantly related to that clade. Clade 3 includes species of the genus *Cetrariastrum* and *Everniastrum lipidiferum* (Hale & Wirth) Hale ex Sipman (1986: 241). *Cetrariastrum* has been distinguished from *Everniastrum* based on an irregular branching pattern of the lobes, smaller asci, thicker hypothecium in *Cetrariastrum*, and a different apothecial stalk (Sipman 1986). Clade 4 includes all species currently placed in the genus *Everniastrum*, with the exception of *E. lipidiferum*. *Hypotrachyna* s.str. is the well supported clade 5. This clade and clade 6 have a well-supported sister-group relationship. Clade 6 includes species currently placed in *Hypotrachyna* and *Parmelinopsis*. The latter genus has traditionally been separated from *Hypotrachyna* based on the presence of cilia and less richly branched rhizines, characters that are regarded as species-specific but unreliable at higher rank in other groups of parmelioid lichens, such as *Parmotrema* (Divakar & Upreti 2005; Elix 1994; Krog & Swinscow 1981).

Characters, such as elongate lobes or presence of usnic acid, have evolved several times independently within the *Hypotrachyna* clade, suggesting that they have an adaptive value in certain habitats. The traditionally accepted genera in the *Hypotrachyna* clade were almost entirely circumscribed based on characters of the vegetative thallus, with the exception of the genus *Cetrariastrum*. Vegetative characters have repeatedly shown to be highly plastic in various groups of lichenized fungi (Högnabba 2006; Lumbsch et al. 2010; Parmmen et al. 2010; Stenroos & DePrist 1998; Tehler & Irestedt 2007). Thus it is not surprising that the morphology-based genera within the *Hypotrachyna* clade were not confirmed by our phylogenetic analysis.

**Taxonomic conclusions:**—Based on our phylogenetic analysis, we propose to reduce the genera *Cetrariastrum*, *Everniastrum*, and *Parmelinopsis* to synonymy with *Hypotrachyna*. An alternative classification would recognize all well-supported clades at generic level. This, however, would require the description of additional new genera that would be difficult to circumscribe phenotypically, and further, would leave the bulk of *Hypotrachyna* s.lat. species (sister-group to clade 2, Fig. 1) in an unresolved position. As an alternative, we propose here to recognize the well-supported clades at subgeneric level and leave the remaining species unclassified within the genus. Recognition at the subgeneric level also has the advantage that monophyletic lineages that are clustered within the paraphyletic *Hypotrachyna* s.lat. can be recognized without producing paraphyletic taxa (Hörandl & Stuessy 2010). We propose to recognize the *H. longiloba* group in clade 1 as *Hypotrachyna* subgen. *Longilobae*, clade 2 as *Hypotrachyna* subgen. *Simuosae*, clade 3 as *Hypotrachyna* subgen. *Cetrariastrum*, clade 4 as *Hypotrachyna* subgen. *Everniastrum*, and clade 6 as *Hypotrachyna* subgen. *Parmelinopsis*. As a consequence of the revised generic concept of *Hypotrachyna*, several new subgenera need description and new combinations are necessary, and these are proposed below.
New subgenera:

**Hypotrachyna subgen. Cetrariastrum** (Sipman) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. et stat. nov.* MycoBank No.: MB 803542


A subgenus in the genus *Hypotrachyna*, corresponding to clade 3 in Fig. 1, including all species placed in *Cetrariastrum* by Sipman (1980, 1986) plus *Everniastrum lipidiferum*. The latter is included provisionally because it appears more distantly related to the other species.


A subgenus in the genus *Hypotrachyna*, corresponding to clade 4 in Fig. 1, including all species placed in *Everniastrum* by Sipman (1980, 1986) excluding *Everniastrum lipidiferum*.

**Hypotrachyna subgen. Longilobae** Divakar, A. Crespo, Sipman, Elix & Lumbsch, *subgen. nov.* MycoBank No.: MB 803544


A new subgenus in the genus *Hypotrachyna*, corresponding to clade 1 (excl. *H. fissicarpa*) in Fig. 1, characterized by separate, linear lobes, densely rhizinate lower surface and the presence of atranorin, alectoronic, anziaic, α- and β-collatolic, and gyrophoric acids. All species included are distributed at higher elevation mainly in the Neotropics, but also in the southern United States and East Africa.

**Hypotrachyna subgen. Parmelinopsis** (Elix & Hale) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. et stat. nov.* MycoBank No.: MB 803545


A subgenus in the genus *Hypotrachyna*, corresponding to clade 6 in Fig. 1, including all species currently placed in *Parmelinopsis* plus *Hypotrachyna* species with sparsely dichotomously branched rhizines, and containing gyrophoric, lecanoric and olivetoric acids in the medulla.

**Hypotrachyna subgen. Sinuosae** Divakar, A. Crespo, Sipman, Elix & Lumbsch, *subgen. nov.* MycoBank No.: MB 803546

Type species:—*Hypotrachyna sinuosa* (Sm.) Hale (1975: 63). *Lichen sinuosus* Smith (1809: tab. 2050).

A new subgenus in the genus *Hypotrachyna*, corresponding to clade 2 in Fig. 1, characterized by combination of features in having mostly separate, linear lobes, densely rhizinate lower surface and the presence of usnic acid, galbinic, norstictic, stictic and salazinic acids. All species included are mainly distributed at higher elevation.
New combinations

Subgenus Cetrariastrum:

**Hypotrachyna dubitans** (Sipman) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov.* MycoBank No.: MB 803547

*Cetrariastrum dubitans* Sipman (1980: 342).

**Hypotrachyna ecuadoriensis** (R. Sant.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov.* MycoBank No.: MB 803548


**Hypotrachyna kaernefeltii** Divakar, A. Crespo, Sipman, Elix & Lumbsch, *nom. nov.* MycoBank No.: MB 803549


**Hypotrachyna lipidifera** (Hale & M. Wirth) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov.* MycoBank No.: MB 803550


Subgenus Everniastrum:

**Hypotrachyna africana** (Hale) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov.* MycoBank No.: MB 803551


**Hypotrachyna alectoricalica** (W.L. Culb. & C.F. Culb.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov.* MycoBank No.: MB 803552


**Hypotrachyna americana** (Meyen & Flot.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov.* MycoBank No.: MB 803553


**Hypotrachyna angolensis** (W.L. Culb. & C.F. Culb.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov.* MycoBank No.: MB 803554


**Hypotrachyna arsenei** (Hale & M. Wirth) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov.* MycoBank No.: MB 803555


**Hypotrachyna arvidssonii** (Sipman) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov.* MycoBank No.: MB 803595

Hypotrachyna billingsii (W.L. Culb. & C.F. Culb.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803556

Hypotrachyna catawbiensis (Degel.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803557
Parmelia soroccheila var. catawbiensis Degelius (1941: 64); Cetrariastrum catawbiense (Degel.) Culberson & Culberson (1981: 281); Everniastrum catawbiense (Degel.) Hale ex Sipman (1986: 237).

Hypotrachyna chilensis (Kurok.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803558

Hypotrachyna cirrhata (Fr.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803559
Parmelia cirrhata Fries (1825: 283); Cetrariastrum cirrhatum (Fr.) Culberson & Culberson (1981: 283); Everniastrum cirrhatum (Fr.) Hale ex Sipman (1986: 237).

Hypotrachyna columbiensis (Zahlbr.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803560

Hypotrachyna constictovexans (Sipman) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803561
Everniastrum constictovexans Sipman in Lumbsch et al. (2011: 53).

Hypotrachyna diffractaica (Y.M. Jiang & J.C. Wei) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803562

Hypotrachyna fragilis (Sipman) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803563

Hypotrachyna latiloba (Sipman) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803564

Hypotrachyna limiformis (Taylor) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803565

Hypotrachyna mexicana (Egan) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803566

Hypotrachyna neocirrhata (Hale & M. Wirth) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803567
Hypotrachyna neohalei Divakar, A. Crespo, Sipman, Elix & Lumbsch, nom. nov. MycoBank No.: MB 803568

Hypotrachyna neotropica Divakar, A. Crespo, Sipman, Elix & Lumbsch, nom. nov. MycoBank No.: MB 803569

Hypotrachyna nepalensis (Taylor) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803570

Hypotrachyna nigrociliata (de Lesd.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803571

Hypotrachyna plana (Sipman) Divakar, A. Crespo, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803594

Hypotrachyna pseudonepalensis (Hale & M. Wirth) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803572

Hypotrachyna rhizodendroidea (J.C. Wei & Y.M. Jiang) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803573

Hypotrachyna scabrida (Elix & Pooprang) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803574

Hypotrachyna sinensis (J.B. Chen & J.C. Wei) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803575

Hypotrachyna sorocheila (Vain.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803576
Parmelia sorocheila Vainio (1899: 123); Cetrariastrum sorocheilum (Vain.) Culberson & Culberson (1981: 292); Everniastrum sorocheilum (Vain.) Hale ex Sipman (1986: 242).

Hypotrachyna subnepalensis (Hale) Divakar, A. Crespo, Sipman, Elix & Lumbsch, comb. nov. MycoBank No.: MB 803577
**Hypotrachyna subplana** (Sipman) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov*. MycoBank No.: MB 803578

**Hypotrachyna subsorocheila** (Y.M. Jiang & J.C. Wei) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov*. MycoBank No.: MB 803579

**Hypotrachyna subvexans** (Sipman) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov*. MycoBank No.: MB 803580

**Hypotrachyna vexans** (Zahlbr. ex W.L. Culb. & C.F. Culb.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov*. MycoBank No.: MB 803581

Subgenus *Parmelinopsis*:

**Hypotrachyna bonariensis** (Adler & Elix) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov*. MycoBank No.: MB 803582

**Hypotrachyna cleefii** (Sipman) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov*. MycoBank No.: MB 803583

**Hypotrachyna ectypa** (Brusse) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov*. MycoBank No.: MB 803584

**Hypotrachyna expallida** (Kurok.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov*. MycoBank No.: MB 803585

**Hypotrachyna heteroloba** (Zahlbr.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov*. MycoBank No.: MB 803586

**Hypotrachyna jamesii** (Hale) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov*. MycoBank No.: MB 803587

**Hypotrachyna megadactyla** (Aptroot) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov*. MycoBank No.: MB 803588

Hypotrachyna nagalandica (K. Singh & Sinha) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov.* MycoBank No.: MB 803590

Hypotrachyna neodamaziana (Elix & J. Johnst.) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov.* MycoBank No.: MB 803591

Hypotrachyna neoprotocetrarica Divakar, A. Crespo, Sipman, Elix & Lumbsch, *nom. nov.* MycoBank No.: MB 803592

Hypotrachyna schindleri (Hale) Divakar, A. Crespo, Sipman, Elix & Lumbsch, *comb. nov.* MycoBank No.: MB 803593

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