

*ANASTROPHYLLUM ELLIPTICUM* INOUE (JUNGERMANNIALES, MARCHANTIOPHYTA),  
A NEW SPECIES FOR RUSSIAN LIVERWORT FLORA

*ANASTROPHYLLUM ELLIPTICUM* INOUE (JUNGERMANNIALES, MARCHANTIOPHYTA) –  
НОВЫЙ ВИД ДЛЯ ФЛОРЫ ПЕЧЁНОЧНИКОВ РОССИИ

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Abstract

An integrative taxonomy approach based on analyses of morphological, ecological, geographical and nucleotide sequences (ITS1-2 nrDNA, *trnL*-F and *trnG*-intron cpDNA) data allowed determining *Anastrophyllum ellipticum* Inoue, a species found in the Altai Mts. (South Siberia) and new for Russia. Detail description and illustrations are provided, its morphological differences from related *A. lignicola* D.B. Schill & D.G. Long are discussed.

Резюме

Комплексный подход, основанный на анализе морфологических, экологических, географических и нуклеотидных (ITS1-2 ядДНК, *trnL*-F и интрона гена *trnG* хпДНК) данных, позволил выявить новый вид для флоры печёночников России – *Anastrophyllum ellipticum* Inoue, найденный в горах Алтая (Южная Сибирь). Приводятся детальное описание и рисунки, обсуждаются морфологические отличия от близкого вида *A. lignicola* D.B. Schill & D.G. Long.

KEYWORDS: *Anastrophyllum ellipticum*, *Anastrophyllum lignicola*, *trnL*-F, *trnG*-intron cpDNA, ITS1-2 nrDNA, Altai Mts., South Siberia, Russia,

INTRODUCTION

During a field trip in the Katunsky State Nature Biosphere Reserve (the Altai Mountains, South Siberia, Russia) in September 2012, the senior author collected a liverwort specimen which differed from all known *Anastrophyllum* species in Russia by a combination of the following features: very small size, 2-celled ellipsoid gemmae on the tips of shoots with unmodified leaves and dioecious condition (only male plants were found). To facilitate determination, we tested this *Anastrophyllum* specimen for its phylogenetic relationships with other Holarctic *Anastrophyllum* s.l. taxa with known DNA sequences. On the obtained trees, our Altai specimen was found in one clade with a sample of *A. lignicola* D.B. Schill & D.G. Long, kindly provided to KPABG herbarium by Prof. D.G. Long (CHINA: Yunnan Province, Digging Pref., Bai Ma Chan, 6.VI.1993 Long # 24067). *Anastrophyllum lignicola* has been recently described by Schill & Long (2002) and is known from Bhutan and China (Yunnan). However, a comparison of morphological features of both discussed *Anastrophyllum* specimens revealed some differences. Following a suggestion of Prof. Long, we compared Altaian plants with Japanese species *Anastrophyllum ellipticum* Inoue (Inoue, 1978) that resembled *A. lignicola* in morphology. This poorly known

species has long been considered as endemic of Japan (Higuchi, 2011), but recently has also been reported from southwest Sichuan, China (Long, 2011). Unfortunately, we were unable to study specimens of *A. ellipticum* Inoue morphologically and molecularly, but the *Anastrophyllum* plants from the Altai fit the type description of *A. ellipticum* perfectly.

In this study, we analyse ITS1-2 nrDNA, *trnL*-F and *trnG*-intron cpDNA nucleotide sequences, demonstrate phylogenetic relationships of the new Altai specimen to the known *Anastrophyllum* s.l. taxa, and provide its morphological description.

MATERIAL AND METHODS

**Taxon sampling.** Together with the enigmatic *Anastrophyllum* specimen from the Altai, our DNA analysis involved *A. assimile* (Hook.) Stephani, *A. michauxii* (F. Weber) H.Buch, *A. lignicola*, *A. sphenoloboides* R.M. Schust., *Sphenolobus minutus* (Schreb.) Berggr., *S. saxicola* (Schrad.) Steph. and *Crossocalyx hellerianus* (Nees ex Lindenb.) Meyl. gathered from different localities of Russia, Norway, South Korea, China, and USA. In total 15 specimens of four *Anastrophyllum* s.str. species were included in the analyses. *Barbilophozia lycopodioides* (Wallr.) Loeske was chosen as outgroup basing on our published results (Vilnet *et al.*, 2010). We re-run ITS1-2

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Table 1. List of taxa, specimen vouchers and GenBank accession numbers. In *Anastrophyllum ellipticum*, ITS1 and ITS2 have different accession numbers, marked by asterisk \* or double asterisk \*\* correspondingly.

Taxon	Specimen voucher (Herbarium)	GenBank accession numbers		
		ITS1-2	<i>trnL</i> -F	<i>trnG</i> -intron
<i>Anastrophyllum assimile</i>	Russia: Altai Territory, M. Ignatov, #4/1 (KPABG)	KF836651	KF836661	KF836640
	South Korea, S.-S. Choi, Hepaticae Korea, Exsiccatae F.II #51, 115517 (KPABG) 1	KF836650	KF836660	KF836639
	South Korea, V. Bakalin, Kor-5-12-11 (VBGI), 115596 (KPABG) 2	KF836652	KF836662	KF836641
<i>Anastrophyllum ellipticum</i>	U.S.A., N. Konstantinova, A 137-18-95 (KPABG)	EU791776	EU791664	no data
	Russia: Altai Territory, Yu. Mamontov, 330/2 (KPABG)	KF836654*	KF836664	KF836642
<i>Anastrophyllum lignicola</i>	China, D. Long, 24067 (KPABG)	KF836644	KF836665	no data
<i>Anastrophyllum michauxii</i>	Russia: Buryatiya Rep., N. Konstantinova, 17-1-02 (KPABG) 1	DQ875125	DQ875087	no data
	Russia: Buryatiya Rep., V. Bakalin, 22-1-27, 102860 (KPABG) 2	KF836646	KF836656	KF836635
<i>Anastrophyllum sp.</i>	Russia: Kemerovo Prov., N. Konstantinova, 35-1a-00, 101837 (KPABG)	KF836647	KF836657	KF836636
	Russia: Komi Rep., M. Dulin, Bryophyta rei publicae Kimi Exciccatae F.I. NN 1-10, 109820 (KPABG)	KF836645	KF836655	KF836634
<i>Anastrophyllum sp.</i>	South Korea, S.-S. Choi, Hepaticae Korea Exsiccatae F.II #54, 115520 (KPABG)	KF836648	KF836658	KF836637
	Russia: Amur Prov., V. Bakalin, 15-20-00, 101577 (KPABG)	KF836649	KF836659	KF836638
<i>Anastrophyllum sphenoloboides</i>	Russia: Murmansk Prov., V. Bakalin, 23-03-01 (KPABG)	EU791778	EU791663	no data
	Russia: Yakutiya Rep., V. Bakalin, 101592 (KPABG)	KF836653	KF836663	KF836633
<i>Barbilophozia lycopodioides</i>	Norway: Svalbard, N. Konstantinova, K 50-3-06 (KPABG)	EU791777	EU791662	no data
	Russia: Murmansk Prov., Konstantinova N., 185-89 (KPABG)	HQ896993	HQ897100	HQ897071
<i>Crossocalyx hellerianus</i>	Russia: Kareliya Rep., V. Bakalin, 06.08.1997 (KPABG)	EU791788	AY327780	no data
	Russia: Sakhalin Prov., Sakhalin I., V. Bakalin, Exsiccatae #82 (VLA, KPABG)	KF836643	KF836666	no data
<i>Sphenolobus minutus</i>	Russia: Kareliya Rep., V. Bakalin, 24.07.1998	EU791790	AY327766	no data
	Norway: Svalbard, N. Konstantinova, K 68-1-06 (KPABG)	EU791789	EU791667	no data
<i>Sphenolobus saxicola</i>	Russia: Buryatiya Rep., N. Konstantinova, 123-3-02 (KPABG)	DQ875124	DQ875086	no data

nrDNA, *trnL*-F and *trnG*-intron cpDNA sequences for twelve specimens, nucleotide data for nine specimens were borrowed from the previous studies (Yatsentyuk *et al.*, 2004; Vilnet *et al.*, 2010; Vilnet *et al.*, 2012). All analyzed specimens are listed in Table 1, including GenBank accession numbers and voucher details.

**DNA isolation, PCR amplification and DNA sequencing** followed protocols described in Konstantinova & Vilnet (2011).

**Phylogenetic analysis.** Three dataset, ITS1-2, *trnL*-F, *trnG*-intron, were automatically aligned in BioEdit 7.0.1 (Hall, 1999) with ClustalW option and then manually corrected. The preliminary phylogenetic analyses revealed incongruence between ITS1-2 and both chloroplast loci data. The topologies obtained from *trnL*-F and *trnG*-intron were similar, thus we produced a combined dataset for both cpDNA loci, marked absent *trnG*-intron sequences for ten samples as missing data. All positions of the ITS1-2 and *trnL*-F+ *trnG*-intron alignments were included in the phylogenetic analysis.

Both datasets were analyzed by Maximum Likelihood estimation (ML) with PhyML (Guindon & Gascuel, 2003) and Maximum Parsimony method (MP) with TNT (Goloboff *et al.*, 2003). The program ModelGenerator

(Keane 1193024931 *et al.*, 2004) determined that the TrN+I+G model was the best-fit evolutionary model of nucleotide substitutions for ITS1-2 dataset and HKY+I+G - for *trnL*-F+*trnG*-intron. These models were used in ML analysis and the heterogeneity rate among sites was modeled using gamma distribution with four rate categories. Bootstrap support (BS) for individual nodes was assessed using a resampling procedure with 500 replicates.

The MP analysis for both datasets involved a New Technology Search with a search for the minimum-length tree by one reiteration and 1000 bootstrap resamplings; the default settings were used for other parameters, indels were taken into account by a modified complex coding algorithm in SeqState (Müller, 2005).

Infrageneric and infraspecific variability of each DNA locus was evaluated as *p*-distances between samples and species calculated in Mega 5.1 (Tamura *et al.*, 2011) using the pairwise deletion option for counting gaps.

## RESULTS

The nucleotide sequences of ITS 1-2 and *trnL*-F were obtained for 12 samples, *trnG*-intron – for 10 samples. The parameters of sequence alignments for each studied loci are shown in Table 2. Despite combined *trnL*-F+*trnG*-intron aligned sequences were 23% longer than ITS 1-2

Table 2. Characteristics of performed ITS1-2, *trnL*-F, *trnG*-intron nucleotide alignments.

	Conservative sites			Variable sites		Parsimony-informative sites	
	Total sites	base pairs	%	base pairs	%	base pairs	%
ITS1-2	848	683	80.54	157	18.51	90	10.61
<i>trnL</i> -F	476	421	88.44	53	11.13	32	6.7
<i>trnG</i> -intron	617	564	91.41	48	7.78	12	1.9
<i>trnL</i> -F+ <i>trnG</i> -intron	1093	985	90.12	101	9.24	44	4.03

ones, both cpDNA loci were in 10% more conservative than ITS1-2, and number of nested variable and parsimony-informative sites was half as much as for ITS1-2.

The MP analysis of ITS1-2 dataset yielded two equally parsimonious trees 322 steps long, with CI=0.814286 and RI=0.856618 calculated in Mega 5.1. A single tree which was 163 steps long was found in MP analysis for *trnL*-F+*trnG*-intron, CI=0.878049 and RI= 0.883721. The arithmetic means of Log likelihood obtained in ML estimation were 2414.716403 for ITS 1-2 dataset, 2184.997967 for *trnL*-F+*trnG*-intron.

Tree topologies obtained by the two methods for each data set were highly congruent, thus bootstrap support (BS) values for ML trees in Figs. 1-2 are indicated from both ML and MP analyses. The studied samples of the genus *Anastrophyllum* s. str. united in one clade (more than 94% BS in all trees). The incongruence between topologies calculated from nuclear and chloroplast datasets consists in different relationships of a subclade composed of the tested *Anastrophyllum* species and *A. lignicola*. On ITS topology, it is in sister affinity to *Anastrophyllum assimile*-subclade (66% BS in ML, without support in MP), on *trnL*-F+*trnG*-intron topology – to *A. michauxii*+*A. sphenoloboides*-subclade (55% BS in ML, 61% BS in MP). The phylogenetic relationship of the tested *Anastrophyllum* species and *A. lignicola* from cpDNA dataset obtained lower support than from ITS1-2 (64% BS in ML and 66% BS in MP opposite to 99% and 82%, respectively). Four samples of *A. assimile* were distributed into two subclades, separated by long branches comparatively with the branch length in subclades of *A. sphenoloboides* or *A. michauxii*. The sample of *Anastrophyllum* sp. from Amur Province (Udokan Range) determined by collector V. Bakalin as *Anastrophyllum michauxii* was phylogenetically distinct from *A. michauxii*-subclade and got placed into a separate phylum in relation to *A. michauxii*+*A. sphenoloboides*-subclade in all topologies (Figs. 1, 2). Representatives of genera *Sphenobolus* and *Crossocalyx* located in separate clades diverged in ITS1-2 and *trnL*-F+*trnG*-intron calculations.

For infraspecific and infrageneric *p*-distance calculations, samples were grouped according to clades and phyla obtained in phylogenetic reconstruction. Nine groups were segregated, *Anastrophyllum* sp., *S. saxicola* were placed into monotypic groups, samples of *A. assimile* from South Korea were put into a separate group, *A. lignicola* and the tested Altaian *Anastrophyllum* species were combined in one group. The results of the analyses are summarized in Table 3. The infraspecific variability was detected in all multiply sampled species in ITS1-2.

It counts less than 1% in *A. sphenoloboides*, *A. assimile* (Altai and USA) and *S. minutus*. *Crossocalyx hellerianus*, *A. michauxii*, and *A. assimile* from South Korea appear to be more variable taxa (>1%) in ITS1-2. The values of *p*-distances in *trnL*-F are zero or less than 1% in all taxa with an exception of *C. hellearianus* which could be explained by incorrect sequence reading in accession AY327780 previously deposited in GenBank. Due to the absence of sequence data, *p*-distances for *trnG*-intron were calculated only for *A. michauxii* and *A. assimile* from South Korea. *A. lignicola* and the tested *Anastrophyllum* species differ from each other by 0.8% in ITS1-2 and 0.4% by *trnL*-F, differences from other species vary from 0.9% for *A. michauxii* and *A. sphenoloboides* in *trnL*-F to 6.9% for *Anastrophyllum* sp. in ITS1-2. Two samples of *A. assimile* from South Korea are genetically more distinct from each other than samples from Altai Territory and USA, both subclades of *A. assimile* also highly differ genetically. *P*-distances between species demonstrated that *Anastrophyllum* sp. differs almost equally from both *A. michauxii* and *A. sphenoloboides*.

#### DISCUSSION

Nowadays exploring DNA data in species identification is becoming a routine procedure. Unfortunately, nucleotide sequence data were obtained for no more than 10% of all known *Anastrophyllum* s.l. species (not synonymized binomials). A single example of special taxonomical study based on integrative approach to morphological, ecological and molecular data was the study implemented to prove the species status of *A. alpinum* Steph., which had been synonymized previously with *A. joergensenii* Schiffn. (Long *et al.*, 2006). Other published data on the genus *Anastrophyllum* s.l. concern predominantly liverwort molecular phylogenetic and taxonomic studies (Schill *et al.*, 2004; Vilnet *et al.*, 2010) or estimation of liverwort divergence time (Feldberg *et al.*, 2013). More or less representative data of infraspecific DNA variability in *trnG*-intron and *rps4* were obtained only for *A. tubulosum* (Nees) Grolle, *A. auritum* (Lehm.) Stephani and *A. (Sphenobolus) minutum* (Schreb.) R.M. Schust. by de Roo *et al.* (2006).

The tested *Anastrophyllum* plants from the Altai and *A. lignicola* were found in one clade. A low level of molecular differentiation suggests their recent divergence compared with other species of this genus (Table 3). Morphologically plants from the Altai are similar to both *A. ellipticum* and *A. lignicola* in size and dioecious condition. At the same time, only male shoots were found in our Altaian sample, which is the case known for *A. ellipticum*, whereas the Chinese sample of *A. lignicola* in-

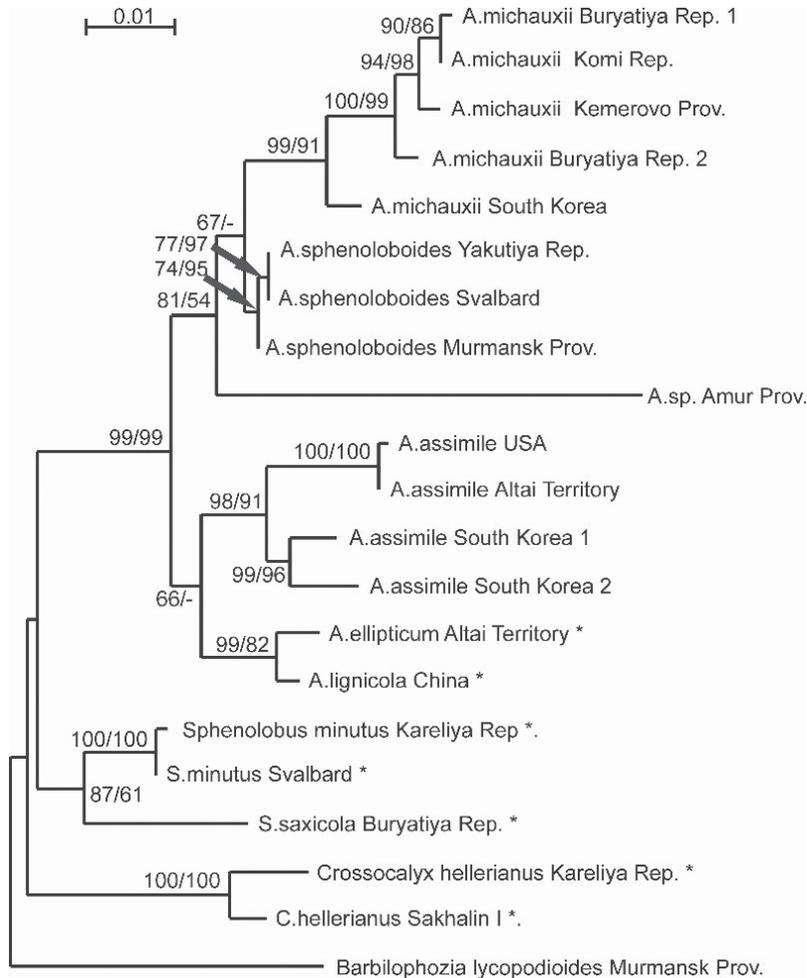


Fig. 1. Maximum likelihood phylogenetic tree for the genus *Anastrophyllum* and related taxa based on ITS1-2 nrDNA nucleotide sequences. Bootstrap support values over 50% are indicated from ML/MP analyses. Species with ambiguous position in ML tree constructed on *trnL-F-trnG*-intron dataset are marked by asterisks.

cludes both male and female plants as noted in its type description. The tested *Anastrophyllum* specimen and *A. ellipticum* (as described by Inoue, 1978) are characterized by uniformly 2-celled gemmae that are located at the tips of shoots with unmodified leaves. *Anastrophyllum lignicola* produced 1-2-celled gemmae on ascending to erect gemmiferous shoots with reduced and appressed leaves (like those of *Crossocalyx hellerianus* and *Sphenolobus minutus*). Basing on morphological investigations, we doubt to classify the tested Altaian *Anastrophyllum* species to *A. lignicola*. Molecular differentiation between them also implies that the species are most likely different due to the level of ITS1-2 sequence variation compared with more or less morphologically invariable *A. sphenoloboides*, *A. assimile* from USA and Altai Territory, *Sphenolobus minutus* (Table 3). Taking into account also similar habitat preference, we attribute the *Anastrophyllum* specimen from the Altai to *A. ellipticum*.

Further we provide description of *Anastrophyllum ellipticum* Inoue based on the specimen from Altai Mts.

***Anastrophyllum ellipticum*** Inoue – Bull. Nat. Sci. Mus., Ser. B, 4: 13. f. 1–2. 1978. Fig. 3.

Plants brownish-green, with no trace of secondary red or purple pigmentation, grow as single shoots among other liverworts. Shoots 2.25–5.0 mm long, 0.25–0.8 mm

wide, ascending. Stem 80–110  $\mu\text{m}$  in diameter, pale brown, 6–8 cells across, with 1-2-layered cortex of thick-walled cells gradually dragging into the medullary cells nearly as large as the cortical and equally thick-walled. Leaves remote, erect to obliquely spreading from somewhat seating base, not decurrent on both sides, entire-margined, loosely to distinctly conduplicate, ovate to elliptical when flattened, 290–350 $\times$ 390–490  $\mu\text{m}$ , 1.35–1.38 times as long as wide, bilobed to 0.3–0.37 of the length, sinus rounded to subacute. Lobes equal to subequal, triangular, apex acute to obtuse, or narrowly rounded. Leaf cells nearly equally thick-walled with indistinct bulging trigones; cuticle covered by fusiform to rounded low papillae. Cells of lobes apex and margins rounded-quadrate to slightly elongate, 1–1.6 times as long as wide, 9–15 $\times$ 13–22  $\mu\text{m}$ , midleaf cells 10–17 $\times$ 16–26  $\mu\text{m}$ , 1–1.7 times as long as wide. Gemmae yellowish to reddish, elliptical to fusiform in outline, straight or somewhat incurved, smooth or with scarce angulation, 2-celled, 8.5–12.5 $\times$ 20–29  $\mu\text{m}$ , (1.7–)2.5(–3.4) times as long as wide. Gemma formation limited to the apices of shoots with unmodified leaves.

Plants dioecious. Male shoots were found only. Androecia intercalary, with bracts in 1–3 pairs; bracts similar to leaves, but strongly concave at base and more markedly canaliculate; antheridia globose, 1 per bract.

Groups	within group <i>p</i> -distances, %		between groups <i>p</i> -distances, %									
	ITS1-2 <i>trnL</i> -F	<i>trnG</i>	<i>A. sphenoloboides</i>	<i>A. michauxii</i>	<i>A. sp., Amur</i>	<i>A. assimile</i> excl. S Korea	<i>A. Altain+</i>	<i>A. lignicola</i>	<i>A. assimile</i> S Korea	<i>S. minutus</i>	<i>S. saxicola</i>	
<i>A. sphenoloboides</i>	0.08	0.3	no									
<i>A. michauxii</i>	1	0	2/0.8/1.8									
<i>A. sp., Amur</i>	no	no	5/1/2.3	6.1/0.6/2.9								
<i>A. assimile</i> excl. SKorea	0.13	0	3.3/1.9/1.7	4.3/1.7/1.8	6.6/1.7/2.5							
<i>A. ellipticum</i> + <i>A. lignicola</i>	0.8	0.4	2.6/0.9/1.7	4/0.9/1.8	6.9/1.1/2.5	3.4/1.7/1						
<i>A. assimile</i> SKorea	1.3	0	2.9/2.1/1.8	4.4/1.9/2	6.1/1.9/2.6	2.2/0.6/0.5	3.2/1.9/1.5					
<i>S. minutus</i>	0.13	0.5	3.7/3.5/-	5/2.8/-	7/2.8/-	4.6/3.6/-	4.9/3.5/-	4.3/3.7/-				
<i>S. saxicola</i>	no	no	4.6/3.7/-	5.8/3/-	7.8/2.8/-	5.2/3.6/-	5/3.4/-	4.6/3.8/-	2.7/1.2/-			
<i>C. hellerianus</i>	1.3	3.6?	5.4/6.6/-	6.4/5.9/-	8.6/6.1/-	6.3/6.1/-	5.7/6.2/-	5.9/6.5/-	3.8/5.3/-	4.5/5.8/-		

Table 3. *P*-distances, calculated from ITS1-2, *trnL*-F, *trnG*-intron nucleotide sequences within and between studied species. The *p*-distances for *trnG*-intron are not calculated for *Sphenolobus* and *Crossocalyx* due to absence of nucleotide sequence data.

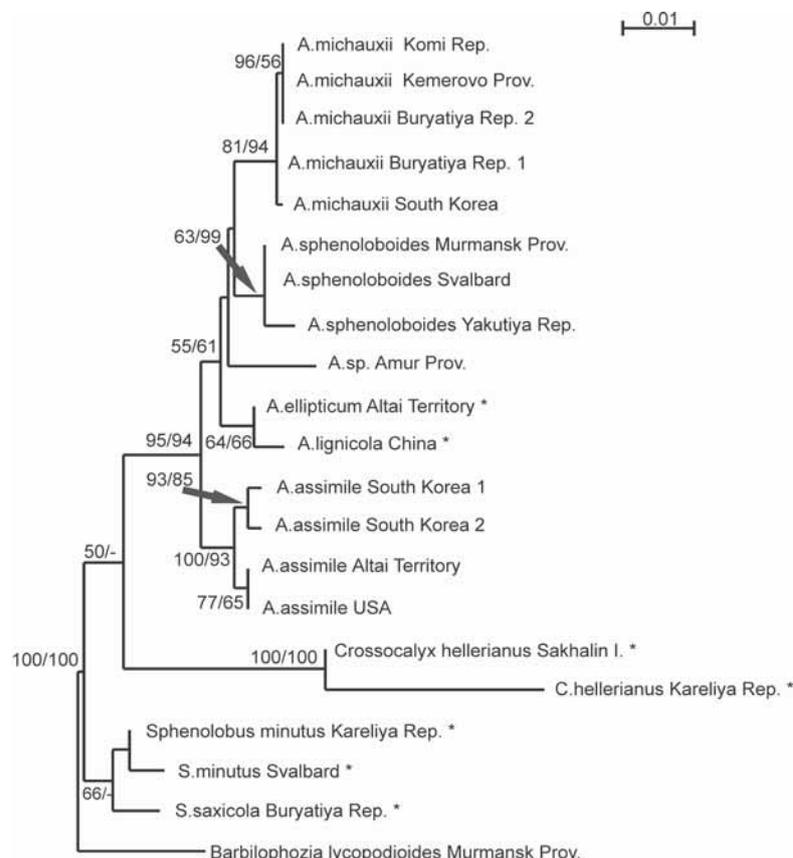


Fig. 2. Maximum likelihood phylogenetic tree for the genus *Anastrophyllum* and related taxa based on combined *trnL*-F-*trnG*-intron nucleotide sequences. Bootstrap support values over 50% are indicated from ML/MP analyses. Species with ambiguous position in ML tree constructed on ITS1-2 nrDNA dataset are marked by asterisks.

**Variation and differentiation:** The Altaian plants deviate in some dimensions from the Inoue's description of *Anastrophyllum ellipticum* (Table 4). Particularly, the Japanese plants are larger, with broader leaves (usually length to width ratio 1-1.2:1 (vs. 1.35-1.38:1), and more deeply bilobed, to about 0.37-0.50 of the length. In contrast, the gemmae of Japanese plants are slightly smaller, and have lower length/width ratio (Table 4). *Anastrophyllum lignicola* hardly differs from both Japanese and Altaian *A. ellipticum* in size characters, but is distinguished in having ascending to erect gemmiferous shoots with reduced and appressed leaves (Schill & Long, 2002: Fig. 1), and by gemmae morphology. The gemmae of *A. lignicola* are 1-2-celled, ellipsoid to rounded, and broader (Fig. 4) than those in *A. ellipticum*. Only male plants are still known for *A. ellipticum*, whereas both male and female shoots were common in one sample of *A. lignicola*. These two species differs also by their ecology. *Anastrophyllum ellipticum* was collected exclusively on decaying wood (like *Crossocalyx hellerianus*), whereas *A. lignicola* grows on rotten logs and stumps, but occasionally on living tree trunks (Schill & Long, 2002). It should be noted that these two species could be misidentified in the southwestern China where both of them are known.

Table 4. A comparison of *Anastrophyllum ellipticum* and *A. lignicola*.

Character	<i>A. ellipticum</i> Altai	<i>A. ellipticum</i> Japan, type description	<i>A. lignicola</i> Yunnan
Shoot width, mm	0.25-0.8	0.6-0.8	to 1.4
Shoot length, mm	2.25-5.0	8-15	to 14
Stem diameter, µm	80-110	100-130	(90-)120-180(-220)
Leaf width, µm	290-350	(350-)380-420	(280-)400-500(-790)
Leaf length, µm	390-490	400-450	(320-)400-550(-820)
Gemmae width, µm	8.5-12.5	8-10	8-15
Gemmae length, µm	20-29	20-28	15-27
Gemmae length/width ratio	(1.7-)2.5(-3.4)	(1.75-)2.3(-2.8)	(1.1-)1.7(-2.1)

**Ecology and distribution:** Our specimens of *Anastrophyllum ellipticum* were collected in the Katunsky Range (49°56' N, 85°51' E, 1700 m alt.) of the Altai Mts. (Republic of Altai). It was growing on decaying wood of a large log (probably of *Pinus sibirica* Du Tour) lying over the water of a rivulet in a subalpine coniferous grass-moss forest dominated by *Pinus sibirica* and *Picea obovata* Ledeb. and containing an understorey of *Abies sibirica* Ledeb., *Spiraea* L. sp., *Juniperus* L. sp., *Vaccinium vitis-idaea* L., and *V. myrtillus* L. In this habitat, *Anastrophyllum ellipticum* was found as single shoots in mixed mats composed by *Blepharostoma trichophyllum* (L.) Dumort., *Cephalozia bicuspidata* (L.) Dumort., *C. lunulifolia* (Dumort.) Dumort., *Lepidozia reptans* (L.) Dumort., *Lophozia lantratoviae* Bakalin, *L. ventricosa* var. *longiflora* (Nees) Macoun, *Riccardia palmata* (Hedw.) Carruth., *Schistochilopsis incisa* (Schrad.) Konstant., and *Tritomaria exsecta* (Schmidel ex Schrad.) Schiffn. ex Loeske. The type locality of *Anastrophyllum ellipticum* is Gongen Peak of Southern Yatsugatake Volcanic Group (35°58' N, 138°22' E) located in the Nagan Pref., Honshu, Japan (Inoue, 1978). It was collected on decaying wood in subalpine (ca. 2300 m alt.) coniferous forest dominated by *Tsuga diversifolia* (Maxim.) Mast. – *Abies veitchii* Lindl., with Siberian dwarf pine *Pinus pumila* (Pall.) Regel also growing in this subalpine zone. This species was associated with *Tritomaria exsecta*, *Bazzania denudata* (Torr. ex Gottsche, Lindenb. & Nees) Trevis., *Scapania ampliata* Steph., and several mosses (Inoue, 1978). Recently *Anastrophyllum ellipticum* has also been found in Southwest Sichuan (about 28°54' N, 101°41' E), China (Long, 2011); the area with subtropical highland climate. In this area, *A. ellipticum* was collected in conifer-dominated (*Abies* Mill., *Picea* A. Dietr. and *Larix* Mill. species) humid forests (about 3300-4200 m alt.) that contained an understorey of smaller woody broadleaves, such as *Acer* L., *Betula* L., *Rhododendron* L. and *Sorbus* L. species. *Anastrophyllum ellipticum* was found there as common on rotten stumps and logs, where *Jamesoniella* (Spruce) Carrington, *Schistochilopsis incisa* and *Tritomaria exsecta* grow as well (Long, 2011). On the basis of the above it can be assumed that *Anastrophyllum ellipticum* is a mountain species with a disjunctive, presumably relic Asian distribution.

**Specimens examined:** Russia: Altai Republic, Katunskiy State Biosphere Reserve, Katunskiy Range, Poperechnaya River valley, 19.IX.2012 Mamontov # YuSM-330-2-2 (KPABG); idem, 19.IX.2012 Mamontov # YuSM-330-2-5 (KPABG); idem, 19.IX.2012 Mamontov # YuSM-330-2-6 (KPABG); idem, 19.IX.2012 Mamontov # YuSM-330-2-7 (KPABG).

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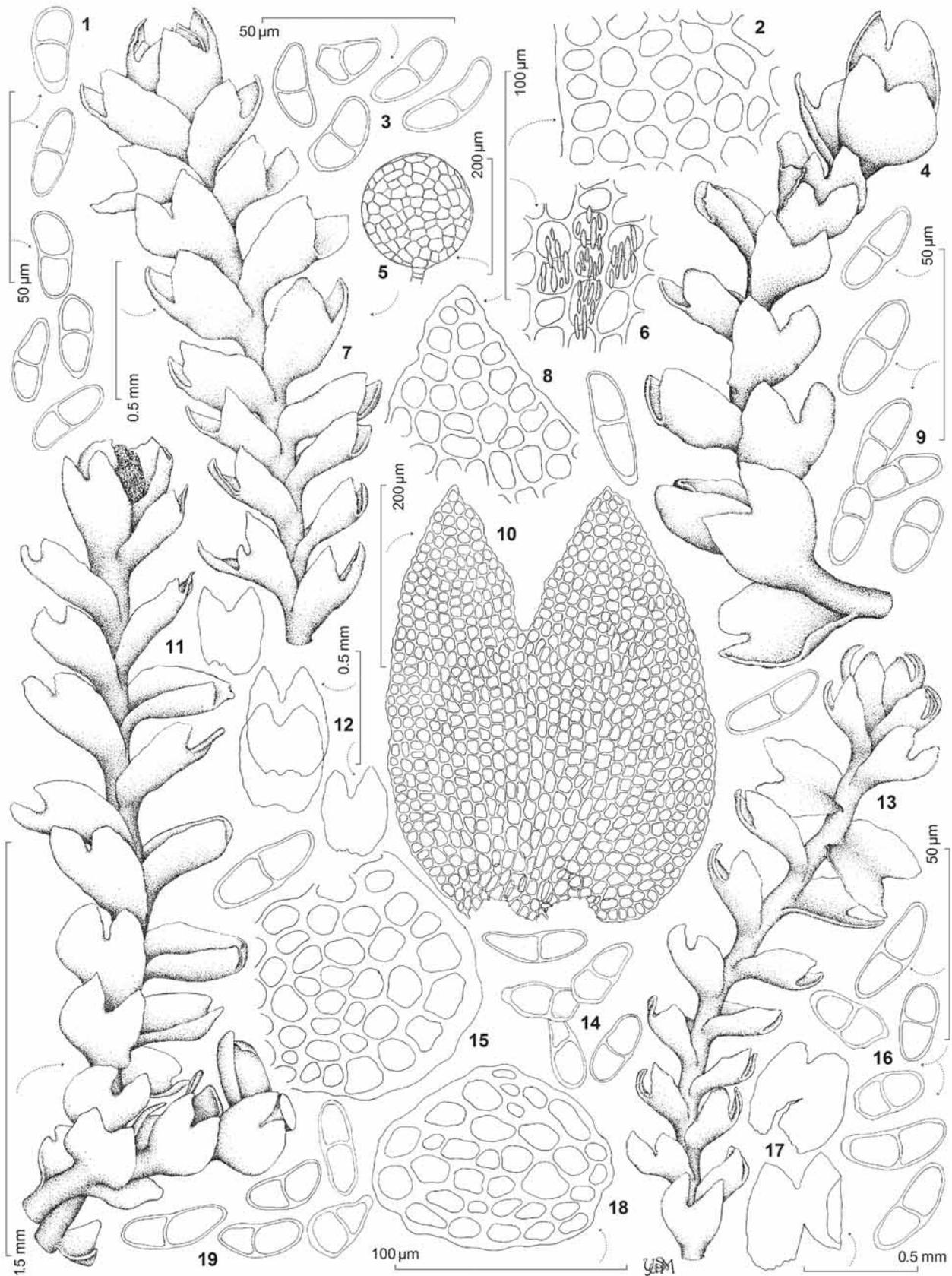


Fig. 3. *Anastrophyllum ellipticum*: 1, 3, 9, 14, 16, 19 – gemmae; 2 – cells of the leaf middle; 4 – habit, lateral aspect; 5 – an antheridium; 6 – leaf cells near the base, with striolate papillose cuticle indicated; 7, 11, 13 – habit, postical aspect; 8 – leaf lobe apex; 10 – an enlarged leaf with cells indicated; 12 – leaves; 15, 18 – stem cross section, 17 – two male bracts. All from Altai Republic, 19.IX.2012 Mamontov # YuSM-330-2-2 (KPABG).

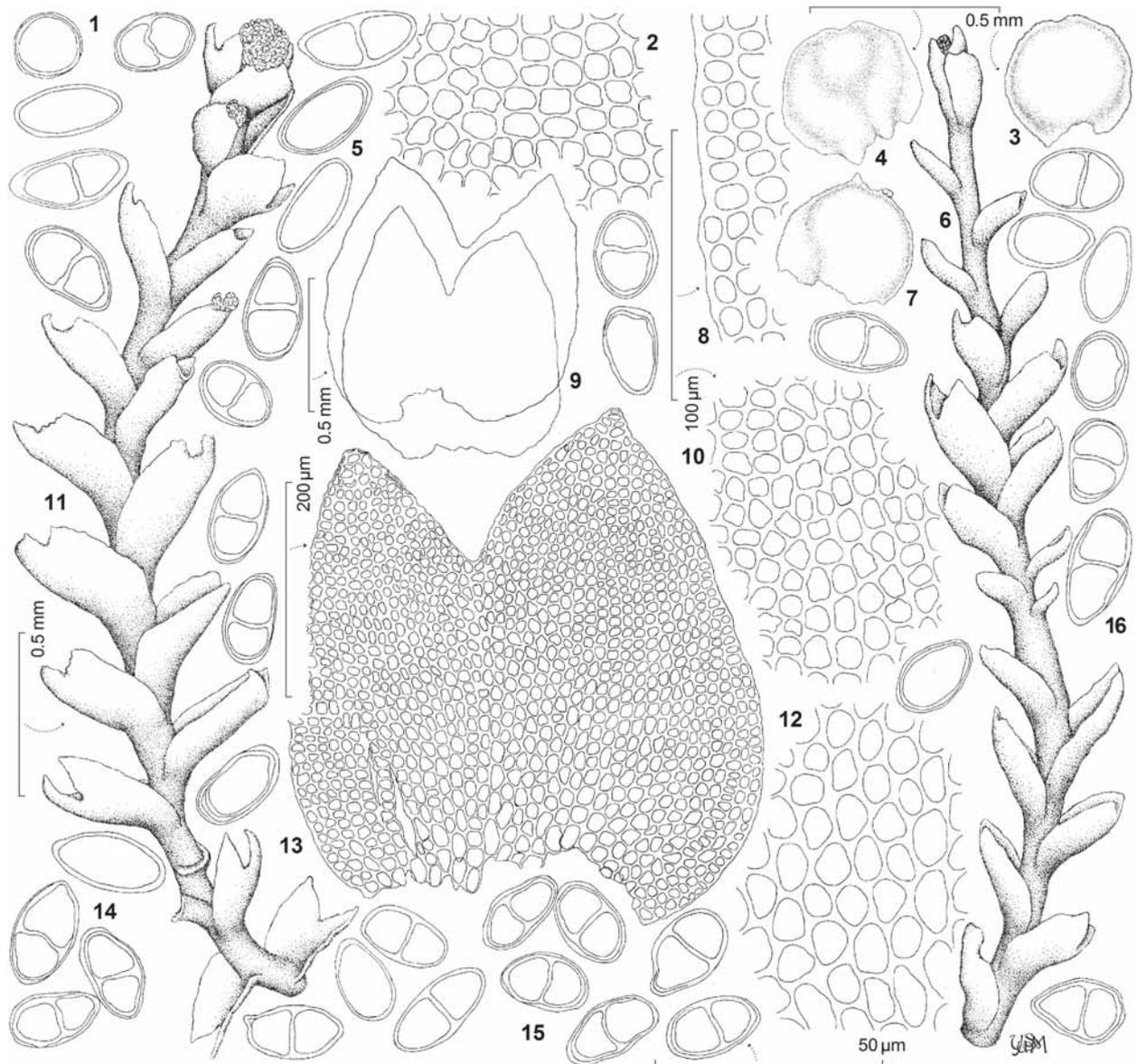


Fig. 4. *Anastrophyllum lignicola*: 1, 5, 11, 14-16 – gemmae; 2 – cells of leaf lobe middle; 3, 4, 7 – leaves of elongated gemmiferous shoot apices; 6 – suberect gemmiferous shoot with reduced leaves; 8 – cells of margin of leaf middle; 9 – two leaves; 10 – cells of leaf middle; 11 – habit, postical aspect; 12 – cells of leaf base; 13 – an enlarged leaf. All from China, Yunnan Province, 6.VI.1993 Long # 24067 (KPABG).

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