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Citation	McCune, B., Di Meglio, J., & Curtis, M. J. (2014). An unusual ascospore shape and a new species, <i>Umbilicaria nodulospora</i> (Umbilicariaceae), from California and Oregon. <i>The Bryologist</i> , 117(2), 170-178. doi:10.1639/0007-2745-117.2.170
DOI	10.1639/0007-2745-117.2.170
Publisher	The American Bryological and Lichenological Society, Inc.
Version	Accepted Manuscript
Terms of Use	http://cdss.library.oregonstate.edu/sa-termsfuse

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**An unusual ascospore shape and a new species, *Umbilicaria nodulospora* (Umbilicariaceae),
from California and Oregon**

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DOI: editor complete

1 **ABSTRACT.** We describe *Umbilicaria nodulospora*, a distinctive new species occurring on steep
2 rock faces on old lava flows in California and Oregon. The species is unusual among lichenized
3 ascomycetes in consistently having one or two shallowly bulging knobs at one end of each
4 ascospore, suggesting a T, Y, or L shape; otherwise they are consistent with the appearance of
5 ascospores in most *Umbilicaria* species. The species is readily distinguished in the field by a
6 grayish tone to the brown upper surface, in combination with a thickly rhizinate lower surface.
7 Distinctiveness of the species was supported by analysis of the ITS and LSU regions of nrDNA.
8 No close relative or sister taxon was found. *Umbilicaria nodulospora* is so far known only from
9 geologically recent flood basalts in central Oregon to northeastern California.

10

11 **KEYWORDS.** California, ITS, Lecanorales, lichenized ascomycetes, lichenized fungi, lichen
12 systematics, LSU, Oregon, rDNA, *Umbilicariaceae*, western North America.

13 Despite Llano's (1950) thorough monograph of the Umbilicariaceae, closer study has
14 revealed a number of new species or the need to resurrect previously synonymized species (Poelt
15 & Nash 1993; Davydov et al. 2010; McCune & Curtis 2012). Continued collecting in western
16 North America has revealed some problems with the current taxonomy. One of those problems
17 came to our attention as two small specimens from Lava Beds National Monument in
18 northeastern California. Further study and collecting showed this to be a previously
19 unrecognized species. Furthermore, it revealed an ascospore shape that is unusual within
20 lichenized fungi. The purpose of this paper is to describe this new species, its unusual spores,
21 and to use DNA sequence data to evaluate the relationship between this species and other species
22 in the Umbilicariaceae.

23 **MATERIALS AND METHODS**

24 ***Specimen sampling.*** We studied collections of *Umbilicaria* from many herbaria, but no
25 collection had specimens of the target species. Instead we obtained sufficient material by
26 collecting in likely areas.

27 All specimens were examined for spores. Hand sections of apothecia were suspended in
28 water and studied by standard light microscopy. A selection representing various geographic

29 locations and with minor variations in thallus form were extracted for DNA. Secondary
30 substances were analyzed by thin-layer chromatography (TLC) using solvents A and C of
31 Culberson (1972). Fragments of specimens were extracted in acetone at room temperature,
32 spotted on aluminum-backed silica gel plates (Merck 5554/7 Silica gel 60 F₂₅₄), lightly brushed
33 with 10% H₂SO₄, and gently charred in an oven at 100°C.

34 ***DNA extraction and PCR amplification.*** We chose to analyze nuclear internal transcribed
35 spacer (ITS) and large subunit (LSU) rDNA regions in keeping with others working on species-
36 level problems in *Umbilicaria* (Davydov et al. 2010; Hestmark et al. 2011; Ivanova et al. 1999;
37 Krzewicka et al. 2009). Total DNA was extracted from ~ 100 mg of homogenized (FastPrep-24,
38 MP Biomedicals, Inc) fresh, frozen and herbarium material following the Fast DNA® Spin Kit
39 (MP Biomedicals, Inc.) protocol. Two µL of total DNA extract was used as template in PCR
40 reactions of 30 µL final volume. Each reaction included 15 µl of Dream Taq Green PCR Master
41 Mix (2x; Thermo Scientific Inc.), 12.8 µl of nuclease-free H₂O, and 1.2 µl of each primer.
42 Primers (final concentration: 400 nM) used for amplifying were ITS1F (Gardes & Bruns 1993)
43 and ITS4 (White et al. 1990) for ITS, and LROR and LR6 (Vilgalys & Hester 1990) for LSU.
44 The reactions were run with the following parameters for ITS: initial denaturation at 94°C for 2
45 min, 34 cycles of denaturation at 94°C for 30 sec, annealing at 50°C for 30 sec, and extension at
46 72°C for 1 min 20 sec. For amplification of LSU, the parameters were as follows: initial
47 denaturation at 94°C for 2 min, 34 cycles of denaturation at 94°C for 45 sec, annealing at 53°C
48 for 45 sec, and extension at 72°C for 2 min. Ten µL of PCR product from each reaction was
49 analyzed for purity by electrophoresis through a 0.8% agarose gel with GelRed stain (Biotium,
50 Inc.) in water.

51 PCR product from each reaction was processed for sequencing as follows: Individual
52 PCR gel bands were cut out of the gel and purified following the QIAquick gel extraction kit
53 protocol (Qiagen, Inc.). Two µl of purified PCR product was added to 8.8 µL H₂O and 1.2 µL
54 sequencing primer (final concentration: 100 nM), and then sequenced by the Center for Genome
55 Research and Biocomputing (Oregon State University). In addition to the amplification primers,
56 the following primers were used for sequencing: ITS2 and ITS3 (White et al. 1990). Staden
57 version 1.6.0 (SourceForge.net) was used to quality check the raw sequence, align the four
58 sequencing runs per PCR product, and generate a consensus sequence for phylogenetic analyses.

59 Not all attempts yielded good sequences, so we ended up with four ITS and three LSU sequences
60 of the new species.

61 **Phylogenetic analyses.** We inferred phylogenetic relationships from sequences of rDNA
62 from 5 specimens of the putative new species, along with 22 *Umbilicaria* specimens represented
63 in GenBank (**Table 1**). We also included *Boreoplaca ultrifrigida*, *Hypocenomyce scalaris*, and
64 *Ophioparma ventosa* as outgroups (**Table 1**) following Hestmark et al. (2011). We interpret the
65 accession of *Umbilicaria krascheninnikovii* in GenBank as *U. polaris* (Schol.) Zahlbr., based on
66 a revised understanding of this group (Davydov et al. 2011). ITS and LSU sequences selected
67 from GenBank represented species across *Umbilicaria*. Sequences were aligned with Geneious
68 alignment using default settings (cost matrix: 65%, gap open penalty 12, gap extend penalty 3).
69 The ends of the alignments were then trimmed to a nearly equal number of sites for all
70 sequences. Alignment gaps were treated as missing data.

71 Phylogenetic trees were obtained by maximum likelihood analysis of the ITS and partial
72 LSU data, using the GTR (general time-reversible) model and Genious defaults, except we used
73 the “BEST” (slower) topology search, using the PhyML (Guindon et al. 2010) plug-in to
74 Geneious 5.4.3 (Drummond et al. 2011). Statistical support for branches was evaluated with
75 1000 bootstrap resamplings. We compare the results for ITS and LSU by constructing
76 phylogenetic trees for each subset of the data. The resulting trees were then visually compared
77 for conflicts (taxa found in two distinct clades, each with more than 70% bootstrap support).
78 Excluding the outgroups, the alignments had 155 variable sites of 504 in the ITS and 106 of 812
79 in the LSU.

80 **RESULTS**

81 We describe a new species, *Umbilicaria nodulospora*, to accommodate distinctive
82 specimens from northern California and central Oregon. The species is distinctive in gross
83 morphology (Fig. 1-2), ascospore morphology (Fig. 3), and in ITS and LSU sequences (Fig. 4),
84 as described below.

85
86 **Ascospore morphology.** *Umbilicaria nodulospora* has distinctive ascospore morphology (**Fig. 1**).
87 We know of this spore shape in lichenized ascomycetes only in *U. calvescens* group from South
88 America. Most ascospores of *U. nodulospora* are asymmetrical at one end, owing to a shallow

89 lateral bulge or nodule. This nodule can be seen on most free spores on a microscope slide, but it
90 is difficult to see when the spores are still in the ascus. Also, depending on the angle of repose of
91 the spore on the microscope slide, the bulge can be nearly invisible in a small fraction (ca. 10-
92 20%) of the spores.

93

94 **Phylogenetic reconstruction.** *Umbilicaria nodulospora* was readily distinguished from other
95 *Umbilicaria* species by their ITS and LSU sequences. Although these sequences could be
96 concatenated and analyzed in a single tree, we chose to keep them separate to help clarify the
97 minimum effort needed to detect these species (e.g. by barcoding). Phylogenetic reconstruction
98 for both ITS (**Fig. 4A**) and LSU (**Fig. 4B**) showed the species to be distinct and forming a well-
99 supported monophyletic group. However, relationships among *U. nodulospora* and other species
100 are obscure, because the backbone of the trees within *Umbilicaria* had little support, and no
101 sister group emerged for *U. nodulospora*.

102

103 THE SPECIES

104 ***Umbilicaria nodulospora*** McCune, Di Meglio & M. J. Curtis, sp. nov. (Figs. 1-3)

105 TYPE: U.S.A.: California: Modoc Co., Lava Beds National Monument, just below east-facing lip
106 of Mammoth Crater on its west side, 41.69200° N 121.54623° W, 1618 m, on volcanic rock,
107 *McCune 32546*. (holotype, OSC; isotypes UC, US).

108 **Description.** Thallus umbilicate, monophyllous (Fig. 1A) to more often dividing as it
109 expands into larger polyphyllous colonies (Fig. 1B); upper surface brown to gray brown, faintly
110 to distinctly grayish pruinose (Fig. 2), often grayer near the umbo, matte to slightly shiny, mostly
111 1–2(3) cm diam, about 0.2 mm thick excluding the rhizines; upper surface smooth to broadly
112 areolate and reticulately cracked, the cracks often deep so that the thallus readily divides into part
113 thalli; submarginal areas occasionally minutely perforate (hold up to light); margins entire to
114 irregularly lacerate or lobulate; lower surface brown to black but apparently lacking
115 thalloconidia, smooth to finely papillose or verrucose, usually developing a dense mat of parallel
116 or tangled rhizines over part or all of the lower surface (Fig. 1D, Fig. 2), the mat about 1–2 mm
117 thick, often interspersed with brown to black trabeculae, sometimes patches apparent without
118 rhizines or trabeculae and thus exposing the papillose lower cortex; upper cortex with superficial
119 POL- (i.e. dark under polarized light) necrotic layer, 0–10 µm thick; cortex 7–12 µm thick,

120 brown and POL- above, hyaline and POL+ below; medulla about 100 μm thick overall, POL-,
121 the algal layer about 60–70 μm , the lower part hyaline to gray and densely crystalline, rather
122 compact; lower cortex very thick, paraplectenchymatous but the cells thick walled and with
123 narrow lumina, the lowermost layer brown; rhizines mostly 25–115 μm diam and 1–4 mm long,
124 cylindrical or sometimes flattened and grading into trabeculae, brown to black, sometimes tan;
125 apothecia sessile, black, gyrose, to 1.2(2.0) mm diam, initially angular to stellate (Fig. 1C), with
126 age protruding more and becoming convex and roundish in outline; ascospores simple, hyaline, 8
127 per ascus, \pm ellipsoidal but usually with one or two blunt shallowly bulging knobs at one end and
128 forming a Y, T, or L shape, (9.5)10.5–13.0(17.8) \times (5.9)6.2–7.5(8.8) μm (**Fig. 3**); pycnidia
129 occasional, embedded in thalline swellings and with a dark ostiole; spermatia bacilliform to
130 narrowly ellipsoid, minute, 3.3–4.3 \times 1.0–1.4 μm ; thallus containing gyrophoric acid and related
131 compounds by TLC. Photobiont chlorococcoid.

132 ***Distribution and habitat.*** So far the species is known only from central Oregon to
133 northeastern California (Fig. 5). In all cases it has been found on steeply sloping surfaces of
134 relatively recent basalt lava flows (i.e. 2,000–12,000 ybp). In most cases it has been found on
135 relatively cool aspects, for example the north-facing lip of collapsed lava tubes.

136 ***Selected specimens examined*** (McCune specimens in OSC; Sheehy specimens at Lava
137 Beds National Monument). U.S.A. CALIFORNIA: Modoc Co., just outside SE corner of Lava Beds
138 National Monument, 41.6922° N 121.4466° W, 1314 m, *McCune 32518, 32519*. Siskiyou Co.,
139 Lava Beds National Monument, east of East Sand Butte, 1316 m, 41.6820° N 121.3722° W,
140 *McCune 32507, 32510*; 0.5 km ENE of Skull Cave, *McCune 32530*; near entrance to Boulevard
141 Cave, 1429 m, *McCune 32543*; Devils Homestead upper parking, 1240 m, *Sheehy LABE-36*; Hill
142 Road at fire danger sign, 1240 m, *Sheehy LABE-62*; Merrill Cave Road, 1295 m, *Sheehy LABE-31*
143 and 32; near summit of Schonchin Butte, 1615 m, *McCune 32536, 32539, 32540*; near bottom of
144 Mammoth Crater, 1547 m, *McCune 32551*; Tickner Road, 1 mile east of Medicine Lake Road,
145 41.68695° N 121.5326° W, 1592 m, *Sheehy 774*. OREGON. Lake Co., lava flow by Cougar
146 Mountain, 43.41086° N 120.87568° W, 1371 m, *McCune 34466*; W edge of Four Craters Lava
147 Field, 43.37427° N 120.68981° W, 1426 m, *McCune 34506*; east side of East Lava Field,
148 43.43548° N 120.70260° W, 1371 m, *McCune 34487*.

149

150 **DISCUSSION**

151 *Ascospore morphology.* We found *Umbilicaria nodulospora* to have an ascospore shape
152 unusual among ascomycetes, lichenized or not. One end of the spore typically has one or two
153 shallow bulges suggesting a T, L, or Y shape. Although we initially thought these might
154 represent a developmental aberration, every specimen examined from each of the fifteen known
155 localities for the species showed this spore morphology. Thus, the spore morphology is
156 consistent within the species and cannot be considered an aberration. Ascospores from all other
157 fertile species of *Umbilicaria* known from western North America have also been examined,
158 revealing no other examples of nodulose spores.

159 The only other description of this kind of ascospore that we have found is Frey (1949),
160 who described and illustrated similar spores in *U. krempelhuberi* Müll. Arg., now considered
161 part of *U. calvescens* Nyl. by Hestmark et al. (2011). Llano (1950) described the spores of *U.*
162 *krempelhuberi* as "spherical to ellipsoid, or irregular and somewhat constricted medially...
163 peculiar constriction occasionally displayed by some spores, suggestive of a triangle or heart-
164 shape." He described the spores of *U. calvescens* as "ellipsoid to irregular or somewhat
165 constricted medially, becoming brown, muriform." While the spores of *U. nodulospora* are very
166 similar to those of *U. krempelhuberi*, both in size and shape, we have seen no tendency for the
167 spores of *U. nodulospora* to become septate, muriform, or brown as Llano reported for *U.*
168 *calvescens*. Furthermore Llano's spore measurements for *U. calvescens* are distinctly larger than
169 we observed for *U. nodulospora* (though Nylander's measurements from *U. calvescens* are
170 similar to ours *U. nodulospora*; see Table 15, p. 180 in Llano (1950)). Hestmark et al. (2011)
171 considered *U. krempelhuberi* to be a synonym of *U. calvescens*, but did not address either the
172 unusual spore shapes or differences in spores between *U. krempelhuberi* and *U. calvescens*.

173 The nodulose spore shape appears gradually in spore development, with spores initially
174 oval, becoming slightly peanut shaped when immature (Fig. 3A, row 1, left side), then finally
175 variously shaped at maturity. The nodulose end of the spore appears is commonly oriented
176 toward the base of the ascus (Fig. 3B), but spores were also seen variously oriented in the ascus.

177 We considered but rejected two alternative hypotheses for the nature of these spores: one
178 that the spores represent a hymenial parasitic ascomycete, or that the spores represent mitotically
179 produced macroconidia. We rejected the parasite hypothesis, because apothecia were collected
180 from fifteen sites and every single apothecium examined had nodulose spores. We considered it
181 highly unlikely that a hymenial parasite is uniformly present in its host. We rejected the

182 mitospore hypothesis because the nodulose spores clearly occur in groups of eight within asci.
183 Asci with spores were always seen in conjunction with the spores loosened by sectioning.

184 Any adaptive or ecological significance of this spore shape remains obscure; nor do we
185 presume that the spore shape is necessarily adaptive. It seems plausible, however, that the
186 nodulose shape affects the mechanics of spore discharge from asci. The knobby spores might
187 impede spore release, perhaps as a mechanism to influence the environmental conditions
188 sufficient for spore discharge, for example desensitizing a moisture-based trigger.

189 ***Phylogenetic relationships.*** *Umbilicaria nodulospora* is a distinctive species in field
190 appearance, habitat, spore shape, and DNA sequences. Specimens of *U. nodulospora* formed a
191 well-supported monophyletic group in phylogenetic trees (Fig. 4). The relationship of this
192 species to other *Umbilicaria* species is, however, obscure, since no support for a sister taxon was
193 found (Fig.4).

194 The phylogenetic reconstruction based on ITS and LSU offered no clues to the origin of
195 this species, since the species connects directly with the poorly resolved backbone of
196 *Umbilicaria*. Morphologically the species shares some characters with *U. torrefacta*, such as
197 smaller ascospores than most *Umbilicaria* species, occasional presence of trabeculae on the
198 lower surface, and occasionally perforations in the thallus near the margins. Neither of the last
199 two characters are as strongly developed as in *U. torrefacta*. Other rhizinate *Umbilicaria* occur in
200 western North America, but so far we have not found them cohabiting with *U. nodulospora*, with
201 the exception of those species with a distinctly gray upper surface in the *U. vellea* group.

202 While *U. nodulospora* is morphological similar to the South American *U. calvescens*
203 group, some differences are apparent. The lower surface of *U. krempehuberi* is pale buff to
204 brown and has sparse to few rhizines, while *U. nodulospora* is brown to black below and thickly
205 rhizinate. Typical *U. calvescens* differs from *U. nodulospora* in lacking rhizines, but *U.*
206 *calvescens* var. *hypomelaena* is black below and rhizinate, while *U. calvescens* var. *subvellea* is
207 densely rhizinate, similar to *U. nodulospora*, but pale to brown in color. All of these variants
208 were included in the concept of *U. calvescens* by Hestmark et al. (2011), because they lacked
209 phylogenetic support based on ITS, nuLSU, and mitSSU.

210 We hypothesize that *U. nodulospora* is most closely related to the *U. calvescens* group,
211 based on morphological similarity and the occurrence of this unusual spore type, although this
212 hypothesis lacks bootstrap support. Phylogenetic reconstructions from both the ITS and LSU

213 regions showed *U. nodulospora* to be distinct from the *U. calvescens* group; furthermore we did
214 not find support for a sister relationship.

215 The apparent restriction of *U. nodulospora* to lava flows is unusual, but perhaps reflects
216 our scattered lichenological exploration of western North America. Many species frequent basalt,
217 as opposed to other kinds of rock, but we know of no species in this region that have been
218 demonstrated to have an obligate requirement for basalt as a substrate.

219 Similarly the species poses a distributional puzzle. So far the species is known only from
220 central Oregon and extreme northeastern California, a very narrow range considering the ease
221 with which it can be found in this area. Narrow endemics are seldom seen with lichens, much
222 less in species frequenting subcontinental or continental climates. Is this species a narrow
223 geographic endemic? Is it truly restricted to lava flows? The only resolution to these puzzles is
224 more extensive searching for the species, which we hope this paper will stimulate.

225

226 **ACKNOWLEDGMENTS**

227 We thank Steve Sheehy for sending to us the original collections of this species. Lava Beds
228 National Monument, including Nancy Nordensten and staff kindly cooperated with field visits.
229 Lakeview District of the Bureau of Land Management partially funded the Oregon field work
230 through Northwest Lichenologists and Daphne Stone. We thank Elisa Alphanary for assistance
231 with TLC and PCR, Jeff Stone and Evgeny Davydov for discussion on ascospore morphology,
232 Patricia Muir and Martin Hutten for assistance and with field work, Martin Hutten for field
233 photography, and Peter Nelson and anonymous reviewers for reviewing the manuscript.

234

235 **LITERATURE CITED**

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Table 1. Voucher information for the species sampled and the associated GenBank accession numbers for ITS and nuLSU. All new sequences are vouchered in OSC unless otherwise specified. The term “morph” indicates recognizable morphological variants of uncertain taxonomic value.

Species	Voucher	GenBank Number	
		ITS	LSU
<i>U. nodulospora</i>	California, <i>McCune 32521</i>	---	xxxxxx
<i>U. nodulospora</i>	California, <i>McCune 32526</i>	xxxxxx	---
<i>U. nodulospora</i> -- holotype	California, <i>McCune 32546</i>	xxxxxx	xxxxxx
<i>U. nodulospora</i> -- isotype	California, <i>McCune 32546</i>	xxxxxx	xxxxxx
<i>U. nodulospora</i>	Oregon, <i>McCune 34506</i>	xxxxxx	---
Previously published sequences			
<i>U. angulata</i> Tuck.	Oregon, <i>McCune 30050</i>	JQ764746	JQ764756
<i>U. angulata</i>	Oregon, <i>McCune 30483</i>	JQ764734	---
<i>U. angulata</i>	Oregon, <i>McCune 31231</i>	JQ764738	JQ764747
<i>U. calvescens</i> Nyl.	Argentina, <i>Hestmark 09002</i>	HM161506	HM161601
<i>U. calvescens</i>	Argentina, <i>Hestmark 09003</i>	HM161507	HM161602
<i>U. calvescens</i>	Argentina, <i>Hestmark 09005</i>	HM161508	HM161604
<i>U. calvescens</i>	Peru, <i>Hestmark 05060B</i>	HM161558	HM161516
<i>U. calvescens</i>	Chile, <i>Hestmark 98025</i>	HM161559	HM161517
<i>U. calvescens</i> var. <i>subvellea</i> Nyl.	Peru, <i>Hestmark 05083B</i>	HM161485	HM161546
<i>U. calvescens</i> var. <i>subvellea</i>	Peru, <i>Hestmark 05061B</i>	HM161460	HM161519
<i>U. calvescens</i> var. <i>hypomelaena</i> Nyl.	Bolivia, <i>Hestmark 05019B</i>	HM161463	HM161524
<i>U. calvescens</i> var. <i>hypomelaena</i>	Peru, <i>Hestmark 05084B</i>	HM161486	HM161547
<i>U. cinereorufescens</i> (Schaer.) Frey	Bolivia, <i>Hestmark 05010B</i>	HM161503	HM161598
<i>U. cinereorufescens</i>	Ecuador, <i>Hestmark 094079</i>	HM161511	HM161605
<i>U. crustulosa</i> (Ach.) Lamy	Norway, <i>Hestmark 09017</i>	HM161496	HM161590
<i>U. decussata</i> (Vill.) Zahlbr.	Antarctica, <i>Ott 2007</i>	AY603122	AY603113
<i>U. haplocarpa</i> Nyl.	Bolivia, <i>Hestmark 05110B</i>	HM161467	HM161528
<i>U. haplocarpa</i>	Bolivia, <i>Hestmark 05052B</i>	HM161487	HM161537
<i>U. havaasii</i> Llano	Oregon, <i>McCune 31230</i>	JQ764739	JQ764748
<i>U. hirsuta</i> (Sw. ex Westr.) Ach.	Norway, <i>Hestmark 09015</i>	HM161494	HM161588
<i>U. hirsuta</i>	Norway, <i>Hestmark 09016</i>	HM161495	HM161589
<i>U. phaea</i> Tuck.	California, <i>McCune 30358</i>	JQ764736	JQ764755
<i>U. phaea</i>	California, <i>McCune 30442</i>	JQ764741	JQ764751
<i>U. phaea</i>	Oregon, <i>McCune 30545</i>	JQ764733	---
<i>U. polaris</i> (Schol.) Zahlbr. (as <i>U. krascheninnikovii</i>)	Antarctica, <i>Lumbsch 19046a</i>	AY603134	AY603118
<i>U. polyrrhiza</i> (L.) Fr.	Oregon, <i>McCune 30484</i>	JQ764737	JQ764749
<i>U. semitensis</i> Tuck. morph 1	Oregon, <i>McCune 30049</i>	JQ764742	JQ764757
<i>U. semitensis</i> morph 1	California, <i>McCune 30407</i>	JQ764735	JQ764753
<i>U. semitensis</i> morph 2	California, <i>McCune 30410</i>	JQ764745	JQ764754
<i>U. semitensis</i> morph 3	California, <i>McCune 30432</i>	JQ764743	JQ764752
<i>U. torrefacta</i> (Lightf.) Schrad.	Oregon, <i>McCune 30482</i>	JQ764744	JQ764750
<i>U. torrefacta</i>	unknown, Brunauer et al.	DQ660906	---
Outgroup:			
<i>Boreoplaca ultrifrigida</i> Timdal	Russia, <i>Haugan & Timdal YAK03/84</i>	HM161512	DQ986797

<i>Hypocenomyce scalaris</i> (Ach. ex Lilj.) M. Choisy	----, <i>Amtoft 47763</i>	DQ782852	DQ782914
<i>Ophioparma ventosa</i> (L.) Norman	Norway, <i>Bjelland 60</i>	AY011013	AY853380

Figure 1. *Umbilicaria nodulospora*. **A.** Habit in situ, moist, monophyllous example (*McCune 32546*, type; photo by M. Hutten). **B.** Habit in situ, dry, of polyphyllous colony in situ (*McCune 32519*). **C.** Detail of upper surface showing young apothecia (*Sheehy LABE31*). **D.** Detail of lower surface showing rhizines, trabeculae, and verrucose bare patches (*Sheehy LABE36*).

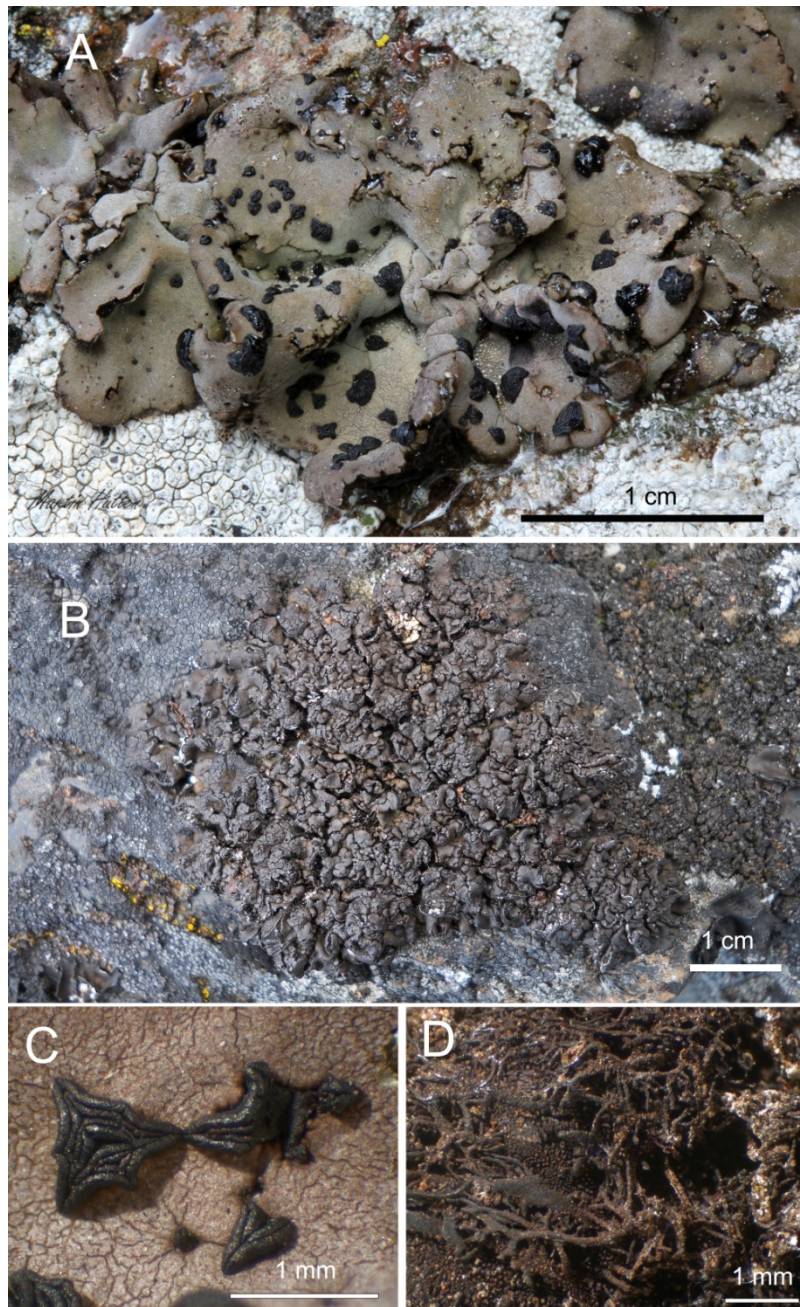


Figure 2. Variation in upper and lower surfaces of *Umbilicaria nodulospora*. **A.** Nearly epruinose examples (*McCune 34506*). **B.** Pruinoso example (*Sheehy LABE31*).

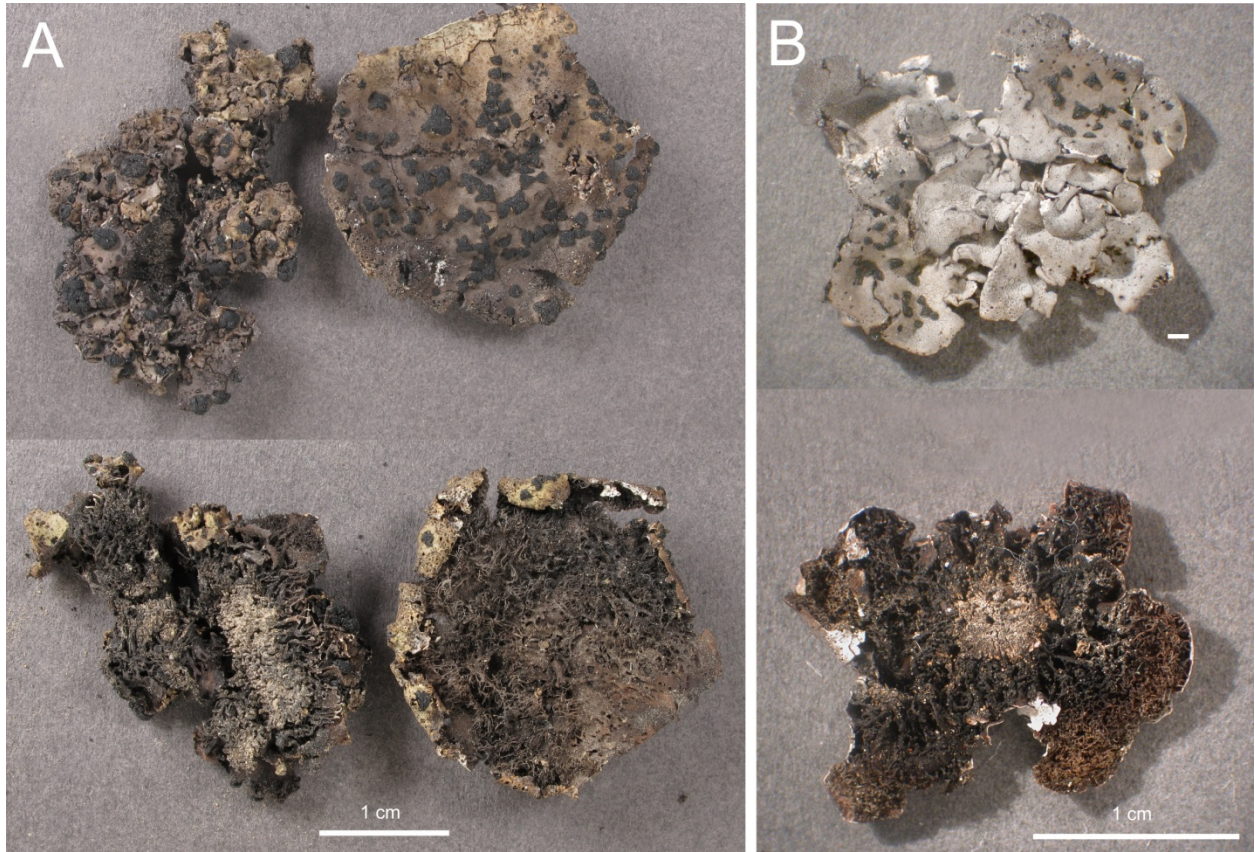


Figure 3. Ascospores and asci from *Umbilicaria nodulospora*. A. Spores selected at random from *Sheehy 774*, *McCune 32546*, and *Sheehy LBE-36*. Four spores on the left of 774 are smaller immature spores. B. Hymenium and dark brown incurved exciple, showing spores in ascus in IKI, *Sheehy 774*.

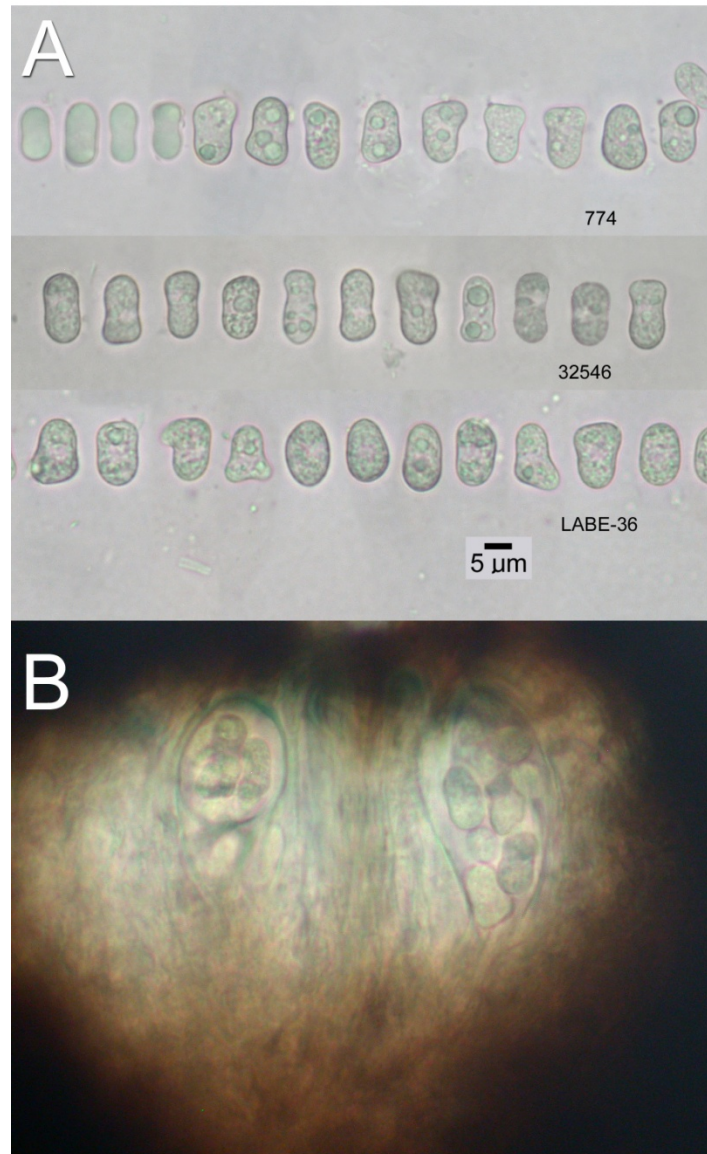


Figure 4. Most likely phylogenetic relationships among sampled *Umbilicaria* species inferred from ITS or nuLSU sequences and based on rooting with *Boreoplaca*, *Hypocenomyce*, and *Ophioparma* chosen as outgroups. **A.** Tree from ITS data. **B.** Inferences from LSU data. Bootstrap percentages above 80% are shown above branches; branch lengths are based on estimated number of substitutions per site assuming a GTR model of substitution. Countries of origin for *U. calvescens* var. *calvescens* are given because of geographically-related variation: A = Argentina, C = Chile, P = Peru.

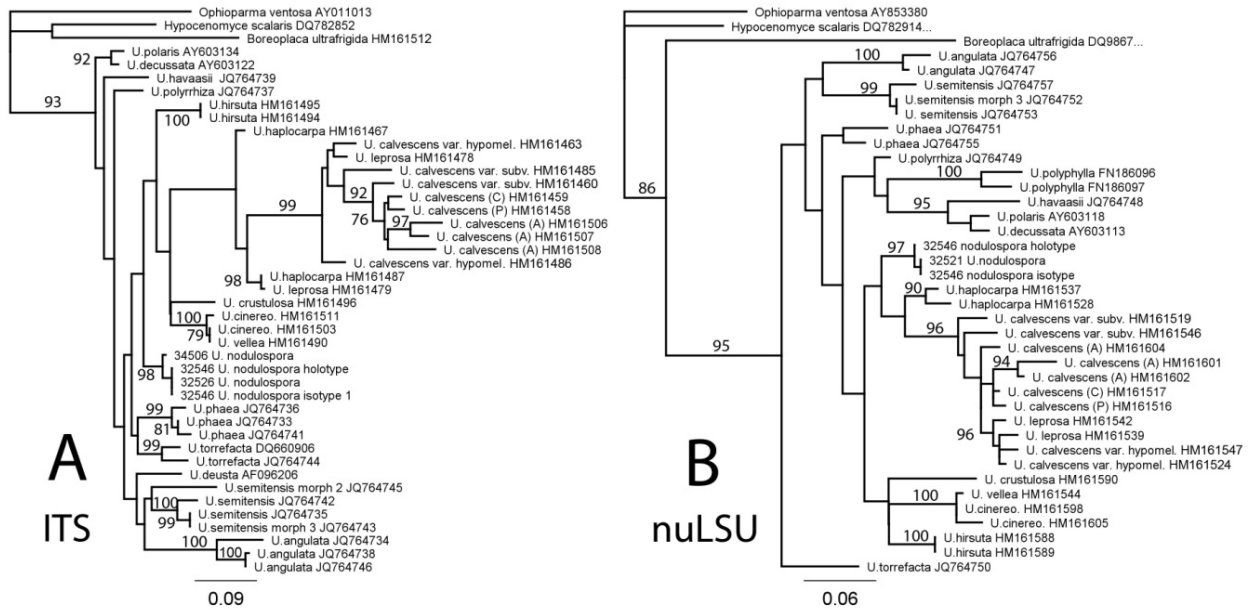


Figure 5. Distribution of *Umbilicaria nodulospora*. **A.** All known sites. **B.** Detail showing the cluster of sites in and near Lava Beds National Monument, California.

