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Two new species of *Xerocomus* (Boletales) from the Indian Himalaya

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Abstract

Xerocomus garhwalensis and *Xerocomus rishikeshinus* (Boletales, Basidiomycota) are described as species new to science from specimens collected in the Himalayas of northwestern India. Both were found in forests dominated by banj oak (*Quercus leucotrichophora* A. Camus), and they presumably form ectomycorrhizal associations with this tree species. *Xerocomus* has been variously defined morphologically, and a number of the species now assigned to the genus are sometimes considered to be members of the genus *Boletus*. The two new species were placed in *Xerocomus* largely on the basis of DNA sequence data, which are still rather limited for the assemblage of macrofungi present in northwestern India.

Keywords – banj oak – Basidiomycota – Boletaceae – ectomycorrhizal fungi – new taxa

Introduction

The genus *Xerocomus* Quél (Boletales, Basidiomycota) *sensu lato* encompasses more than 160 described species worldwide. *Xerocomus* has been variously defined morphologically (Husbands 2013), and species now assigned to the genus are sometimes considered to be members of the genus *Boletus* (Drehmel et al. 2008). Indeed, in all but the most recent taxonomic treatments of members of the family Boletaceae, many of the species now considered to belong to *Xerocomus* have been placed in the genus *Boletus* (Smith & Thiers 1971, Bessette et al. 2000). No comprehensive molecular phylogenic study of the Boletaceae yet exists, but available data suggest that *Xerocomus* is not monophyletic, since species show up in several different clades. Nuhn et al. (2013), who carried out a relatively comprehensive phylogenetic investigation of the entire suborder Boletineae (which consists of the families Boletaceae and Paxillaceae), identified a "*Xerocomus* clade" that included the type species *X. subtomentosus* (L.) Quél. but did not include certain other species assigned to the genus *Xerocomus*. The results obtained from a molecular phylogenetic study of just the family Boletaceae (Wu et al. 2014) also indicated that *Xerocomus* is not monophyletic.

The purpose of this paper is to describe two new species of *Xerocomus* which were collected during an ecological study of the successional dynamics of banj oak (*Quercus leucotrichophora* A. Camus [Fagaceae]) and chir pine (*Pinus roxburghii* Sarg. [Pinaceae]) forests in northwestern India (Nautiyal 2015). These two species (*Xerocomus garhwalensis* and *Xerocomus rishikeshinus*) are described largely on the basis of DNA sequence data.

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Materials & Methods

The specimens upon which the two new species are based were collected during fieldwork carried out in the Garhwal region of northern Uttarakhand during the monsoon season on 2 August 2012, and important information collection information was recorded (Rathnayaka et al. 2024). Sporocarps were photographed in the field with a digital camera and then air-dried as soon as possible. However, because of the warm, moist conditions that existed at the time, sporocarps degraded rather rapidly once they had been collected. It was not possible to prepare an adequate spore print from any specimen, but small tissue samples were obtained to be used as described below. Colors were described from fresh material based on the color plates in Kornerup & Wanscher (1978), with the code of the relevant color plate provided (in parentheses) in the descriptions of the two species. Index Fungorum and Facesoffungi numbers were obtained as per the instructions of Index Fungorum (2024) and Jayasiri et al. (2015).

Examination of spores

Scanning electron microscope (SEM) images of spores from air-dried sporocarps were obtained with a JSM-6390 LA (SEM) at 10–15 kV using material mounted on copper stubs using double-sided sticky film and sputter-coated with gold. In addition, spores were also examined with a Zeiss light microscope with a differential interference contrast (LM) Zeiss Axio Imager A1 using the program Axio Vision 4.8.0.0 (Carl Zeiss Imaging Solutions). Measurements of spores given herein were determined for a minimum of 20 spores for each of the two species.

DNA extraction, PCR, and sequencing

Approximately 0.5 g of fungal tissue was removed from the interior (trama) of the fruiting body of each specimen. These tissue samples were placed into sterile 1.5 ml microcentrifuge tubes. Samples were disrupted and homogenized by a Geno/Grinder 2010 using 3.0 mm glass beads (10 min, 1620 rpm). DNA extraction of homogenized tissue was carried out using the NucleoSpin Plant II kit (Macherey NagelMacherey-Nagel, Bethlehem, PA). Protocol steps were modified from the manufacturer's original protocol to achieve optimal DNA extraction. Modifications included dividing the volumes of PL1 Buffer solution, Rnase A and PC Buffer solution by half, and performing one wash with 350 ml PW1 Buffer solution. DNA samples were eluted in 25 µl of PE Buffer solution.

DNA extracted from the fungal tissue was amplified via the polymerase chain reaction (PCR) using the fungal-specific primers ITS1F and ITS4 (White et al. 1990). PCR amplifications were performed in a T100 thermal cycler (Bio-Rad Inc., USA). The PCR program consisted of an initial denaturation at 95 °C for 5 min, followed by 37 cycles of denaturation at 95 °C for 20 s, annealing at 56 °C for 30 s, and amplification at 72 °C for 1.30 min, and a final extension at 72 °C for 7 min. PCR products were verified via electrophoresis in a 1.5% agarose gel in 0.5× TAE buffer, stained by SYBR safe. MassRuler Express Forward DNA Ladder Mix (Thermo Scientific) was used as a size standard. DNA was sent for single-pass Sanger sequencing to Beckman-Coulter Genomics (Danvers, MA).

Sequences were edited using the software SeqMan-program version 7.1.0 (44.1) and manually corrected before alignment to obtain a consensus sequence. For a DNA-based identification, all sequences were in-silico compared with the results of a nucleotide search using the Basic Local Alignment Search Tool (BLAST) available at the National Center for Biotechnology Information (NCBI; www.ncbi.nlm.nih.gov).

Phylogenetic analyses

DNA sequences of the internal transcribed spacer (ITS) nuclear ribosomal RNA genes of each specimen were aligned with a selection of homologous sequences from *Xerocomus* spp. obtained using the NCBI BLAST search tool and the UNITE database (https://unite.ut.ee/). In addition, ITS sequences of closely related genera (Table 1) were chosen for alignment and subsequent phylogenetic analysis based on the recommendations of Šutara (2008). Homologous sequences were aligned using

the MUSCLE algorithm in MEGA version 6 (Tamura et al. 2013) and then edited visually. Aligned sequences were then used for subsequent phylogenetic analysis.

Maximum likelihood (ML) phylogenetic analysis was performed using RAxML-HPC2 (8.2.4) (Stamatakis 2014) on XSEDE via the CIPRES science gateway (www.phylo.org) with 1000 bootstrap replications. The resulting ML tree was visualized with the program FigTree (http://tree.bio.ed.ac.uk/software/figtree/). ML values greater than 50 were reported in the final tree. The nomenclature used for fungi in this paper follows that listed in Index Fungorum (http://www.indesfungorum.org/names/Names.asp)

Taxonomy

Xerocomus garhwalensis A. Nautiyal, M. Ben Hassine Ben Ali & S. L. Stephenson, sp. nov.
Figs. 1 & 3A

Index Fungorum: IF 902540; Facesoffungi number: FoF 16744

Etymology – the name refers to the region (Garhwal) in India where the type specimen was collected.

Pileus 5–10 cm broad, 1–3 cm tall, at first convex to broadly convex but becoming plano-convex with age, at first deep yellow (4A8) but darkening with age; surface smooth but marked with light orange (5A4) discolorations; tube surface pastel yellow (3A4); tubes angular, 0.5–1.8 mm at the margin, 0.8–4.0 mm in the central portion and 1.5–3.8 mm near the stipe, where they become somewhat sub lamellate; Stalk solid, 6.0–7.0 cm long and 7–9 mm wide, white (1A1) at the base and greyish yellow (4C7) towards the apex; no partial veil present; Spores probably brownish yellow in mass, (10–) 11–12 × 4–5 µm (Q = 2.6), subfusiform, appearing smooth but with a bacillate spore surface ornamentation under SEM (Figure 3B).

Holotype – Nautiyal AN12-6.

Habit, habitat and distribution – Occurring on the ground as solitary fruiting bodies or in small groups, associated with banj oak. Currently known only from the collecting site in northern India.

Specimens examined – India, Uttarakhand, near the village of Lamkot (30.34° N, 78.43° E, elevation 1954 m), 2 August 2012, A. Nautiyal AN-06. Deposited the herbarium (LE) of the Komarov Botanical Institute in St. Petersburg, Russia.

Fig. 1 – *Xerocomus garhwalensis*. A. Sporocarps as observed in the field. B. Single sporocarp.

GenBank accession numbers – ITS: KU761592.

Comments – *Xerocomus* is known to form ectomycorrhizal associations with trees. Since the sporocarps of *X. garhwalensis* were found in a forest dominated by banj oak, this new species is

presumably ectomycorrhizal with this tree species. The sporocarps degraded rather rapidly once they had been collected. *Xerocomas garhwalensis* can be readily distinguished from *X. rishikeshinus* based on the color of the pileus, which is yellow for the former and brownish red to violet-brown for the latter. *Xerocomas garhwalensis* also has a wider pileus compared to the latter (5–10 cm vs 4.5–5.5 cm).

Xerocomus rishikeshinus A. Nautiyal, M. Ben Hassine Ben Ali & S. L. Stephenson, sp. nov.
Figs. 2 & 3B

Index Fungorum: IF 902541; Facesoffungi number: FoF 16745

Etymology – the name refers to the largest city (Rishikesh) near the site in India where the specimen was collected.

Pileus 4.5–5.5 cm broad, 0.8–1.0 cm tall, at first broadly convex but becoming plano-convex with a slightly upturned margin with age; pileus brownish red to violet brown (10D6 to 10E6); surface velutinous; tube surface greyish yellow (2B7), tubes angular, 0.1–0.7 mm at the margin, 0.6–2.3 mm in the central portion and 0.9–2.1 mm near the stipe, where they become somewhat sub lamellate; stipe solid, 4.5–5.7 cm long and 6–8 mm wide, yellow (3A7) at the apex, with some brownish red discolorations (8B-C8), and dark yellow (4C8) below; spores probably brownish yellow in mass, 10–11 (–12) × 4.5–5.0 µm (Q = 2.2), subfusiform, smooth.

Holotype – Nautiyal AN12-08.

Habit, habitat and distribution – Occurring as solitary fruiting bodies or in small groups, associated with banj oak. Currently known only from the collecting site in northern India.

Specimens examined: India, Uttarakhand, near the village of Lamkot (30.34° N, 78.43° E, elevation 1954 m), 2 August 2012, A. Nautiyal AN-08; *ibid*., A. Nautiyal AN12-01; *ibid*., A. Nautiyal AN12-05. Deposited in the herbarium (LE) of the Komarov Botanical Institute in St. Petersburg, Russia.

GenBank accession numbers – AN-08 - ITS: KU761593

Comments – Sporocarps of *X. rishikeshinus* were collected in a forest dominated by banj oak and thus are presumably ectomycorrhizal with this tree species. Interestingly, all sporocarps occurred adjacent to decaying logs on the forest floor. As was also the case for *X. garhwalensis*, the sporocarps of *X. rishikeshinus* degraded rather rapidly once they had been collected. As noted under *X. garhwalensis,* the two species can be easily distinguished on the basis of pileus color and the width of the pileus.

Fig. 2 – *Xerocomus rishikeshinus.* A. Sporocarps as observed in the field. B. Two sporocarps showing the tube surface.

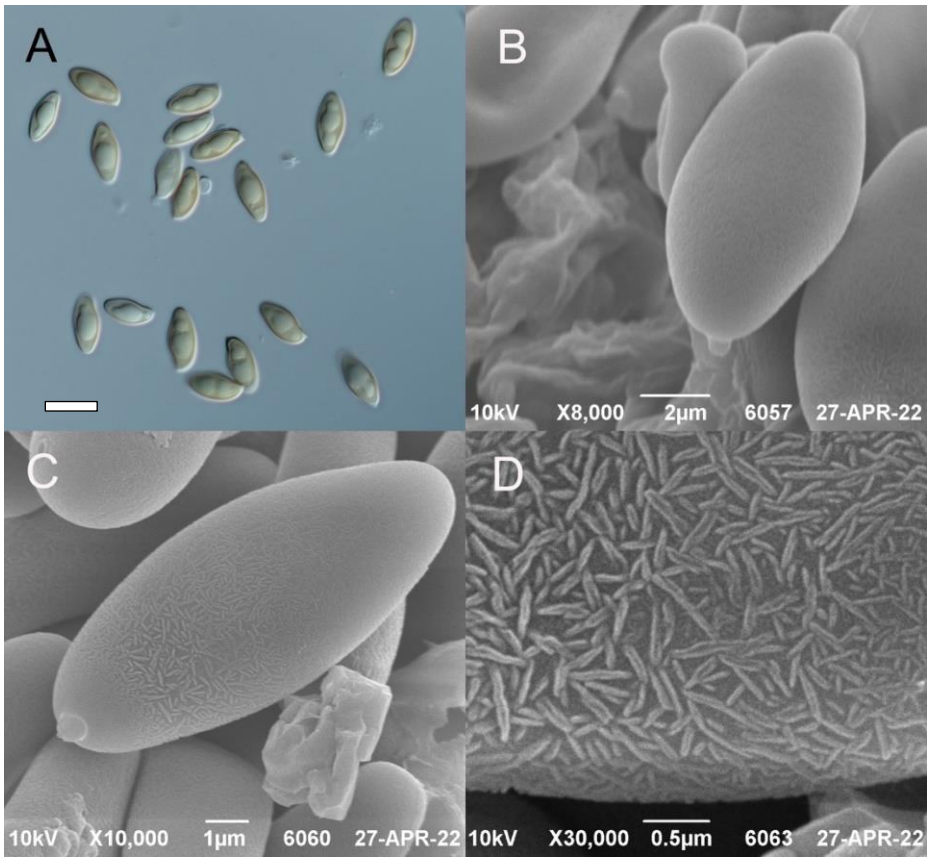

Fig. 3 – Spores of the two new species described herein. A. Subfusiform spores of *Xerocomus garhwalensis* as viewed by light microscopy. B. Spores of *Xerocomus garhwalensis* as viewed by scanning electron microscopy. C. Spores of *Xerocomus rishikeshinus* as viewed by scanning electron microscopy. D. Bacillate spore surface ornamentation in *Xerocomus rishikeshinus.* Scale bars: A = 10 µm, B = 2 µm, C = 1 µm, D = 0.5 µm.

Table 1. Fungal ITS sequences obtained from NCBI GenBank for phylogenetic analysis of the two new species described herein.

Species	GenBank accession no.	Species	GenBank accession no.
Alessioporus ichnusanus	KJ729491	*Phylloporus rufescens*	JQ967263
Boletus chrysenteron	FJ596906	*Phylloporus scabripes*	JQ003622
Boletus citrinovirens	DQ066405	*Pseudoboletus parasiticus*	KM248932
Boletus dryophilus	AY372283	*Pulchroboletus roseoalbidus*	KJ729489
Boletus impolitus	AJ419187	*Xerocomellus armeniacus*	JF908795
Boletus rubellus	KJ802928	*Xerocomellus chrysenteron*	JF908799
Boletus sinopulverulentus	KC579402	*Xerocomellus cisalpinus*	KT271743
Boletus spadiceus	DQ066411	*Xerocomellus porosporus*	KM085410
Boletus zelleri	AY750158	*Xerocomellus sarnarii*	KT271745
Bothia castanella	DQ867114	*Xerocomellus zelleri*	DQ974704
Hemileccinum sp.	KP012755	*Xerocomus amazonicus*	KT339240
Octaviania cyanescens	HQ328784	*Xerocomus armeniacus*	AJ419221
Octaviania tasmanica	HQ328789	*Xerocomus badius*	KM409434
Phylloporus alborufus	JQ003624	*Xerocomus chrysenteron*	HQ207693
Phylloporus bellus	JQ003618	*Xerocomus chrysonemus*	DQ066384
Phylloporus bogoriensis	JQ003619	*Xerocomus cisalpinus*	HM190084
Phylloporus centroamericanus	JQ003631	*Xerocomus cyaneibrunnescens*	JQ751259
Phylloporus colligatus	KT339267	*Xerocomus depilatus*	AY127032
Phylloporus cyanescens	JQ003621	*Xerocomus ferrugineus*	HQ207698
Phylloporus foliiporus	JQ003641	*Xerocomus illudens*	JQ003658

Table 1 Continued.

Species	GenBank accession no.	Species	GenBank accession no.
Phylloporus gajari	KP780417	*Xerocomus impolitus*	HM347650
Phylloporus leucomycelinus	JQ967249	*Xerocomus magniporus*	JQ678697
Phylloporus maculatus	JQ678696	*Xerocomus parvogracilis*	JQ751261
Phylloporus orientalis	JQ003651	*Xerocomus perplexus*	JQ003657
Phylloporus pachycystidiatus	KF053003	*Xerocomus porosporus*	HM190086
Phylloporus parvisporus	JQ967257	*Xerocomus potaroensis*	JN168784
Phylloporus pelletieri	DQ534566	*Xerocomus pruinatus*	AF402140
Phylloporus purpurellus	JQ003630	*Xerocomus rubellus*	EF644119
Phylloporus rhodoxanthus	DQ533980	*Xerocomus spinulosus*	KR819011
Phylloporus rubeolus	JQ967261	*Xerocomus subtomentosus*	DQ066359
Phylloporus rubiginosus	KF053004	*Xerocomus zelleri*	DQ822794
Phylloporus rubrosquamosus	JQ967260		

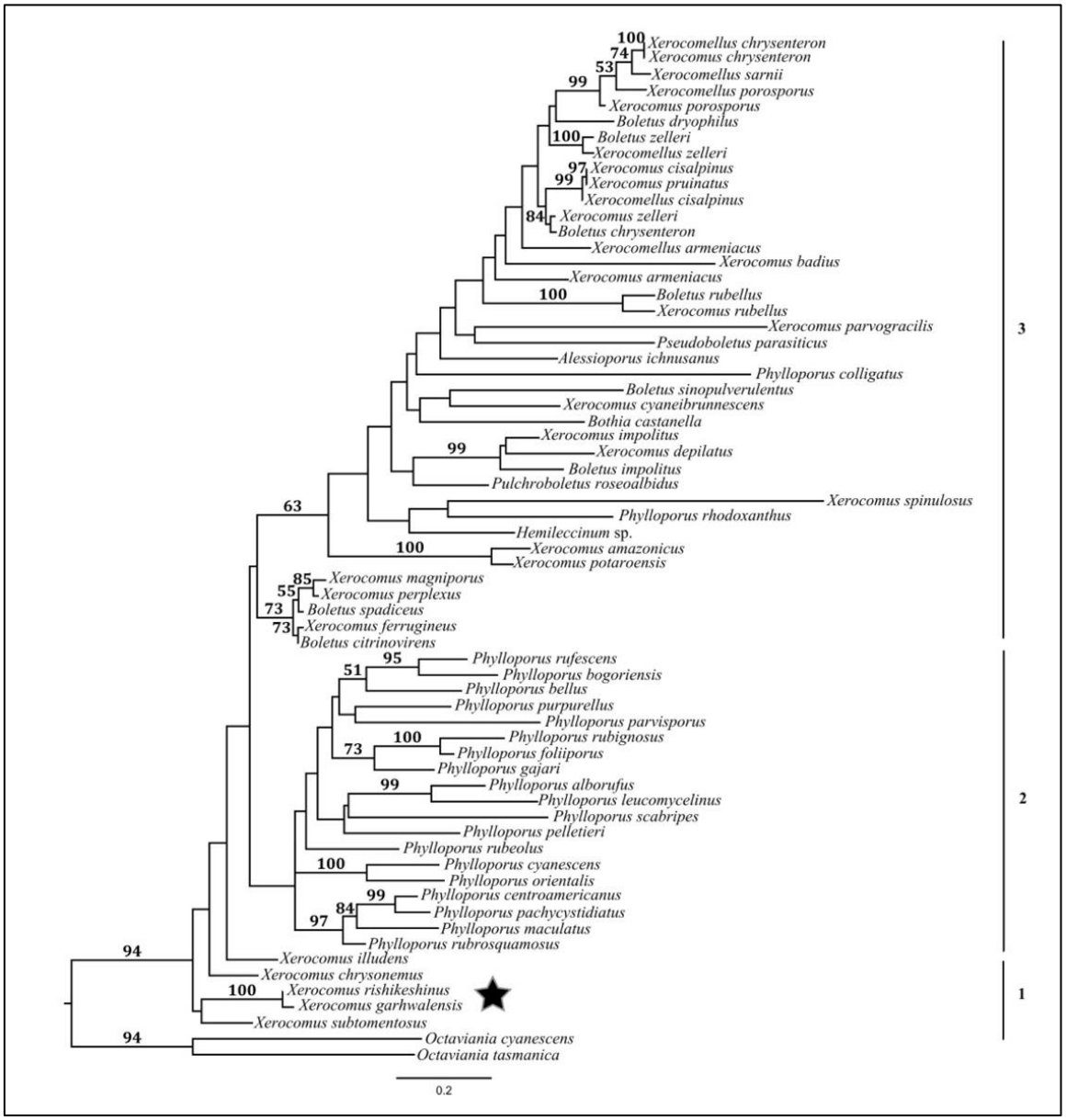

Fig. 4 – Maximum likelihood phylogenetic analysis of *Xerocomus rishikeshinus* and *X. garhwalensis* ITS sequences with closely related species and genera. Likelihood values greater than 50 are reported. The star denotes the location of the two new species.

Discussion

As noted in the introduction, the genus *Xerocomus* is difficult to circumscribe morphologically, since it appears to share several features in common with *Boletus*. Indeed, some authors (e.g., Smith & Thiers 1971) have questioned whether or not the former should be recognized as distinct. In most instances, species of *Xerocomus* have been differentiated based on having subangular to angular tubes that are sublamellate near the stipe. However, Ladurner & Simonini (2003), who conducted an intensive study of the species of *Xerocomus* known from Europe, commented on the extreme variability of morphological characters in the material they examined. Although the use of molecular data to delimit species would seem to represent a more effective approach, the results obtained from the phylogenetic studies that have been carried out (e.g., Drehmel et al. 2008) indicate that the genus does not represent a monophyletic group.

The ITS region is considered the universal DNA barcode marker for fungi (Bellemain et al. 2010, Schoch et al. 2012, Das & Deb 2015). In the present study, maximum likelihood phylogenetic analysis of ITS sequences obtained from the specimens reported herein and other sequences available for closely related taxa revealed a distinct clade (Fig. 4; clade 1) that contains both the two new species (on a well-supported branch) and *X. subtomentosus* (L.) Quél., the type for the genus *Xerocomus*. These three species form a basal *Xerocomus* clade, based on ITS sequence data. Although *Xerocomus garhwalensis*, *X. rishikeshinus*, and the type species *X. subtomentosus* are members of the same clade and thus are closely related, they can be distinguished rather easily based on their morphological features. *Xerocomus subtomentosus* and *X. garhwalensis* are similar in size, but the pileus of the former is ochraceous-brown to medium brown in color, whereas that of the latter is deep yellow. Moreover, the stipe of *X. subtomentous* has a sparse reticulum at the apex, which is absent in *X. garhwalensis*. *Xerocomus rishikeshinus* is smaller than either species (4.5–5.5 cm vs 3–9.5 cm and 5–10 cm) and has a brownish red to violet-brown pileus. *Xerocomus illudens* (Peck) Singer (1946) and *X. chrysonemus* A.E. Hills & A.F.S. Taylor (2006) appear to be most closely related to the other species whose sequence data were used to produce the phylogenetic tree described above (Fig. 4). The former is similar in size to *X. garhwalensis* but differs in having a pileus that is pale brownish yellow and slightly hairy to velvety. *Xerocomus chrysonemus* is comparable in size to *X. rishikeshinus* but has a yellow-ochre to yellow-olive pileus and a bright yellow stipe that arises from a yellow basal mycelium (Janda et al. 2013).

Interestingly, species of *Phylloporus* also form a distinct clade for ITS sequence data (Fig. 4; clade 2), but the relationships among many of the other taxa in the tree remain unresolved (clade 3). The ITS sequence data for the two new species shared 97.5% identity, with 17 variable sites (including gaps) across 671bp of ITS. This appears to be a greater similarity than the accepted threshold for most fungal ITS sequences of 97% for conspecific sequences, but given the lack of resolution between other species of *Xerocomus* in this ITS phylogeny, it would appear that the 97% threshold is not an adequate metric for species delineation in this genus. For instance, a comparison of *X. cisalpinus and X. pruinatus* homologous ITS sequence data shows a 99.9% identity at ITS (1bp over 568 bases). Therefore, it appears that consideration of the morphological characters that distinguish these two new species from one another, the ITS sequence variation between them, and the fact that the two new species cluster near the type species supports their placement in the genus *Xerocomus* as distinct species.

The first species of *Xerocomus* described from India appears to have been *X. bakshii* (Singer & Singh 1971). The authors indicated that it was an ectomycorrhizal associate of chir pine. Both pine and oak have been reported as ectomycorrhizal hosts for species of *Xerocomus* (Moser 1978), so the association of the two new species described herein with banj oak is not unexpected. Other more recent reports of *Xerocomus* from India include Sagar & Lakhanpal (1991), De (2006), Das et al. (2016), Chakraborty et al. (2017), and Das (2017).

As noted earlier, obtaining an adequate spore print from any of the specimens we collected was not possible. However, Ladurner & Simonini (2003) reported that they found no relevant differences in spore color for the species they examined. Typically, the spores are brownish yellow, which is presumed to be the case for the two new species. These authors also indicated that the spores themselves displayed some differences in features such as the surface and thickness of the wall, but

the most consistently useful feature to differentiate the spores of different species was their length/width quotient (Q). As a general observation (Fig. 3), spores of the two new species are remarkably similar in overall shape, but they do differ in their Q values (2.6 for *Xerocomas garhwalensis* and 2.2 for *X. rishikeshinus*).

In summary, the assemblage of ectomycorrhizal fungi associated with banj oak in northern India includes two species of *Xerocomus* not previously recognized as new to science. These two species can be distinguished rather easily based on differences in both the overall size and color of the pileus. However, each of the two species cannot yet be reliably differentiated from several other species in the same genus on the basis of morphology, but this situation is not unusual in this genus. However, they are clearly distinct from all other species of *Xerocomus* based on the molecular data presented herein.

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Accessibility of data

GenBank assession numbers are KU761592 and KU761593 for *Xerocomus garhwalensis* and *Xerocomus rishikeshinus*, respectively. Specimens of both species have been deposited in the herbarium (LE) of the Komarov Botanical Institute in St. Petersburg, Russia

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