Description and DNA barcoding of three new species of *Leohumicola* from South Africa and the United States

H.D.T. Nguyen¹, K.A. Seifert¹

Abstract  Three new species of *Leohumicola* (anamorphic Leotiomycetes) are described using morphological characters and phylogenetic analyses of DNA barcodes. *Leohumicola levissima* and *L. atra* were isolated from soils collected after forest fires in Crater Lake National Park, United States. *Leohumicola incrustata* was isolated from burned fynbos from the Cape of Good Hope Nature Reserve, South Africa. The three species exhibit characteristic *Leohumicola* morphology but are morphologically distinct based on conidial characters. Two DNA barcode regions, the Internal Transcribed Spacer (ITS) nuclear rDNA region and the cytochrome oxidase subunit I (Cox1) mitochondrial gene, were sequenced. Single-gene parsimony, dual-gene parsimony and dual-gene Bayesian inference phylogenetic analyses support *L. levissima*, *L. atra*, *L. incrustata* as distinct phylogenetic species. Both ITS and Cox1 barcodes are effective for the molecular identification of *Leohumicola* species.

Key words  auroconidium  chlamydospore  cytochrome oxidase subunit I (Cox1)  internal transcribed spacer (ITS)  *Leotiomycetes*

INTRODUCTION

The hyphomycete genus *Leohumicola* was described for four species (*L. verrucosa*, *L. minima*, *L. terminalis*, and *L. lenta*) by Hambleton et al. (2005). *Leohumicola* species produce two-celled auroconidia, with a round to elliptoidal, dark-brown terminal cell with slightly thickened walls, and a basal cell that is either cupulate or cylindrical, and hyaline to pale brown. Globose to ellipsoidal, intercalary or terminal chlamydospores are produced by all known species. Conidium ontogeny is usually monoblastic, with sympodial extension of the conidigenous cells sometimes occurring. Secession is rhexolytic, with the remnants of the empty basal cell remaining attached to the terminal cell. Most *Leohumicola* strains grow slowly and sporulate sparsely or not at all; they must be grown on various media to stimulate conidial production.

Hambleton et al. (2005) noted that many internal transcribed spacer (ITS) sequences of unidentified soil or root-associated fungi in GenBank belonged to the *Leohumicola* clade, but did not correspond with the species they described. Several of the known species of *Leohumicola* were associated with burnt ecosystems, especially commercial blueberry cultivation, and were isolated by heat treatment of soil suspensions or from surface-sterilised roots of ericaceous host plants. This association with the plant family Ericaceae led us to obtain soil samples from a burned area of fynbos in the Cape Floristic Region (Cape of Good Hope Nature Reserve, South Africa), a hotspot of biodiversity for this plant family (Cowling & Richardson 1995). We also obtained soil from a part of Crater Lake National Park, United States, recently affected by forest fires.

The original study of *Leohumicola* supplemented morphological information with phylogenetic analysis of the ITS. Here, we add analyses of cytochrome oxidase subunit I (Cox1) mitochondrial gene sequences. The ITS is a widely accepted DNA marker for identifying fungi. Cox1 is the DNA barcode gene that has been tested most extensively in the animal kingdom, with a 648-bp region in the 5’ end usually providing species-level resolution (e.g. Ward et al. 2005, Hajibabaei et al. 2006). The Cox1 barcode region was somewhat effective in identifying species of *Penicillium* (Seifert et al. 2007) but has otherwise been little explored in fungi. This study assesses the utility of both ITS and Cox1 as DNA barcodes for the identification of *Leohumicola* species.

MATERIALS AND METHODS

Isolation, observation and preservation of cultures

Soil samples from South Africa were collected at Olifantsbos, Cape of Good Hope Nature Reserve, with the kind assistance of Dr Karin Jacobs and her students from the Department of Microbiology, University of Stellenbosch. The sampled region was a fynbos with abundant *Erica* and *Protea* species, which had been burned one or two years previously. Samples of surface and rhizosphere soil were collected in sterile 15 mL BD Falcon conical bottom tubes and mailed to Ottawa. Soil samples from Crater Lake National Park, Montana, USA, were collected by Matt Trappe in a region with visible signs of forest fire damage. Approximately 50 g samples were collected into zip lock bags and mailed to Ottawa. All samples were kept at room temperature until processing.

Fungi were isolated using a method modified from Jackson et al. (1995). After using a layer of cheesecloth to remove large particles from the soil sample, 2–4 mL of fine dry soil were placed into 50 mL BD Falcon conical bottom tubes. Sterile 0.1 % (w/v) peptone broth was added to the 25 mL mark, then the tube was vortexed for 30 s. The tube was submerged in a 75 °C water bath until the suspension reached this temperature (~ 15 min),
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then incubated for a further 30 min with manual shaking every 5 min to ensure even temperature distribution. The tube was cooled at room temperature for 30 min. A well homogenised 1 mL aliquot of the suspension was mixed with 100 mL of molten and cooled (50 °C) half-strength potato-dextrose agar (PDA (Difco), BD, Sparks, Maryland, USA) with 40 mg/L chloramphenicol to inhibit bacterial growth. The mixture was dispensed in polystyrene Petri dishes (~ 20 mL per dish) and then left to solidify. Petri dishes were sealed with Parafilm and incubated upright at 25 °C under ambient light conditions.

Isolation plates were checked for *Leohumicola* colonies every 1–2 d for 2 wk. Petri dishes with no visible growth after 2 wk were incubated for up to 3 mo before disposal. *Leohumicola* colonies were recognised by their slow growth combined with the release of yellow pigments into the medium. Putative *Leohumicola* colonies were transferred to new full-strength PDA plates, then incubated as above for 3 wk at room temperature (22–25 °C) before performing morphological studies and DNA extraction.

For morphological studies, suspected *Leohumicola* colonies were grown on oatmeal agar (OA, Samson et al. 2004), corn meal agar with dextrose (CMA (Difco), BD, Sparks, Maryland, USA) and PDA. To induce sporulation, PDA was inoculated with a suspension of macerated mycelium as described by Hambleton et al. (2005). Cultures were checked for aleurioconidia and chlamydospores monthly. Cultures that did not sporulate after 3 mo were transferred to potato-carrot agar (PCA, Samson et al. 2004), incubated at 25 °C under ambient light conditions for 2 mo, and then rechecked for conidia. Measurements and photographs were taken from material mounted in 85 % lactic acid using an Evolution MP digital microscope camera on an Olympus BX50 compound microscope with differential interference contrast (DIC) optics and captured using ImagePro 6.0 (Media Cybernetics, Bethesda, Maryland, USA). Colony photographs were taken after 2 wk and 2 mo. Some microphotographs and colony photographs were digitally retouched using Adobe Photoshop CS2 for aesthetic reasons, to reduce background clutter and to remove unwanted reflections, as noted in the figure legends. Colony colours were assessed using Komerup & Wanscher (1978).

Twenty-three strains selected to represent the genetic diversity of the isolated species were deposited in the Canadian Collection of Fungal Cultures (DAOM), Ottawa, Canada (Table 1). Additional strains are deposited in the Seifert Lab collection at Agriculture and Agri-Food Canada.

**DNA extraction, PCR, sequencing and sequence editing**

DNA extractions were performed using UltraClean Microbial DNA Isolation Kits (MO BIO Laboratories Inc., Carlsbad, California, USA) from mycelia scraped from PDA colonies using a sterile scalpel. DNA concentration and quality were determined by Nanodrop ND-1000 spectrometer (Thermo Scientific, Wilmington, Delaware, USA) and preparations were diluted to 1–5 ng/µL of DNA template.

The ITS and Cox1 regions were amplified and sequenced using the primers ITS5 and ITS4 (White et al. 1990) and newly designed primers for the Cox1 of the *Pezizomycotina*, PezizF (5’-TCAGGRTTAYTAGGWACAGCATT-3’) and PezizR (5’-ACCTCAGGRGTGYYCCGAAGAT-3’) (S. Gilmore, pers. comm.). Primers ITS1, ITS2, and ITS3 (White et al. 1990) were sometimes used as internal sequencing primers when the DNA sequence quality obtained from ITS5 and ITS4 was inadequate. Primer binding sites for Cox1 are illustrated in Fig. 1.

For the PCR master mix, 0.1 mM dNTP’s, 0.08 µM forward primer, 0.08 µM reverse primer, 1X Titanium Taq buffer (Clontech, Mountain View, California, USA), 0.5X Titanium Taq enzyme (Clontech, Mountain View, California, USA), and 1.00 µL of DNA template (1–5 ng/µL) were mixed in sterile HPLC water totalling 10 µL per reaction. The PCR reaction was run in a Mastercycler gradient S thermal cycler (Eppendorf, Mississauga, Ontario, Canada). The following profile was used to amplify ITS: 95 °C for 3 min (initial denaturation), then 40 cycles at 95 °C for 45 s (denaturation), 60 °C for 45 s (annealing), 72 °C for 1.5 min (extension), then 72 °C for 8 min (final extension). The following parameters were used to amplify Cox1: 95 °C for 3 min (initial denaturation), then 40 cycles at 95 °C for 1 min (denaturation), 51 °C for 1 min (annealing), 72 °C for 1.5 min (extension), then 72 °C for 8 min (final extension).

For sufficient amplification of Cox1 for *Leohumicola* sp. DAOM 239516, a touchdown PCR was performed. The Cox1 touchdown profile was the same as the profile described above except that the annealing temperature started at 54 °C (5 cycles), then changed to 51 °C (5 cycles), then to 49 °C (5 cycles), then finally to 46 °C (35 cycles), for a total of 50 cycles. For sufficient Cox1 amplification from *Myxotrichium deflexum* UAMH 6365, a step-up PCR was performed. The Cox1 step-up profile differed with the annealing temperature initially at 46 °C (10 cycles), then 49 °C (10 cycles), then finally 51 °C (30 cycles), for a total of 50 cycles. PCR products were separated by electrophoresis on a 1 % agarose gel, stained with ethidium bromide and visualised under UV light.

Both forward and reverse strands were sequenced using Big Dye Terminator (Applied Biosystems, Foster City, California, USA) in 10 µL reactions with the same protocol described by de Cock & Levesque (2004). The following profile was used for the sequencing reaction of ITS: 95 °C for 3 min, then for 40 cycles at 95 °C for 30 s, 50 °C for 15 s, 60 °C for 2 min. For Cox1, the sequencing reaction profile was 95 °C for 3 min, then 40 cycles at 95 °C for 30 s, 51 °C for 15 s, 60 °C for 4 min.

![Fig. 1 Primer binding sites for the 628 bp Leohumicola Cox1 barcode region. Reference positions based on the mitochondrial genomic sequence of Saccharomyces cerevisiae.](image-url)
Contigs were assembled and edited using SeqMan II v7.0 from DNA Star (www.dnastar.com/). To confirm that the newly designed PCR primers amplified the expected gene, BLAST analyses were performed with our putative Cox1 sequences to verify that they were homologous with other fungal Cox1 sequences. All sequences are deposited in GenBank and the Barcode of Life Database (BOLD, www.barcodinglife.org) (see Table 1).

**Sequence alignment and phylogenetic analyses**

Internal Transcribed Spacer (ITS) and Cox1 sequences were aligned using MAFFT v6 (Katoh et al. 2005). A few minor adjustments were made to the ITS alignment using Se-Al v. 1.0 (Rambaut 1996). No manual adjustments were required for the Cox1 alignment, which had no indels. Alignments are deposited in TreeBASE (www.treebase.org/treebase/), study accession no. S2134. To test whether the ITS and Cox1 data sets contained congruent phylogenetic signals and could be combined for analysis, a partition homogeneity test (Farris et al. 1994) was performed using PAUP 4.0 (Swofford 2002) using a heuristic search with 1 000 replicates, TBR branch swapping, unordered and unweighted characters and gaps treated as missing.

 Parsimony analyses of ITS alone (Fig. 4a), Cox1 alone (Fig. 4b), and for both genes combined (Fig. 4c), were performed using heuristic searches in PAUP 4.0 (Swofford 2002), with uninformative characters excluded. Bootstrap analyses (1 000 replicates) were undertaken using full heuristic searches for the two single-gene parsimony analyses, and using fast-stepwise addition for the dual-gene analysis. For all parsimony analyses, parsimony tree scores were calculated and the 70 % consensus tree was computed.

For Bayesian analysis, MrModeltest v. 2.2.6 (Nylander 2004) was used to select the most appropriate models of sequence evolution for data sets that contained *Leohumicola* species only, according to the Akaike information criterion (AIC) (Akaike 1974). The HKY+I model (Hasegawa et al. 1985) and the K80+G (Kimura 1980) model were selected for Cox1 and ITS, respectively. Bayesian inference was performed with MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003) using the dual-gene data set with two designated partitions (ITS and Cox1), the appropriate model of sequence of evolution applied to each partition, and *L. lenta* DAOM 231149 set as outgroup (see Fig. 4b). Two independent MCMC runs were performed simultaneously. Each MCMC ran for 2.0 × 10^6 generations, and the first 10 000 trees were discarded as burn-in. The 10 001 trees from each independent MCMC (total 20 002 trees) were combined into one consensus tree with 50 % majority rule consensus (Fig. 4d).

Myxotrichum deflexum was initially chosen as an outgroup to root all analyses, based on its position as near neighbour to the *Leohumicola* clade in the 18S analyses by Hambleton et al. (2005). We could not obtain satisfactory sequences for the Cox1 of two other potential outgroups, *Myxotrichum arcticum* UAMH 9243 and *Scytalidium lignicola* DAOM 231160. Therefore, *M. deflexum* was used as the outgroup for the single-gene parsimony analyses. In the Bayesian analysis, the branch
connecting *M. deflexum* to the ingroup was too long, obscuring the phylogenetic structure of the ingroup. Therefore, *L. lenta* was used to root the tree for the Bayesian and dual-gene parsimony analyses because of its basal position in the single-gene parsimony analyses.

Two *Leohumicola* isolates (DAOM 239499, 239516) had an intron in the *Cox1* region. Internal sequencing primers LHM1R (5’-GGCGTTCTTAGTTCTCCATTTAGT-3’), LHM5F (5’-TGATAGTGGGGTACAAAGTCA-3’) and LHM4F (5’-GGTTATAGAAAATGGAGCAGGTA-3’) were designed and used to sequence the poorly resolved region at the ends of the exonic region for *Leohumicola* sp. DAOM 239499. Similarly internal sequencing primers LHM2R (5’-GGCGTTCTTAGTTTTCCATT-3’), LHM3F (5’-CCGCCTAGTTATTATTATTTTA-3’) and LHM4F were used for the intron of *Leohumicola* sp. DAOM 239516.

**RESULTS**

By heat treating soil, three distinct species exhibiting characteristic *Leohumicola* morphology were isolated. On PDA, colonies...
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 grew slowly, and initially were yellow and slowly maturing to grey or olive colours, with brown or olive soluble pigments released into the surrounding media (Fig. 2, 3). Characteristic *Leohumicola* aleurioconidia and chlamydospores were observed for several strains after 3 mo on PDA and CMA, although some strains did not sporulate even after 6 mo in culture. *Leohumicola incrustata* DAOM 239517 only sporulated on PCA. The morphological descriptions of the new species *L. atra*, *L. incrustata*, and *L. levissima* are presented in the taxonomy section, and the characters of all known species are summarized in Table 2.

The internal transcribed spacer (ITS) nrDNA sequences were 462 bp long for all strains of *L. levissima*; 463 bp for most *L. incrustata* strains (except DAOM 239503, HNLHM91, HNLHM103, 464 bp, and DAOM 239500 462 bp) and 462 bp for both *L. atra* strains. ITS sequences of the isolated strains closely matched reference *Leohumicola* sequences in GenBank using BLAST searches. The barcode region of the cytochrome oxidase subunit I (Cox1) mitochondrial gene was 628 bp for all strains, except DAOM 239499 and DAOM 239516, which had an intron making the PCR product roughly 1500 bp. There are currently few fungal Cox1 reference sequences in GenBank, but BLAST results of Cox1 sequences from our strains matched fungal sequences for that gene at a maximum of 87 % DNA sequence identity. The sequences generated for *Leohumicola* and the outgroup *Myxotrichum deflexum* are currently the only Leotiomycetes with Cox1 DNA barcode sequences.

Parsimony analyses of ITS and Cox1 alignments (Fig. 4a, b) revealed that all previously recognized and newly discovered *Leohumicola* species form monophyletic groups in strict consensus trees, with weak bootstrap support for some clades. In the ITS analysis, *L. atra* (bootstrap support 87 %) and *L. incrustata* (98 %) form well-supported clades. *Leohumicola levissima* is paraphyletic with *L. minima* and two unidentified strains, but is resolved as a monophyletic group in the Cox1 tree. In the Cox1 analysis, the three new species are monophyletic, supported by bootstrap values of 73 % for *L. levissima*, 77 % for *L. atra*, and 99 % for *L. incrustata*. The monophyly of the strains of the type species of the genus *L. verrucosa* is not strongly supported by bootstrapping. The topology of the ITS and Cox1 trees present differing sister group relationships. In the Cox1

![Fig. 3](https://example.com/fig3)  
*Fig. 3 Leohumicola colonies on PDA after 2 mo incubation.* a. *L. levissima* HNLHM2B; b. *L. levissima* DAOM 239511; c. *L. levissima* DAOM 239512 with dark brown exudates; d. *L. atra* DAOM 239515; e. *L. incrustata* DAOM 239500 with black exudates; f. *L. incrustata* DAOM 239498; g. *L. incrustata* HNLHM91 with dried clear exudates; h. *L. incrustata* DAOM 239517; i. *Leohumicola* sp. DAOM 239516. — Scale bar = 5 mm.
Fig. 4  ITS and Cox1 phylogenetic analyses. a–c. Single most parsimonious trees based on heuristic analysis. Thick lines indicate branch topology retained in the strict consensus of the MPTs. Green dots represent strains that produced aleuroconidia and chlamydospores. Bootstrap support values above 50 % from the combined ITS and Cox1 data set. The K80+G and HKY+I models were used for the ITS partition and Cox1 partition, respectively. Abbreviations: IC = informative characters, CI = consistency index, RI = retention index, RC = rescaled consistency index.
analysis, *L. terminalis* is sister to *L. verrucosa* whereas it is sister to *L. lenta* in the ITS analysis. Furthermore, *L. incrustata* is sister to the *L. atra/L. minima* clade in the ITS analysis, but most closely related to the *L. verrucosa/L. terminalis* clade in the *Cox1* analysis.

The partition homogeneity test confirmed that the ITS and *Cox1* data sets could be combined (P = 0.50). A dual-gene parsimony analysis (Fig. 4c) and a dual-gene Bayesian inference (Fig. 4d) were performed using *L. lenta* to root the tree.

In the dual-gene parsimony analysis, all three new species form monophyletic groups supported by strict consensus tree topology and bootstrap values of 70% for *L. levissima*, 97% for *L. atra*, and 100% for *L. incrustata*. In the Bayesian analysis (Fig. 4d), *L. atra* and *L. incrustata* samples form monophyletic clusters both with a branch support value of 1.00. However, *L. levissima* is paraphyletic with *L. atra* in the Bayesian analysis. *Leohumicola verrucosa* is more strongly supported as a clade in both dual-gene analyses (79% in parsimony and 0.99 in Bayesian) than in the single-gene analyses. The topology of the dual-gene parsimony and Bayesian analyses are identical and most similar to the *Cox1* parsimony analysis (Fig. 4b).

As reviewed by Seifert et al. (2007), introns are a frequently reported problem in fungal *Cox1* genes. Most of our strains of *Leohumicola* amplified easily but three strains were problematic. In DAOM 230084, chromatograms contained an ambiguous stretch with double peaks from position 574 to 590 of the *Cox1* amplicon; consequently, we removed this strain from all phylogenetic analyses. Both *Leohumicola* sp. DAOM 239516 and *Leohumicola* sp. DAOM 239499 had large introns (about 875 bp) in the target region of the *Cox1* gene. When these introns were removed and the sequences were translated, the amino acid alignment revealed conserved protein sequences in relation to the *Cox1* of most other *Leohumicola* strains. ITS parsimony analyses placed *Leohumicola* sp. DAOM 239499 (a sterile strain from South Africa) in the *L. incrustata* clade (data not shown), which corresponds with its colony characters. However, in a *Cox1* parsimony analysis with the intron

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**Fig. 5** *Leohumicola atra*. a. Sporulating part of colony on PDA; b. aleurioconidial development; c. single-celled aleurioconidium (left) and terminal aleurioconidium (right); d–f. mature aleurioconidia; g, h. lighter coloured aleurioconidia. All panels = DAOM 239515. — Scale bars: a = 50 µm, b–h = 5 µm.
removed, this strain formed a monophyletic clade with another intron-containing strain, *Leohumicola* sp. DAOM 239516 (from Ontario, Canada). The phylogenetic conflicts between ITS and Cox1 were unexpected and thus strains DAOM 239499 and 239516 remain unidentified. Strain DAOM 239499 was removed from all analyses presented here to increase phylogenetic congruency, and allow our ITS and Cox1 data to be combined for dual-gene analysis.

**Taxonomy**

*Leohumicola atra* Nguyen & Seifert, *sp. nov.* — MycoBank MB512015; Fig. 5

Conidia lateralia vel modice terminalia, cellula terminalis 4.5–5.5 × 4.0–5.5 μm, (sub)globosa, atra, laevi; cellula basilari 2.5–4.5 × 2.5–3.5 μm, crateriformis, obconica vel cylindrica. Coloniae in agaro PDA dicto ca. 10 diam post 14 dies.

Holotypus. Cultura ex solo isotata, exsiccata in herbario DAOM 239515, viva ex-typo CCFC.

**Etymology.** Named after the dark-brown or nearly black colour of the terminal conidial cells (*atra* Lat. = dark).

*Conidiogenous hyphae* hyaline, approximately 1–2.5 μm wide, often in fascicles in aerial mycelium (Fig. 5a). *Conidiogenous cells* reduced to a single denticile 0.5–1.0 μm long (mean ± SE = 0.6 ± 0.1, n = 10) and 1.0–2.0 μm wide (1.5 ± 0.1, n = 10). *Conidia* initially two-celled, single or side by side in small clusters, or successively produced sympodially from hyphae, either lateral (Fig. 5b, d–f) or terminal on conidiogenous hyphae. Terminal cell 4.5–5.5 × 4.0–5.5 μm (5.0 ± 0.1 × 5.2 ± 0.1, n = 20), globose to subglobose, at first hyaline like the basal cell, becoming dark brown (Fig. 5h) or almost black; conidial walls slightly thick, remaining smooth after 3 mo. Conidial connection to basal cell 2.5–3.5 μm wide, not constricted. Aleuroconidia sometimes single-celled with terminal cell directly attached to the hypha, with no basal cell (Fig. 5c). Basal cell 2.5–4.5 × 2.5–3.5 μm (3.3 ± 0.1 × 3.1 ± 0.1, n = 20), obconical or cupulate, often symmetrical or sometimes asymmetrical or irregular, hyaline or slightly pale brown, paler than the terminal cell. Ratio of lengths of terminal : basal cell 1.5–2.0 (1.6 ± 0.1). Basal cell of conidium rupturing during secession, resulting in a functionally single-celled conidium bearing the remnant of the basal cell. *Chlamydosporales* sparsely produced, intercalary, single, rarely in chains, concolorous with conidial terminal cell, subglobose to ellipsoidal, 3–11 × 4–7 μm, with thin or slightly thickened walls. *Vegetative mycelium* often with swollen, monilioid, hyaline or subhyaline hyphae 1.5–2 μm wide, septate, with slightly thickened walls.

**Colonies** on PDA after 2 wk (Fig. 2) under ambient light at room temperature roughly 10 mm diam; entirely olive (3E3) at first becoming grey (3E1) in the centre and olive (3E3) at the margins as the colonies mature, convex, wrinkled with a felty appearance. Exudates produced around the colony centre as black droplets; soluble pigments greyish red (8C4) or faint yellow/orange around the colony and becoming darker with age. Margin entire, slightly gnawed, or smooth. Colony reverse dark-brown (7F8).

**Colonies** on OA after 2 wk (Fig. 2) under ambient light at room temperature roughly 13–15 mm diam; grey (4E1) in the centre and olive-brown (4E4) at the margins, sometimes with felty white aerial mycelium; soluble pigments brown (6E4) around the colony. Margin entire and smooth. Colony reverse brown (5F5) to olive (3F5).

**Specimens examined.** USA, Oregon, Crater Lake National Park, 45°56’N 122°08’W, from heated soil, 28 July 2006, M. Trappe, holotype and ex-type strain DAOM 239515. Two strains were isolated from one soil sample (Table 1).

Notes — The terminal cell of the conidia of *L. atra* becomes much darker brown compared to other *Leohumicola* species and is nearly black. It remains smooth-walled even after 5 mo incubation.

*Leohumicola incrusta*tata* Nguyen & Seifert, *sp. nov.* — MycoBank MB512014; Fig. 6

Conidia lateralia vel modice terminalia, cellula terminalis 4.0–5.4 × 4.0–5.0 μm, (sub)globosa, brunnea, incrusta* N* ; cellula basilari 2.5–4.5 × 2.0–3.0 μm, crateriformis vel obconica. Coloniae in agaro PDA dicto 12–18 mm diam post 14 dies.

Holotypus. Cultura ex solo isolata, exsiccata in herbario DAOM 239498, viva ex-typo CCFC.

**Etymology.** Named after the appearance of the terminal conidial cells which are incrusted with a crust-like slime and warts.

*Conidiogenous hyphae* hyaline, 1.5–2.0 μm wide, often in fascicles in aerial mycelium. *Conidiogenous cells* reduced to a single denticile 1.0–3.0 μm long (mean ± SE = 1.4 ± 0.1, n = 15) and 1.5–3.5 μm wide (2.1 ± 0.1, n = 15). *Conidia* initially two-celled, single or side by side in small clusters, or successively produced sympodially (Fig. 6a, e) from hyphae, either lateral or terminal on conidiogenous hyphae. Terminal cell 4.0–5.5 × 4.0–5.0 μm (4.9 ± 0.1 × 4.5 ± 0.1, n = 20), globose to subglobose, at first hyaline like the basal cell, becoming either pale brown to dark brown; conidial walls slightly thick, smooth or slightly verrucose with large warts 0.75–1.5 μm, usually incrusted with a brown coloured slime 1–2 μm thick around the apex (Fig. 6b–d, f–l). Conidial connection to basal cell 2–3 μm wide, not constricted. Basal cell 2.5–4.5 × 2.0–3.0 μm (3.7 ± 0.1 × 2.7 ± 0.1, n = 20), obconical or cupulate, often symmetrical or sometimes asymmetrical or irregular, hyaline to pale brown, paler than the terminal cell. Ratio of lengths of terminal : basal cell 1.0–2.0 (1.5 ± 0.1). Basal cell of conidium rupturing during secession, resulting in a functionally single-celled conidium bearing the remnant of the basal cell. *Chlamydosporales* sparsely produced in submerged mycelium, commonly found in poorly sporulating colonies, intercalary, single, concolorous with conidial terminal cell, subglobose or ellipsoidal or irregularly shaped with a rough and wrinkled appearance, 5–6 × 3–4.5 μm, with slightly thickened walls. *Vegetative mycelium* often with swollen, monilioid, hyaline or brown coloured hyphae 1.5–3 μm wide, septate, with slightly thickened walls.

**Colonies** on PDA after 2 wk (Fig. 2) under ambient light at room temperature 12–18 mm diam; pastel yellow (2A4) or greyish yellow (2B3) or grey (2B1) in the centre and olive-yellow (2C8) or white at the margins; sometimes wrinkled, sometimes splitting the agar near the colony centre, with short and felty appearance. 5–6 × 3–4.5 μm, with slightly thickened walls. *Vegetative mycelium* often with swollen, monilioid, hyaline or brown coloured hyphae 1.5–3 μm wide, septate, with slightly thickened walls.
as small reddish brown droplets, at the colony margins and centre as large clear droplets, or around the colony centre as small dark brown to black droplets; soluble pigments variable ranging from brown (6D8), olive (3E8), and dark yellow (4C8). Margin smooth, entire, sometimes irregular or gnawed. Colony reverse dark-olive (2F6) or dark-brown (5F8).

Colonies on OA after 2 wk (Fig. 2) under ambient light at room temperature roughly 15–20 mm diam; yellowish white (2A2) to pastel-yellow (2A4); soluble pigments sometimes absent and sometimes minimal and purplish white (14A2) around the colony. Margin entire and smooth. Colony reverse pale yellow (3A2) to light yellow (3A5) at the margin and olive (2E3) in the centre.

Specimens examined. South Africa, Western Cape Province, Cape of Good Hope Nature Reserve, 34°20' 18°27'E, from heated soil, 7 April 2006, K.A. Seifert, holotype and ex-type strain DAOM 239498. Thirteen strains were isolated from four soil samples (Table 1).

Notes — Large warts or slime production on the terminal cell are the defining characteristics of L. incrustata aleurioconidia. The conidia are most similar to those of L. verrucosa, but in that species the wall ornamentation forms smaller, discrete warts.

Leohumicola levissima Nguyen & Seifert, sp. nov. — MycoBank MB512013; Fig. 7

Conidia lateralia vel modice terminalia, cellula terminali 4.5–6.0 × 4.0–5.5 µm, (sub)globosa, brunea, laevi; cellula basilari 1.5–4.0 × 2.5–3.5 µm, crateriformis vel obconica. Coloniae in agaro PDA dicto 15–20 mm diam post 14 dies.

Holotypus. Cultura ex solo isolata, exsiccata in herbario DAOM 239506, viva ex-typo CCFC.

Etymology. Named after the smooth walled and unornamented appearance of the terminal conidial cells (levissima Lat. = smooth).
Conidiogenous hyphae hyaline, 1–2 µm wide, often in fascicles in aerial mycelium. Conidiogenous cells reduced to a single denticle, 0.5–1.5 µm long (mean ± SE = 0.8 ± 0.1, n = 12) and 1.0–3.5 µm wide (2.2 ± 0.2, n = 12). Conidia initially two-celled, single (Fig. 7j) or side by side in small clusters, or successively produced sympodially (Fig. 7a) from hyphae, either lateral (Fig. 7b) or terminal (Fig. 7c) on conidiogenous hyphae. Terminal cell 4.5–6.0 × 4.0–5.5 µm (5.3 ± 0.1 × 4.9 ± 0.1, n = 20), globose to subglobose, at first the same colour as the basal cell, becoming dark brown while still attached; conidial walls slightly thick, remaining smooth after 3 mo. Conidial connection to basal cell 2.5–3.5 µm wide, not constricted. Basal cell 1.5–4.0 × 2.5–3.5 µm (2.6 ± 0.1 × 3.1 ± 0.1, n = 20), obconical or cupulate, often symmetrical or sometimes asymmetrical or irregular, hyaline to pale brown, paler than the terminal cell. Ratio of lengths of terminal : basal cell 1.5–2.5 (1.8 ± 0.1). Basal cell of conidium rupturing during secession (Fig. 7e), resulting in a functionally single-celled conidium bearing the remnant of the basal cell (Fig. 7k). Chlamydospores sparsely produced in submerged mycelium, commonly found in poorly sporulating colonies, intercalary, single, concolorous with conidial terminal cell, subglobose to ellipsoidal, sometimes with irregular constrictions, 5.5–7.5 × 5–6 µm, with thin or slightly thickened walls (Fig. 7f–i). Vegetative mycelium often with swollen, monilioid, hyaline or subhyaline hyphae 1–2 µm wide, septate, with slightly thickened walls.

Colonies on PDA after 2 wk (Fig. 2) under ambient light at room temperature 15–20 mm diam; olive (2E4) or grey (2D1) in the centre and greyish yellow (2C4) or yellowish grey (2C2) at the margins, planar or convex, sometimes wrinkled, sometimes splitting the agar near the colony centre, with low, felty, slightly lanose white aerial mycelium. Soluble pigments not produced after 2 wk. Margin smooth and entire. Colony reverse olive-grey (2F2) to olive (2E4).

Colonies on OA after 2 wk (Fig. 2) under ambient light at room temperature roughly 12–17 mm diam; pale yellow (2A3) to light yellow (2A5); soluble pigments minimal around the colony. Margin entire and smooth. Colony reverse olive (2E5) in the centre and light yellow (3A5) at the edge.

Specimens examined. USA, Oregon, Crater Lake National Park, 45°56’N 122°08’W, from heated soil, 28 July 2006, M. Trappe, holotype and ex-type culture DAOM 239506. Nineteen strains were isolated from three soil samples (Table 1).

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**Fig. 7** Leohumicola levissima. a. Aleurioconidial development, with younger aleurioconidia (left) and older aleurioconidia (right); b. lateral aleurioconidia; c. terminal aleurioconidium; d. lateral (left) and terminal (right) aleurioconidia; e. basal cell of aleurioconidium rupturing during secession; f. terminal chlamydospore; g–i. intercalary chlamydospores; j. single-celled aleurioconidium; k. functionally single-celled aleurioconidium bearing the remnant of the basal cell. Panels a, d, e, k = DAOM239511; b, c, j = DAOM 239509; f–i = DAOM 239513. The background of panels a and c were altered digitally for aesthetic reasons. — Scale bar = 5 µm.
Notes — The terminal cell of *L. levissima* conidia remains smooth even after 3 mo, in contrast to the roughened or encrusted terminal cells of *L. verrucosa* and *L. incrustata*. The conidia of *L. atra*, described above, have similarly smooth terminal cells, but are much darker. The colony morphologies of *L. levissima* and *L. atra* are distinct, particularly on OA. On OA, *L. levissima* is light yellow and *L. atra* is grey and olive brown (Fig. 2). Also, *L. levissima* grows faster on PDA than *L. atra*. Based on the similarity in aleurioconidia and the topology of the parsimony analyses, perhaps these two species share a common ancestor. PDA colonies of *L. levissima* after 6 wk incubation are less variable than they are after 2 wk. Older colonies eventually produce pale olive, soluble pigments.

**DISCUSSION**

This study proposes three new species of *Leohumicola*, namely *L. atra*, *L. incrustata*, and *L. levissima*, using morphological characters and DNA barcoding. The three species exhibit the characteristic two-celled aleurioconidia of the genus, which become functionally single-celled after sessation. Brown to olive pigments diffuse into agar media, and colonies grow slowly. The new species can be distinguished by features of the terminal cells of the aleurioconidia. In *L. levissima* they are smooth and brown, whereas they are smooth and almost black in *L. atra*, and covered with warts (that sometimes appear slimy rather than composed of cell wall material) in *L. incrustata*. Chlamydospores, similar in pigmentation to the aleurioconidia, are produced by the three new species and the four previously described species. A revised key to the seven known species of *Leohumicola* is provided below.

Dense mycelial growth, and abundant soluble pigment production on PDA, renders microscopic observations of *Leohumicola* conidia difficult. They are more conspicuous on the optically clear CMA medium, where the mycelia are sparser and soluble pigments are reduced; sporulation is more abundant on inoculum blocks originally transferred from PDA. Generally, strains were more likely to produce conidia after 3 mo on CMA than on PDA, OA, or when macerated on PDA. As indicated on the phylogenetic trees, not all strains of *L. incrustata* and *L. levissima* sporulated. Of note, *Leohumicola* sp. DAOM 239516 produced almost exclusively chlamydospores and only one aleurioconidium was seen. This isolate is phylogenetically distinct from other *Leohumicola* species, but we chose not to describe it here because of the paucity of diagnostic morphological characters in the single culture available.

The results of our phylogenetic analyses are in agreement with the morphological data. Most *Leohumicola* species are monophyletic, although *L. levissima* is paraphyletic with *L. minima* in the ITS parsimony analysis and with *L. atra* in the dual-gene Bayesian analysis. Bootstrap support is variable for some groups and the sister relationships among species are inconsistent. Although this renders the phylogenetic structure of the genus uncertain, it does not interfere with monophyletic species recognition. Perhaps as additional species are discovered and the species sampling of this genus is more complete, the phylogenetic structure will be clearer.

As DNA barcodes, the ITS and Cox1 loci provide similar sequence variation and reveal similar phylogenetic groupings of *Leohumicola* species (Table 3). However, Cox1 provides slightly better species resolution, particularly for the minima/levissima/atra clade. Both Cox1 and ITS sequences are suitable DNA barcodes for the currently known *Leohumicola* species because the mean sequence divergence between species is about 10 times greater than the mean divergence within species.

**Table 3** Comparison of ITS and Cox1 markers for DNA barcoding.

<table>
<thead>
<tr>
<th>Marker</th>
<th>No. of isolates analysed</th>
<th>No. of species</th>
<th>Sequence length</th>
<th>Mean interspecific divergence (%)</th>
<th>Mean intraspecific divergence (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>ITS</td>
<td>45</td>
<td>7</td>
<td>462</td>
<td>0.35</td>
<td>0.04–0.78</td>
</tr>
<tr>
<td>Cox1</td>
<td>45</td>
<td>7</td>
<td>628</td>
<td>0.24</td>
<td>0.11–0.32</td>
</tr>
</tbody>
</table>

Genetic anomalies in the target region of the Cox1 gene were found in three *Leohumicola* isolates. *Leohumicola* sp. DAOM 230084 contained a short ambiguous stretch of double peaks that may indicate multiple copies of the Cox1 gene. *Leohumicola* sp. DAOM 239499 and DAOM 239516 contained introns. They were partially sequenced from the 5' and 3' ends, but additional sequencing primers would be needed to sequence the entire length of the introns.

The search for *Leohumicola* species has only begun. Hambleton et al. (2005) noted that *Leohumicola* ITS sequences correspond (with > 95% identity and BLAST E-value of 0) to many unidentified fungi from environmental studies or plant roots in GenBank. Based on these observations and our discovery of three new species from soil samples from two previously unsampled locations, *Leohumicola* is likely to be a diverse, wide-spread soil-borne genus. The soil heating procedure should be effective for isolating additional *Leohumicola* species from other countries.

**KEY TO THE SPECIES OF LEOHUMICOLA**

1. Colony diam < 5 mm after 2 wk on PDA, terminal cell of conidium 7–10 µm long
   1. Colony diam > 5 mm after 2 wk on PDA, terminal cell of conidium shorter
   2. Conidia terminal and lateral
   3. Conidia terminal only and usually smooth-walled
   4. Terminal cell of conidium globose or subglobose, with a width of about 5 µm diam
   5. Terminal cell of conidium smooth after 3 mo incubation
   6. Terminal cell of conidium verrucose or encrusted

2. Conidia terminal and lateral
   3. Conidia terminal only and usually smooth-walled

3. Terminal cell of conidium mostly ellipsoidal

4. Terminal cell of conidium smooth after 3 mo incubation

5. Terminal cell of conidium verrucose or encrusted

6. Terminal cell of conidium verrucose or encrusted
5. Terminal cell of conidium pale brown ............ L. levissima
5. Terminal cell of conidium dark-brown ............ L. atra
6. Many small warts occurring on the terminal cell of the conidium ............ L. verrucosa
6. Few large warts or slime produced around the apex of the terminal cell ............ L. incrustata

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