Exophiala crusticola anam. nov. (affinity *Herpotrichiellaceae*), a novel black yeast from biological soil crusts in the Western United States

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A novel black yeast-like fungus, *Exophiala crusticola*, is described based on two closely related isolates from biological soil crust (BSC) samples collected on the Colorado Plateau (Utah) and in the Great Basin desert (Oregon), USA. Their morphology places them in the anamorphic genus *Exophiala*, having affinities to the family *Herpotrichiellaceae* (Ascomycota). Phylogenetic analysis of their D1/D2 large subunit nuclear ribosomal RNA (LSU nrRNA) gene sequences suggests that they represent a distinct species. The closest known putative relative to *Exophiala crusticola* is *Capronia coronata* Samuels, isolated from decorticated wood in Westland County, New Zealand. The holotype for *Exophiala crusticola* anam. nov. is UAMH 10686 and the type strain is CP141b^T (= ATCC MYA-3639^T = CBS 119970^T = DSM 16793^T). Dark-pigmented fungi appear to constitute an important heterotrophic component of soil crusts and *Exophiala crusticola* represents the first description of a dematiaceous fungus isolated from BSCs.

Biological soil crusts (BSCs) are formed by communities of micro-organisms that bind together the upper strata of soil and are common in arid lands, such as those found in the Western United States (Belnap & Gardner, 1993). BSCs in arid lands are predominantly composed of cyanobacteria, mosses and lichens. Recent culture-dependent and independent studies have demonstrated that heterotrophic bacteria belonging to the phyla *Actinobacteria*, *Proteobacteria* and *Bacteroidetes* are also major components of BSCs (Smith *et al.*, 2004; Nagy *et al.*, 2005; Gundlapally & Garcia-Pichel, 2006) and an effort has been made to culture and report on isolates from BSCs that are members of these phyla (Reddy & Garcia-Pichel, 2005; Reddy *et al.*, 2006). Although fungi have been identified as components of BSCs (Belnap *et al.*, 2001; Fletcher & Martin, 1948; Garcia-Pichel, 2002; Galun & Garty, 2001), few studies (e.g. Grishkan *et al.*, 2006; States & Christensen, 2001) have investigated the fungal constituents

of BSCs or the contributions that they make to crust ecology. Here, two black yeast-like fungal strains (CP141b^T and OR302-3) isolated from BSCs are described as a novel species of the genus *Exophiala* within the family *Herpotrichiellaceae*.

Members of the family *Herpotrichiellaceae* exhibit a diverse polymorphic life cycle and, therefore, can be difficult to identify by morphology alone. However, the use of nuclear ribosomal RNA (nrRNA) gene sequence data has facilitated identification and classification of these organisms (see Spatafora *et al.*, 1995; Untereiner & Naveau, 1999; de Hoog *et al.*, 2003). The family is represented by the teleomorph genus *Capronia* and the anamorphic genera *Cladophialophora*, *Exophiala*, *Fonsecaea*, *Phaeococcomyces*, *Phialophora*, *Ramichloridium* and *Rhinocladiella* (Untereiner & Naveau, 1999). These fungi, commonly called black yeasts, are characterized by the presence of melanin or melanin-like pigments in the cell walls and by a yeast-like growth during part of their life cycles (Haase *et al.*, 1999). *Exophiala* is also characterized by an annellidic form of blastic conidiogenesis and by conidiogenous cells that are often inconspicuously annellate (de Hoog & Hermanides-Nijhof, 1977). The *Dictionary of Fungi* (Kirk *et al.*, 2001) cites twelve species in the genus *Exophiala*; however, additional species have been described more recently (e.g. de Hoog *et al.*, 2003). Some species of the genus *Exophiala* are known as occasional opportunistic human pathogens (de Hoog *et al.*, 2003; Haase *et al.*, 1999).

Capronia coronata Samuels, having an *Exophiala* anamorph and isolated from decorticated wood in the Westland

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Abbreviations: BSC, biological soil crust; EPS, extracellular polysaccharides; LSU, large subunit; nrRNA, nuclear ribosomal RNA.

The GenBank/EMBL/DDBJ accession numbers for the D1/D2 large subunit nuclear ribosomal RNA gene sequences of strains CP141b^T and OR302-3 are AM048755 and DQ777875, respectively. The accession number for the sequence of the internal transcribed spacer of the nuclear ribosomal RNA gene for strain CP141b^T is AM048756.

Comparisons of the nucleotide sequences of the D1/D2 large subunit nuclear ribosomal RNA gene of *Exophiala crusticola* and related taxa, details of the characteristics that distinguish strains CP141b^T and OR302-3 and an additional phylogenetic tree are available as supplementary material in IJSEM Online.

County of New Zealand (Müller *et al.*, 1987), was the closest known relative of the BSC isolates CP141b^T and OR302-3. However, the sequence divergence value of 3.3 % in the divergent D1/D2 domain of the large-subunit (LSU) nrRNA gene indicates that our isolates belong to a distinct species and refute an anamorph–teleomorph connection (Kurtzman & Robnett, 1998; Peterson & Kurtzman, 1991). The International Code of Botanical Nomenclature currently allows the use of a separate binary name for the fungal anamorph if the teleomorphic relationship is not firmly established (Greuter *et al.*, 2000); therefore, we propose the name *Exophila crusticola* for this novel anamorphic species.

Fungus isolation and characterization

Strains CP141b^T and OR302-3 were isolated from BSC samples collected from the Colorado Plateau (38° 34' 09.84" N 109° 31' 04.51" W) and the Great Basin desert (44° 29' 06.03" N 121° 04' 07.30" W), USA. Initially, 0.5 g crust samples were suspended in Ringer's solution (Lorch *et al.*, 1995), shaken for 30 min and the suspension was allowed to settle. Subsequently, 100 µl supernatant was placed on plates of BG11 minimal medium (Rippka *et al.*, 1979). The plates were incubated under light at room temperature. Fungal colonies were observed on plates where cyanobacteria were also present. Strains CP141b^T and OR302-3 were selected because of their dark pigmentation and replated on a nutrient-rich 10 × PGY-BG11 medium (Lorch *et al.*, 1995). This medium was also used to obtain inoculum for all biochemical tests.

After the initial isolation, strains CP141b^T and OR302-3 were cultured on standard PDA (Yarrow, 1998) and PGY (Lorch *et al.*, 1995) plates, in addition to 10 × PGY-BG11 plates, in order to observe growth and the formation of hyphal elements. The temperature range for growth was determined on 10 × PGY-BG11 between 10–50 °C (in increments of 5 °C). The pH range for growth was determined on 10 × PGY-BG11 buffered in 0.1 M phosphate with the pH ranging from 5 to 12 at intervals of 1 pH unit. Catalase activity was determined by bubble production in 30 % (v/v) aqueous hydrogen peroxide solution. Oxidase activity was tested by the oxidation of 1 % (w/v) tetramethyl-*p*-phenylenediamine (Merck). Carbon assimilation tests were performed by adding each carbon compound at a final concentration of 0.5 % to a base stock of BG11 medium without citric acid (Reddy & Garcia-Pichel, 2005).

Standard methodologies were followed for the maintenance of cultures and the description of yeast-like morphology (Yarrow, 1998). Micromorphological data were gathered using a conventional bright-field microscope (BH2; Olympus) or a microscope in differential interference contrast or bright-field mode (Axio Imager. A1; Zeiss). Microscopic examinations were made from fresh cells in water mounts. Measurements were made at a magnification of ×1000 using a calibrated ocular. Cell and conidia dimension statistics include: $\bar{x}$, the arithmetic mean of the

cell/conidia length by cell/conidia width ($\pm$ SD) for n cells/conidia measured; Q , the quotient of cell/conidia length and cell/conidia width in any one cell/conidium, indicated as the range of variation in n cells/conidia measured; Q_m the mean of Q values. Colour descriptions adhere to the nomenclature and codification system outlined in the *Methuen Handbook of Colour* (Kornerup & Wanscher, 1967).

DNA isolation, PCR and sequence analysis

A rapid mini-DNA isolation method from yeast-like cells was standardized as follows: a 1 ml suspension of CP141b^T culture was centrifuged in an Eppendorf tube at 10 000 r.p.m. for 5 min at room temperature. The cell pellet was suspended in 200 µl lysis buffer (10 mM Tris, 1 mM EDTA pH 8, 1 % SDS), 200 µl Tris-saturated phenol was added and the mixture was incubated at 65 °C for 60 min. The suspension was then centrifuged at 10 000 r.p.m. for 5 min at room temperature and the supernatant collected. The supernatant was treated with 200 µl chloroform/iso-amyl alcohol mixture (24:1), vortexed and centrifuged at 10 000 r.p.m. for 5 min at room temperature. The supernatant was collected and added to 20 µl 3 M sodium acetate and 600 µl ice-cold alcohol. This mixture was vortexed and incubated at –80 °C for 30 min. The suspension was centrifuged at 10 000 r.p.m. for 20 min at 4 °C. The resultant DNA pellet was washed with 70 % alcohol, vacuum-dried and dissolved in 20 µl TE buffer.

The divergent D1/D2 domain was amplified with the combination of the NL-1 (5'-GCATATCAATAAGCG-GAGGAAAAG-3') and NL-4 (5'-GGTCCGTGTTTCAA-GACGG-3') primers of O'Donnell (1993). The ITS4 (5'-TCCTCCGCTTATTGATATGC-3') and ITS5 (5'-GGA-AGTAAAAGTCGTAACAAGG-3') primers of White *et al.* (1990) were used to amplify the internal transcribed spacer (ITS1) of the nrRNA gene. PCR was performed with a final reaction mixture (50 µl) containing ~50 ng genomic DNA, 25 pmol each primer, 200 mM dNTPs, 2.5 mM MgCl₂, 2.0 U *Taq* polymerase and 5 µl 10 × reaction buffer (Takara). The amplification reactions were performed in a PTC 150 Mini Cyclyer (MJ Research) with the following cycling parameters; 5 min at 94 °C, followed by 30 cycles at 30 s at 94 °C, 30 s at 55 °C and 60 s at 72 °C, with a final extension for 5 min at 72 °C. The amplified products were separated on a 1.0 % agarose gel and visualized by staining with ethidium bromide (0.5 µg ml⁻¹). Amplicons were removed from the gel and purified using a gel extraction kit (Qiagen). Direct sequencing of purified PCR products was performed with the ABI Big Dye Terminator kit (Perkin Elmer Applied Biosystems). Both strands of the PCR product were sequenced for the D1/D2 domain and ITS1 using the NL1 and NL4 and ITS4 and ITS5 primers, respectively.

A sequence similarity search was performed using GenBank BLASTN (Altschul *et al.*, 1997) and sequences of closely related taxa were retrieved and aligned using the CLUSTAL W module in the MEGA 3 software package (Kumar *et al.*, 2004).

Pair-wise evolutionary distances between the sequences were calculated using Kimura's two-parameter model (Kimura, 1980). Phylogenetic trees were constructed using three tree-making algorithms: neighbour-joining (NJ), maximum-parsimony (MP) and the unweighted pair group method with arithmetic mean (UPGMA) in the MEGA 3 software package (Kumar *et al.*, 2004). Clade stability in the phylogenetic trees was assessed using 1000 replicate datasets in a bootstrap analysis.

Classification, phylogenetic analyses and ecology

Strains CP141b^T and OR302-3 exhibited similar growth and morphological characteristics. Nearly all physiological characteristics exhibited by these isolates were identical; however, a few minor differences were observed (see Supplementary Table S1 in IJSEM online). Sequence data for the D1/D2 domain suggests that the strains are conspecific as the domain contained only one nucleotide substitution (see Supplementary Table S2 in IJSEM online), thus having less than 1 % sequence divergence (Peterson & Kurtzman, 1991). Strain CP141b^T was chosen as the representative strain for further characterization and as the basis for the species description as it was the first to be isolated.

Specific characteristics (morphological, growth-related and biochemical) of *Exophiala crusticola* anam. nov. are given in the species description. In general, the isolates were metabolically versatile in their use of sugars and small-molecular mass organics, with the exception of amino acids, and were not very proficient at metabolizing complex organics. This may indicate that their ecological role may be as osmotrophs specialized on the photosynthetic exudates from cyanobacteria. Recurrent wetting and drying cycles in soil crusts promote a chronic leaching of organics from these primary producers, creating a significant concentration of dissolved organics in the soil solution, which are then available to consumers such as *E. crusticola*. Both isolates were recovered from minimal media on which cyanobacteria were growing and they appeared to be thriving on cyanobacterial exudates. This type of trophic role was alluded to by de Hoog (1993) who described black yeasts of the family *Herpotrichiellaceae* as secondary saprophytes that are known to inhabit 'bacterial mats'.

Strains CP141b^T and OR302-3 exhibit morphological characters, including a dimorphic habit and inconspicuously annellate conidiogenous cells, which support their placement within the genus *Exophiala*. Morphologically, *E. crusticola* is characterized by mucoid colonies that exhibit very slow growth. Conidiogenous cells are produced on torulose hyphae, normally terminal, and on unswollen hyphae, normally as singular, intercalary, fertile loci. Conidia are globose, subglobose to ovoid (Fig. 1). The ability of *E. crusticola* to produce submerged hyphae that, in turn, produce conidia (Fig. 1) is not common within the genus *Exophiala* and may reflect a growth habit that is

Fig. 1. *Exophiala crusticola* anam. nov. CP141b^T on PDA agar at 25 °C. (a) Anellate yeast-like cell; (b) conidiogenous cells producing conidia; (c) torulose hyphae; (d) fascicle of submerged hyphae protruding from colony margin. Bars, 1 µm (a), 2 µm (b–c), 1 mm (d).

compatible with the BSC habitat. The manner in which *E. crusticola* produces conidia is similar to that found in *Exophiala lecanii-corni* (Benedek & G. Specht) Haase & de Hoog. *E. lecanii-corni*, however, tends to be more conspicuously hyphal, whereas *E. crusticola* exhibits a more consistent yeast-like phase. In addition, the former produces ellipsoidal to reniform conidia that are narrower (1.5–2.4 µm in width) and have a broader range of lengths (3.3–5.9 µm) than conidia found in *E. crusticola* (de Hoog & Hermanides-Nijhof, 1977). Other species of the genus *Exophiala* are more readily distinguished from *E. crusticola*. For example, the elongated, lateral conidiogenous cells found in species such as *Exophiala salmonis* and *Exophiala jeanselmei* var. *jeanselmei* are lacking in *E. crusticola*.

Phylogenetic studies based on nrRNA gene sequences suggest that the family *Herpotrichiellaceae* constitutes a monophyletic entity (Untereiner & Naveau, 1999). Our analysis included sequence data from seven taxa representing the teleomorph genus *Capronia* and twelve taxa representing the anamorphic genera *Cladophialophora*, *Exophiala*, *Fonsecaea* and *Phialophora*, which were extracted from GenBank. *Phaeococcomyces catenatus* (Chaetothyriales, Ascomycetes, Ascomycota) and *Saccharomyces cerevisiae* strain S288C (Saccharomycetales, Saccharomycetes, Ascomycota) were selected for the outgroup. Alignment of the D1/D2 LSU nrRNA gene sequences revealed 40 unique nucleotide signatures for *E. crusticola* in comparison with other closely related anamorphic (*E. jeanselmei*, *Exophiala moniliae* and *Exophiala spinifera*) and teleomorph (*Capronia acutisetata* and *Capronia coronata*) taxa

(see Supplementary Table S2 in IJSEM online). Neighbour-joining and maximum-parsimony analyses (data not shown) placed *E. crusticola* deep within the *Herpotrichiellaceae* clade. Both *C. acutiseta* and *C. coronata* showed a 3.3% sequence divergence from *E. crusticola*. Although analysis using UPGMA, maximum-parsimony (data not shown) and neighbour-joining (Fig. 2) criteria revealed the close relationship between *C. coronata* and *E. crusticola*, the nodes were not strongly supported by bootstrap values. However, the analyses overwhelmingly supported this relationship over that of *C. acutiseta* with *E. crusticola*. When compared with *E. crusticola*, the sequence of *E. jeanselmei* showed a 3.8% sequence divergence and those of *E. moniliae* and *E. spinifera* showed a 4.0% sequence divergence. The topology of trees recovered in a phylogenetic analysis using the ITS sequence (see Supplementary Fig. S1 in IJSEM online) also supported these conclusions. Our results reinforce other studies that have suggested the polyphyletic nature of the genera *Capronia* and *Exophiala* (e.g. Spatafora *et al.*, 1995; Untereiner & Naveau, 1999; de Hoog *et al.*, 2003).

Isolation of strains of *E. crusticola* from Colorado Plateau and Great Basin desert BSCs samples suggests that this anamorphic fungus may be common in BSCs and that it plays a role in crust ecology. Cultivation-independent studies of field samples would be necessary to reinforce this conclusion. However, these results certainly support States and Christensen's (2001) conclusion, based on cultivation, that dark-pigmented fungi are prominent components of BSCs. Furthermore, finding *E. crusticola* associated with BSCs in desert localities is not surprising considering that black yeasts have been isolated from extreme environments and they are known to be able to survive severe drought, excessive temperatures and UV irradiation because of their robust, melanized cell walls (de Hoog, 1993). Extracellular

polysaccharides (EPS) produced by prokaryotic organisms are known to bind soil particles, thus aiding in the establishment of BSCs and slowing erosion in desert soils (Garcia-Pichel *et al.*, 2001). Black yeasts are also known to produce EPS (de Hoog, 1993) and, in culture when supplied with plenty of organics, isolates of *E. crusticola* produce copious amounts of EPS. This suggests that eukaryotic fungal organisms associated with BSCs may also contribute to soil stability in desert systems through EPS production in addition to the aggregation of soil particles by hyphae. The isolation of other EPS-producing yeasts from BSCs, such as *Rhodotorula* (R. Potrafka, personal communication), lends further credence to this hypothesis.

Although other unidentified 'yeasts' have been isolated from BSCs (States & Christensen, 2001), this publication appears to be the first to clearly identify a BSC-associated black yeast. The fact that our isolates represent a novel anamorphic species underscores the need for further investigation into the diversity and ecology of fungal components of BSCs. Overall, the paucity of literature related to fungi associated with BSCs reflects the fact that these organisms are inadequately known and indicates that the field is ripe for future investigation.

Latin diagnosis of *Exophiala crusticola* Bates, Gundlapally & Garcia-Pichel anam. nov.

Coloniae ex CP141b^T in PGY ad 25 °C (±2 °C) *tardae crescentes*, 2.0–3.0 mm *diametro* ad 14 *dies* *attingentes*. In PDA ad 25 °C (±2 °C) *tardae crescentes*, 0.5–1.0 mm *diametro* ad 14 *dies* ad 25 °C (±2 °C) *attingentes*. *Videor mucosae* *quam primum*, *deinde laeves ut verruculosae, siccae et firmae, elevatae ex agarum usque 1 mm ad limites brunneae* (6E4), *fusco-brunneae* (6F4) *ut griseo-brunneae* (6F3), *partes interiores nigellae*. *Margo integer et quam primum acutus designo, inde hyphae submersae lineares vel*

Fig. 2. Neighbour-joining tree based on the analysis of the sequence of the D1/D2 domain of the LSU nrRNA gene (approximately 540 bases) showing the relationship between *Exophiala crusticola* anam. nov. CP141b^T and related taxa. GenBank accession numbers are given in parentheses. Bootstrap values are expressed as percentages of 1000 replications and clades supported by bootstrap values over 65% are indicated (branches in bold). The outgroup, *Phaeococcomyces catenatus* strain CBS 650.76 (AF050277) and *Saccharomyces cerevisiae* strain S288C (NC001144), was trimmed from the figure without modifying the tree topology. Bar, 0.01 substitutions per nucleotide position.

ramificantes gradatim crescentes, emergentes ut punctae fortuitae secus marginem et fasciculae abundante crescentes post 14 dies in PDA. Hyphae aerae deinde crescentes super superficiares ex coloniae. Hyphae cellulae deficiens post 14 dies in PGY. Exsudatum et odoratus deficiens. Ad temperatura extensa ab 5–30 °C crescens, ad vel supra 37 °C moriens.

Cellulae fermentiformis commune, cellulae-singulae, parietes-latae, globosae, subglobosae, ovoideae ut limoni-formes, 5.6–8.0 × 4.8–7.2 µm [$\bar{x}$ = 6.5 ± 0.7 × 5.9 ± 0.9 µm, Qm = 1.1, n = 20], subhyalinae, olivaceae pallidae ut brunneae pallidae, ad apex expeditiones conidia secundariae ex singulae, minutae, inconspicuus annelatus clavae conidiiferitae. Hyphae exinflatae vel torulosae, parietes-latae, septatae, subglobosae, ovoideae, ellipsoideae ut cylindricae et elongatae, ramorae interdum vel regularae, 3.0–8.0 µm diametro, subhyalinae, olivaceae pallidae ut brunneae pallidae; cellulae conidiogenitae non disimiles, parietes-latae, ellipsoideae ut cylindricae et elongatae, subhyalinae, olivaceae pallidae ut brunneae pallidae, ramorae raro vel interdum; conidia gentiae ex minutae, inconspicuus annelatus clavae conidiiferitae, terminales ex hyphae torulosae vel laterales ex singulae, intercalares loci ex hyphae exinflatae (raro terminales). Conidia cellulae-singulae, parietes-teniae, laeves, globosae, subglobosae ut ovoideae, 4.0–4.8 × 3.2–4.0 µm [$\bar{x}$ = 4.3 ± 0.4 × 3.5 ± 0.4 µm, Qm = 1.2, n = 20], subhyalinae, olivaceus pallidus ut brunneus pallidus. Teleomorphus incognitus.

CP141b^T erat positivus pro catalasa, oxidasa, ureasa et infitialis pro lipasa, phosphatasa, gelatinasa, ADNasa, β-galactosidasa, deaminasa phenylalaninum, dihydrolasa argininae, decarboxylasa lysinae et decarboxylasa ornithinae; non poterat utor caseinum vel aesculinum. Fungo poterat utor salis acetii, arabinosum, fructosum, galactosum, glucosum, glycerinum, inulinum, acidum lacticum, lactosum, levulosum, maltosum, mannitol, rafinosum, saccharosum, sucrosus, et xylosum per origo ex carbonis, autem non poterat utor acidum citricum, dextrinum, ethanolaminum, vel acidum succinicum. Cycloheximidum cellularum ex CP141b^T venenum est.

Holotypus: Colorado Plateau (38° 34' 09.84" N 109° 31' 04.51" W), USA – segregatus ex collectio crustae biologicae terrarum. Cultura sicca ex *Exophiala crusticola* (isolatus typus CP141b^T) ad UAMH cum numerus accessionem 10686 deposita est. Isolatus typus CP141b^T (=ATCC MYA-3639^T = CBS 119970^T = DSM 16793^T) modus lyophilizatus conservatus est.

Description of *Exophiala crusticola* Bates, Gundlapally & Garcia-Pichel anam. nov.

Exophiala crusticola (crus.ti'co.la. L. n. crusta crust; L. suff. -cola from L. n. incola an inhabitant; N.L. n. crusticola a crust inhabitant).

Colonies of CP141b^T on PGY at 25 °C (±2 °C) are slow-growing, attaining 2.0–3.0 mm diameter at 14 d. On PDA at 25 °C (±2 °C), colonies are slow-growing, attaining

0.5–1.0 mm diameter at 14 d. Appear mucoid at first, soon becoming smooth to verruculose, dry and firm, elevated from media up to 1 mm, outer part brown (6E4), dark brown (6F4) to greyish brown (6F3) and inner parts blackish. Margin entire and, at first, sharply defined, then submerged linear or branching hyphae gradually develop that emerge randomly around the margin and form abundant fascicles after 14 d on PDA. Aerial hyphae eventually develop over the surface of the colony. Hyphae lacking after 14 d on PGY. Lacking exudates and odour. Growth observed at temperatures ranging from 5–30 °C, growth not observed at or above 37 °C.

Yeast-like cells are abundant, single-celled, thick-walled, globose, subglobose, ovoid to lemon-shaped, 5.6–8.0 × 4.8–7.2 µm [$\bar{x}$ = 6.5 ± 0.7 × 5.9 ± 0.9 µm, Qm = 1.1, n = 20], subhyaline, pale olivaceous to pale brown, developing secondary conidia at the apex from a single, minute, inconspicuously annelate conidiiferous peg. Hyphae unswollen or torulose, thick-walled, septate, subglobose, ovoid, elliptical to cylindrical and elongate, occasionally or regularly branched, 3.0–8.0 µm in diameter, subhyaline, pale olivaceous to pale brown; conidiogenous cells undifferentiated, thin-walled, elliptical to cylindrical and elongate, subhyaline, pale olivaceous to pale brown, rarely to occasionally branched; conidia produced from a minute, inconspicuously annelate conidiiferous peg, terminally on torulose hyphae or laterally as single, intercalary loci on unswollen hyphae (rarely terminally). Conidia single-celled, thin-walled, smooth, globose, subglobose to ovoid, 4.0–4.8 × 3.2–4.0 µm [$\bar{x}$ = 4.3 ± 0.4 × 3.5 ± 0.4 µm, Qm = 1.2, n = 20], subhyaline, pale olivaceous to pale brown. The teleomorph is unknown.

CP141b^T is positive for catalase, oxidase and urease activities and negative for lipase, phosphatase, gelatinase, DNase, β-galactosidase, phenylalanine deaminase and arginine dihydrolase activities, as well as lysine and ornithine decarboxylases. Is not able to hydrolyse casein or aesculin. The fungus is able to utilize acetate, arabinose, fructose, galactose, glucose, glycerol, inulin, lactic acid, lactose, levulose, maltose, mannitol, raffinose, sucrose and xylose as a sole carbon source, but is not able to utilize citrate, dextrin, ethanolamine or succinate. Cells of CP141b^T are sensitive to cycloheximide.

Holotype: Colorado Plateau (38° 34' 09.84" N 109° 31' 04.51" W), USA, isolated from a biological soil crust sample. A dried culture of *Exophiala crusticola* (type strain CP141b^T) is deposited at UAMH (accession no. 10686). The type strain CP141b^T is also maintained freeze-dried at the ATCC (ATCC MYA-3639^T), CBS (CBS 119970^T) and DSMZ (DSM 16793^T) culture collections.

Acknowledgements

The research was funded by the National Science Foundation Biotic Surveys and Inventories grant 0206711 (F.G.-P.) We acknowledge support from Garcia-Pichel lab members in the field as well as in the

lab. Tonya R. Boschmann contributed by reading over the manuscript. Dr L. Sigler kindly offered advice regarding the type specimen. We would also like to acknowledge an anonymous reviewer whose thorough evaluation improved the quality of this publication.

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