The genus Cryptococcus is polyphylectic and is distributed throughout the Hymenomycetous yeasts, with representatives in all four clades (Tremellales, Trichosporonales, Filobasidiales and Cystofilobasidiales). Sequencing of the D1/D2 domain of the large rDNA subunit has been accomplished for all known ascomycete (Kurtzman & Robnett, 1998) and basidiomycete (Fell et al., 2000) species. Strains that differ in this region by at least 2 nt can be considered as potentially novel taxa (Fell et al., 2000). In a previous study by Thomas-Hall & Watson (2002), over 500 yeasts were isolated from Antarctic soil and snow samples, from which 60 isolates were selected (on the basis of physiological and morphological characteristics) for further analysis in the current study. One-dimensional SDS-PAGE of whole-cell protein extracts was employed to identify yeast isolates with similar or visually identical protein banding patterns. This condensed the study group to 27. Phylogenetic analysis of the D1/D2 region of the large rDNA subunit sequence of Cryptococcus nyarrowii and Cryptococcus sp. CBS 7712, CBS 7713, CBS 7743, CBS 8016, KCTC 17061, KCTC 17062 and KCTC 17063, within the Tremellales clade. These two Antarctic isolates are described in this communication as Cryptococcus sp. nov.

Isolation and characterization

Samples of soil and snow were collected in November 1997 and stored at −10 ºC. Yeasts were isolated as described previously (Thomas-Hall & Watson, 2002). Strain 41b was isolated from soil and strain 22c was isolated from stromatolite and shell, from samples that were taken from Watts Lake, Vestvold Hills (68° 29’ S 78° 25’ E), Davis Base, Antarctica. Cultures were maintained on yeast extract/peptone (YPE) plates [2% (w/v) glucose, 0.5% bacteriological peptone, 0.5% yeast extract, 0.3% KH₂PO₄, 0.3% (NH₄)₂SO₄, 1.5% agar] and in aqueous stocks at 6 ºC, with long-term storage in 15% glycerol at −80 ºC. Isolates were characterized by the standard methods described by Yarrow (1998).

DNA sequence analysis

An AquaPure Genomic DNA Isolation kit from Bio-Rad was employed to extract DNA from the yeast isolates. PCR products were obtained by utilizing the Qiagen HotStart PCR kit [2 μl purified DNA, 0.5 μl forward primer (5’-TCCTGTATTACAGACCTGCGG-3’), 0.5 μl reverse primer (5’-TCCTGGCTTTATTGATAG-3’), 21.5 μl MilliQ water, 2.5 μl Q-solution, 25 μl HotStart Mastermix], followed by thermal cycling using the following conditions: 95 ºC for 15 min, followed by 30 cycles of 94 ºC for 1 min, 52 ºC for 1 min and 72 ºC for 1 min, with a final 10 min at 72 ºC. PCR products were purified with the Prep-a-geneclean system (Bio-Rad). A Beckman CEQ2000 Dye Terminator Quick Start kit was used for the sequencing reaction of the D1/D2 domain in a total volume of 20 μl (purified PCR product, 2 μl primer (forward primer MLF

The GenBank/EMBL/DDBJ accession number for the 26S rDNA sequence of Cryptococcus watticus is AY138478.
5’-GCATATACCGGAGGAAAAG-3’, reverse primer MLR 5’-GTTCCGTGTTTCAAGACGG-3’), 4 μl Beckman CEQ DTCs Quickstart mix, 14 μl MillQ water] and was placed in the thermal cycler for 30 cycles of 96°C for 20 s, 50°C for 20 s and 60°C for 4 min. Sequences were obtained with a Beckman CEQ2000 automatic sequencer and aligned visually with BioEdit. Phylogenetic relationships were assessed with MegAlign (DNAStar). Phylogenetic analyses employed the maximum-parsimony program of PAUP 4.0 (Sinauer Associates) with heuristic searches and neighbour-joining analysis. Bootstrap values were determined by using PAUP; values of < 50% were not included in tree figures.

### Fatty acid and protein pattern analyses

Cells were grown to stationary phase in 100 ml YEP broth and fatty acid composition and whole-cell protein patterns were determined as described previously (Thomas-Hall & Watson, 2002).

Sixty isolates from the original 500 yeasts that were isolated in a previous study (Thomas-Hall & Watson, 2002) were chosen for further analysis on the basis of morphological characteristics. One-dimensional SDS-PAGE of whole-cell proteins was employed initially to characterize relatedness among unknown isolates by comparing protein banding patterns. Isolates with visually identical or similar protein banding patterns were grouped together. Two isolates, 22c and 41b, were shown to have protein banding patterns that were indistinguishable from each other, but differed significantly from those of *C. nyarowii* and *H. corniformis* (results not shown). Phylogenetic analyses revealed that the two isolates have identical sequences and have 2 nt difference from the Korean strains KCTC 17061, KCTC 17062 and KCTC 17063, 15 nt difference from *H. corniformis* and 16 nt difference from *C. nyarowii*, resulting in their placement in the Tremellales clade with other isolates from Antarctica (*C. nyarowii* and Cryptococcus strains CBS 7712, CBS 7713 and CBS 7743) (Fig. 1). Fatty acid analysis of strain 41b revealed oleic acid (C18:1) to be the predominant fatty acid present (61%), together with the polyunsaturated fatty acids C18:2 (5%) and C18:3 (3%), whereas strain 22c showed significant amounts of C18:1 (28%) and the polyunsaturated fatty acids C18:2 (31%) and C18:3 (11%). These fatty acid compositions confirmed previous studies that have shown that psychrophilic Antarctic yeasts, such as species of the genera *Candida*, *Leucosporidium* and *Mrakia*, have a high unsaturated fatty acid content (Watson, 1987). The new yeast isolates were placed in the genus *Cryptococcus*, as no sexual state was observed under a variety of conditions. Vegetative reproduction is by multilateral budding (Fig. 2), D-glucuronate and inositol are assimilated and urease and Diazonium blue B reactions are positive (Fell & Statzell-Tallman, 1998; Kurtzman & Fell, 1998).

### FIG. 1.

Phylogenetic tree showing placement of *C. watticus* among related basidiomycetous yeasts, derived from maximum-parsimony analysis of the 26S rDNA D1/D2 domain. Bootstrap replications from 100 full heuristic replications using the neighbour-joining method are displayed. *Cryptococcus aquaticus* and *Mrakia gelida*, which represent the Cystofilobasidiales, are the designated outgroup species in this analysis. Labelled clades have representative species only.

### FIG. 2.

*Cryptococcus watticus* after 3 days at 15°C in YEP broth, showing budding cells. Bar, 10 μm.
**Description of Cryptococcus watticus**

_Cryptococcus watticus_ (wat′ti.cus, N.L. adj. watticus referring to Watts Lake, Antarctica, from where the isolates originated).

After 3 days growth in YEP broth at 15 °C, cells are ovoidal and occur singly or in pairs. Budding is polar. Aerobic growth results in pink, convex, circular colonies with an entire margin. Colonies are viscous in consistency. No sexual state is observed from mixed or pure cultures plated for 3–6 months at 6 or 15 °C on YEP agar, cornmeal agar, malt agar or nitrogen base agar. Growth on yeast nitrogen base agar or cornmeal agar is slower than on YEP or malt agar. Assimilation of carbon compounds is as follows: positive reactions are observed for glucose, galactose, sucrose, trehalose, lactose, melibiose, raffinose, inulin, D-xyllose, D-ribose, L-rhamnose, N-acetyl-D-glucosamine, D-mannitol, methyl α-D-glucoside, salicin, succinate, citrate, inositol and D-glucuronate; negative or weak reactions are observed for D-arabinose, D-glucosamine, glycerol, erythritol, ribitol, D-glucitol, hexadecane, L-sorbose, maltose, cellobiose, melezitose, L-arabinosum, methanol, ethanol, galactitol, D-glucuronate, D-L-lactate. Exiguus respondet amyllum solubile. Respondet nitratum. Incrementum sine vitamina, ex 50 % (w/w) GY agar, 10 % NaCl, 5 % glucose non respondet. Incrementum respondet sine biotino et sine thiamin. Liquatio gelatinis et ureum respondent. Amyllum non creatur. Incrementum ad 25 °C exigus est, ad 30 °C non est.

_In collectione zymotica Centraalbureau voor Schimmelcultures, Utrecht, Nederlandia, CBS 9496^T_ (≡ NRRL Y-27556^T) est Cryptococcus watticus. Haec est isolata ex terra, testa Watts Lake, Vestvold Hills, Davis Base (68° 29′ S 78° 25′ E), Antarctica.

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**References**


