**Aureobasidium tremulum** Inamdar, Roh. Sharma & Adhapure, sp. nov.

**Etymology.** Named after the shaking and trembling behaviour of the yeast when observed under a light microscope (Latin **tremulum** - shaking, trembling).

**Classification —** Aureobasidiaeae, Dothideales, Dothideomycetes.

**Initial growth** as creamy white colonies on potato dextrose agar, later turning brown to dark brown. Colonies appear to be dry and rough. Each colony is round with a convex elevation from a cross-sectional viewpoint and the edges appear to be undulated. Growth is optimal on Sabouraud dextrose agar (SDA). Colonies on nutrient agar did not become dark brown. **Cells** are generally oblong-shaped with very few cells assuming an irregular shape. **Budding** occurs frequently. The average size of mature, non-budding cells is 2.8 x 6.4 μm. **Sexual reproduction** was not observed. **Pseudohyphal** formation not observed. Optimal growth occurred at 20–25 °C, with some growth at 5–15 °C. The following carbon compounds are assimilated: D-glucose, L-arabinose, D-xylose, D-maltose, D-saccharose, D-Trehalose, D-raffinose. No growth observed with glycerol, calcium-2-keto-gluconate, L-lactose while weak assimilation was observed for adonitol, xylitol, D-galactose, D-melezitose, and D-raffinose.

**Habitat —** Aureobasidium tremulum** was isolated as a culture contaminant in the laboratory of Department of Biotechnology and Microbiology of Vivekanand Arts, Sardar Dalipisingh Commerce and Science College, Aurangabad.

**Distribution** — India (Aurangabad, Maharashtra).

**Notes** — An initial BLASTn similarity search using the LSU region sequence in the NCBI type sequences nucleotide database showed the highest similarity to *A. lini CBS 125.21* (GenBank MH866211; 98 % identity, 99 % query cover) followed by *A. melanogenum* strain CBS 105.22 (GenBank MH866219; 98 % identity; query coverage 97 %). The BLASTn similarity search in the NCBI type sequences database using the ITS sequence showed the highest similarity to *Kabatiella bupleuri* CBS 131304 (GenBank NR_121524; 95 % identity, 100 % query coverage) followed by *Aureobasidium iranianum* CCTU 268 (GenBank KM093738; 95 % identity, 99 % query coverage) and *A. melanogenum* CBS 105.22 (GenBank NR_159598, 95 % identity, 99 % query coverage). The neighbour-joining (NJ) phylogenetic analyses of ITS and LSU RNA gene regions were done using sequences of other species of *Aureobasidium*. The phylogenetic tree topology clearly shows that the present strain UN-1 is novel and does not cluster with any known species of the genus. The phylogenetic analysis based on the ITS alignment shows that it forms a sister branch to *A. thailandense* NRRL 58543 (GenBank JX462675) and *A. mangrovei* IBRC-M-30266 (GenBank KY089087). In the phylogenetic analysis based on the LSU alignment, it does not group with known species but was placed at equal evolutionary distance with *A. cauvilorum* CBS 242.64 (GenBank FJ150944).

**Notes** — A BLASTn similarity search using the LSU region sequence in the NCBI type sequences nucleotide database showed the highest similarity to *A. tremulum* (GenBank MH186702; 98 % identity, 99 % query cover) followed by *A. lini* (GenBank MH186701; 98 % identity, 99 % query cover) and *A. melanogenum* strain CBS 105.22 (GenBank MH1866219; 98 % identity; query coverage 97 %). The BLASTn similarity search in the NCBI type sequences database using the ITS sequence showed the highest similarity to *Kabatiella bupleuri* CBS 131304 (GenBank NR_121524; 95 % identity, 100 % query coverage) followed by *Aureobasidium iranianum* CCTU 268 (GenBank KM093738; 95 % identity, 99 % query coverage) and *A. melanogenum* CBS 105.22 (GenBank NR_159598, 95 % identity, 99 % query coverage). The neighbour-joining (NJ) phylogenetic analyses of ITS and LSU RNA gene regions were done using sequences of other species of *Aureobasidium*. The phylogenetic tree topology clearly shows that the present strain UN-1 is novel and does not cluster with any known species of the genus. The phylogenetic analysis based on the ITS alignment shows that it forms a sister branch to *A. thailandense* NRRL 58543 (GenBank JX462675) and *A. mangrovei* IBRC-M-30266 (GenBank KY089087). In the phylogenetic analysis based on the LSU alignment, it does not group with known species but was placed at equal evolutionary distance with *A. cauvilorum* CBS 242.64 (GenBank FJ150944).

**Typus.** India, Aurangabad, Maharashtra, laboratory contaminant, July 2016, A. Inamdar (holotype MCC 1683 preserved as metabolically inactive strain, ITS and LSU sequences GenBank MK503657 and MK503660, MycoBank MB829941).

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