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MICROBIOLOGICAL AND VIRULENCE ASPECTS OF *RHODOTORULA MUCILAGINOSA*

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Supplementary Figure 1: Phylogenetic analysis of *Rhodotorula mucilaginosa*, based on ITS sequences constructed with Maximum likelihood, based on the Tamura-Nei model + Gamma distribution (T92+G) implemented in MEGA v.7. Bootstrap support was calculated from 1000 replicates. (T) = type strain of the species. Bootstrap values > 80 % were considered statistically significant.