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## o *Moniliellomycetes* and *Malasseziomycetes*, two new classes in *Ustilaginomycotina*

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*Ustilaginomycotina* (*Basidiomycota, Fungi*) has been reclassified recently based on multiple gene sequence analyses. However, the phylogenetic placement of two yeast-like genera *Malassezia* and *Moniliella* in the subphylum remains unclear. Phylogenetic analyses using different algorithms based on the sequences of six genes, including the small subunit (18S) ribosomal DNA (rDNA), the large subunit (26S) rDNA D1/D2 domains, the internal transcribed spacer regions (ITS 1 and 2) including 5.8S rDNA, the two subunits of RNA polymerase II (*RPB1* and *RPB2*) and the translation elongation factor 1- $\alpha$  (*EF1- $\alpha$* ), were performed to address their phylogenetic positions. Our analyses indicated that *Malassezia* and *Moniliella* represented two deeply rooted lineages within *Ustilaginomycotina* and have a sister relationship to both *Ustilaginomycetes* and *Exobasidiomycetes*. Those clades are described here as new classes, namely *Moniliellomycetes* with order *Moniliellales*, family *Moniliellaceae*, and genus *Moniliella*; and *Malasseziomycetes* with order *Malasseziales*, family *Malasseziaceae*, and genus *Malassezia*. Phenotypic differences support this classification suggesting widely different life styles among the mainly plant pathogenic *Ustilaginomycotina*.

**Keywords:** FUNGI; MOLECULAR PHYLOGENY; SMUTS; TAXONOMY; YEASTS**Document Type:** Research Article

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