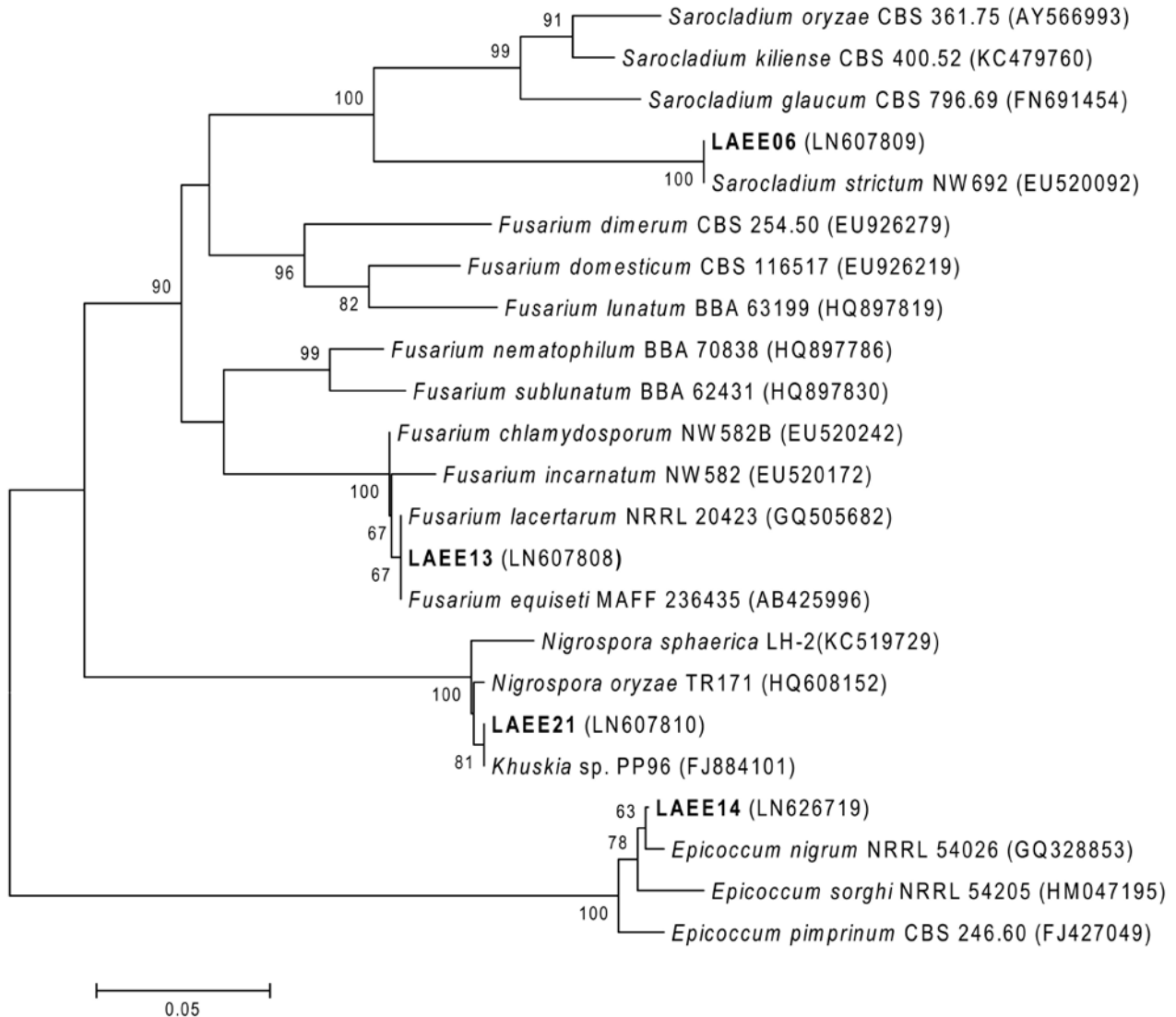


Supplementary Information

Figure S1. Neighbour-joining (Kimura-2 parameter model) phylogenetic tree based on ITS sequences (552 nt) of isolates of this study and strains belonging to culture-collection. Accession numbers are given in parentheses. Numbers at the nodes are bootstrap support values ($\geq 50\%$) for 1000 replicates. The scale bar indicates the number of substitutions per site.



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