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 (≥50%) for 1000 replicates. The scale bar indicates the number of substitutions per site.