

Figure S1. Neighbour-joining phylogenetic tree based on ITS sequences showing the distance of isolated strains with the nearest species of the genus *Exserohilum*. *Alternaria alternata* was used as an out group. Bootstrap percentage values as obtained from 1,000 resamplings of the date set are given at the nodes of the tree. The tree is rooted to midpoint with bootstrap support values greater than 50 shown. The scale bar represents 0.2 substitutions per nucleotide position.



Figure S2. Neighbor-joining phylogenetic tree based on ITS sequences showing the distance of isolated strains with the nearest species of the genus *Curvularia*. *Alternaria alternata* was used as an out group. Bootstrap percentage values as obtained from 1,000 resamplings of the date set are given at the nodes of the tree. The tree is rooted to midpoint with bootstrap support values greater than 50 shown. The scale bar represents 20 substitutions per nucleotide position.

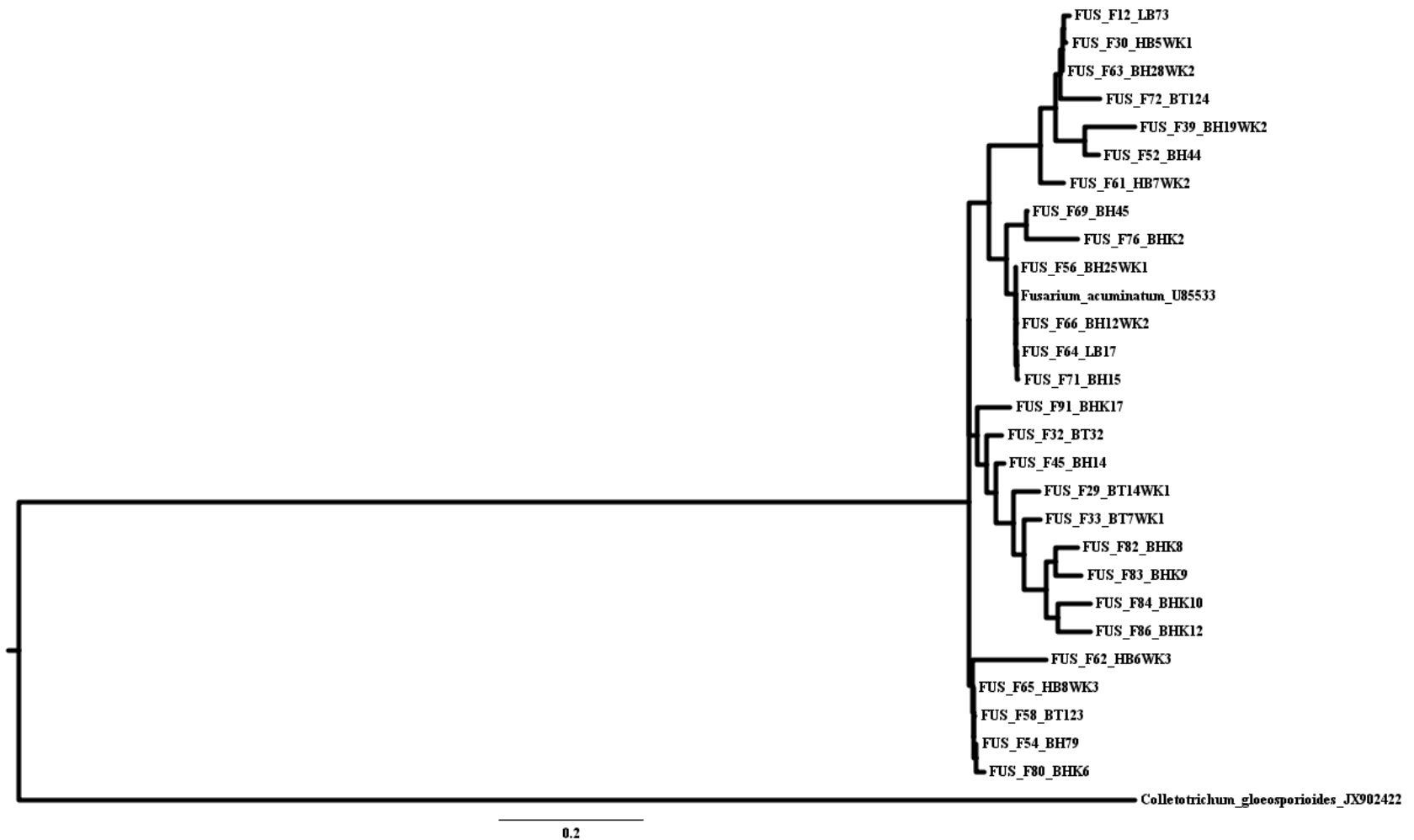


Figure S3. Neighbour-joining phylogenetic tree based on ITS sequences showing the distance of isolated strains with the nearest species of the genus *Fusarium*. *Colletotrichum gloeosporioides* was used as an out group. Bootstrap percentage values as obtained from 1,000 resamplings of the date set are given at the nodes of the tree. The tree is rooted to midpoint with bootstrap support values greater than 50 shown. The scale bar represents 0.2 substitutions per nucleotide position.