

Figure Legends

Figure S1: Amplified fragment length polymorphism analysis showing genotypic diversity among 24 clinical and environmental global *Exserohilum* isolates. The dendrogram was constructed by using UPGMA (unweighted pair group method with arithmetic mean) in combination with the Pearson correlation coefficient and was restricted to fragments of 60-400 bp. Scale bar indicates the percentage similarity.

Figure S2: Phylogram of 24 isolates of species of *Exserohilum* strains based on rDNA ITS sequences using maximum likelihood with the MEGA v6 software, with partial deletion of gaps and using the Kimura-2 parameter substitution model. *Curvularia heteropogonica* was used as outgroup and *Exserohilum* isolates with a "T" are ex-type. Branch support values are indicated by the numbers near the branches.

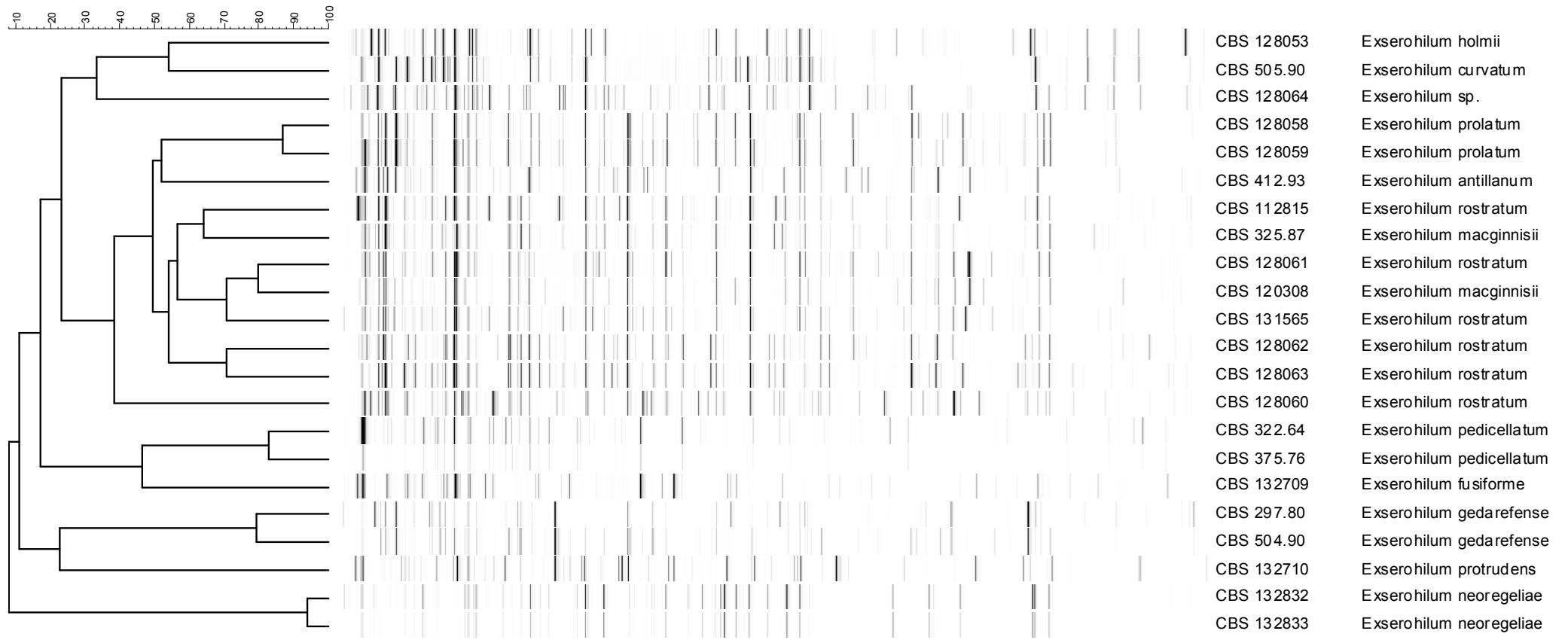


Fig. S2

