



**Supplementary Fig. 2.** Neighbor-joining phylogenetic tree analysis based on *Fusarium* spp. translation elongation factor (*tefI*) partial sequences. *Nectria haematococca* was used as an outgroup. The strains isolated in this study are bolded and values below 70 are not shown. Bootstrap values are based on 1,000 replications. Bar, 0.05 substitutions per nucleotide position. Sequence accession numbers are shown in parentheses.