



Figure S3. A maximum-likelihood phylogeny (with *S. trifoliorum* as outgroup) generated using RAxML showing non-parametric bootstrap analyses (in %) of 1000 repetitions. Nodes are labelled with the species names, isolate number, and accession numbers for publicly available data (all from GeneBank, <https://www.ncbi.nlm.nih.gov/genbank>), except *S. minor* LC41 that can be obtained from the China National GeneBank (CNGB) database). Only bootstrap values above 70 are shown, and the scale bar represent the number of nucleotide substitutions per site. Re-isolations are based on the month isolated, e.g., the October re-isolate is for sclerotia from October inoculated plants, November re-isolate is for sclerotia from November inoculated plants, etc.