

Figure S1a. Phylogeny obtained by Maximum likelihood analysis of the combined LSU-ITS-RPB2 sequence alignment of species from *Mycosphaerellaceae*. ML bootstrap support values above 70 % are shown at the nodes. *Micronematomyces caribensis* strain CBS113380 is used as outgroup. Strains analysed in this study are emphasised in bold. Branches that are crossed by diagonal lines are shortened by 50 %.

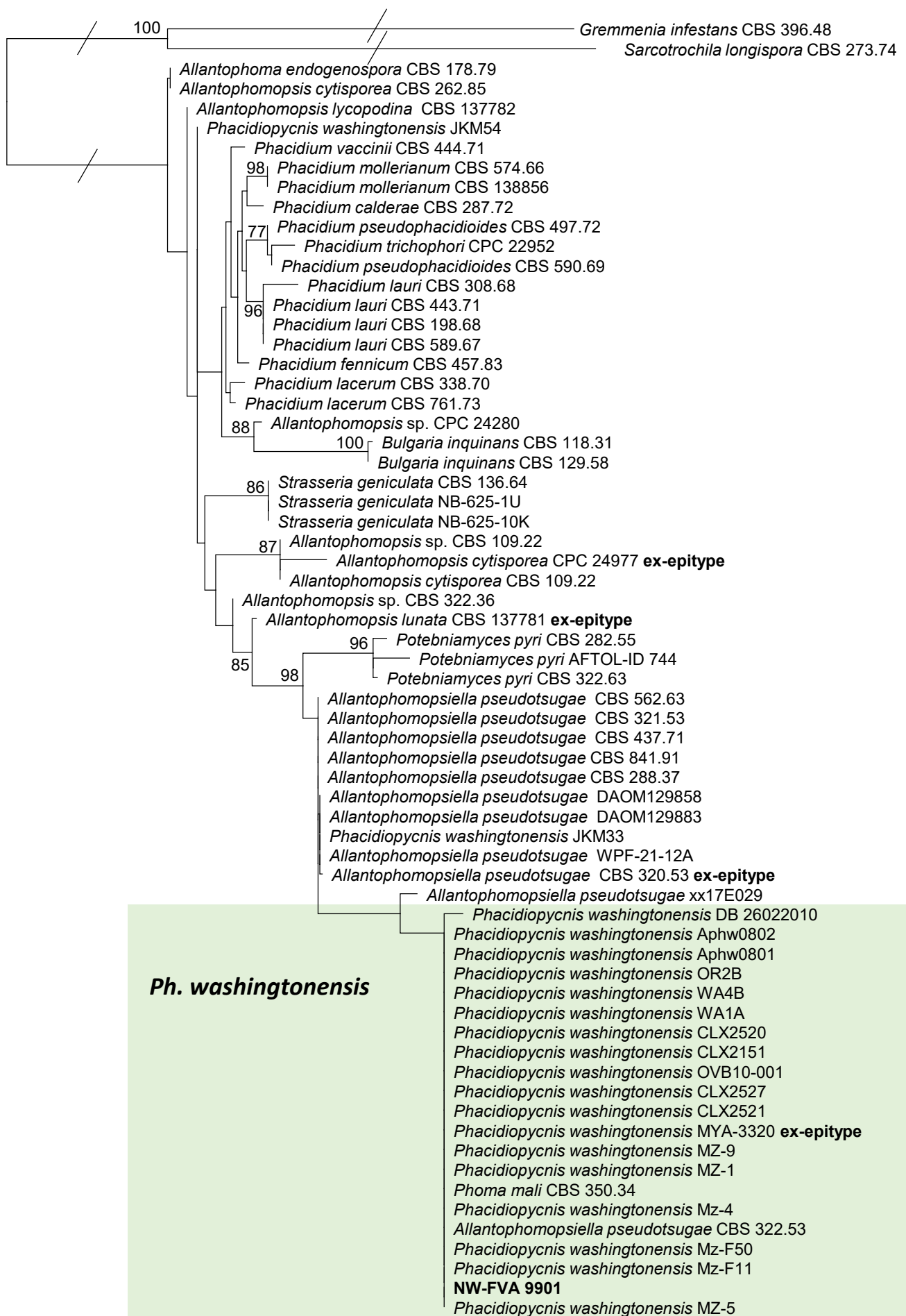


Figure S1b. Phylogeny obtained by Maximum likelihood analysis of the combined LSU-ITS-*RPB2* sequence alignment of species from *Phacidiaceae*. ML bootstrap support values above 70 % are shown at the nodes. *Gremmenia infestans* strain CBS 396.48 and *Sarcotrochila longispora* strain CBS 273.74 are used as outgroup. Strains analysed in this study are emphasised in bold. Branches that are crossed by diagonal lines are shortened by 50 %.



Figure S1c. Phylogeny obtained by Maximum likelihood analysis of the combined LSU-ITS-*EF-1α* sequence alignment of *Coniochaeta* species. ML bootstrap support values above 70 % are shown at the nodes. *Coniochaeta verticillata* strain CBS 816.71 is used as outgroup. Strains analysed in this study are emphasised in bold. Branches that are crossed by diagonal lines are shortened by 50 %.