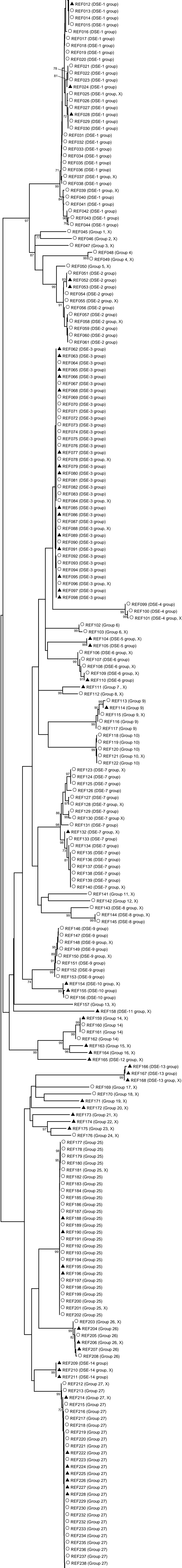


Figure S2 Minimum Evolution tree of the ITS sequences of 24 isolates originating from roots of indigenous (○) and invasive (▲) plants. Name of the groups are shown in brackets. Isolates used in the artificial inoculation experiments are marked (X). Tree was inferred using the Maximum Composite Likelihood model and pairwise deletion at gaps using MEGA 4.0. Bootstrap values obtained from 1000 replicates are shown as percentages and not shown below 70%. Bar = 2 changes/100 characters.



0.02