**Figure S4** The maximum likelihood (ML) tree of the ITS sequences of representatives of group DSE-3 and similar sequences from GenBank. Sequences obtained in this study are shown in bold. *Massarina corticola* (FR668004) was used as outgroup. Accession number, isolation source and geographic origin of sequences from public databases are shown. NJ bootstrap (not shown below 70%) values are above and the Bayesian posterior probabilities as percentage (not shown below 90%) are below the branches. Abbreviations: uncultured (u.), clone (c.). Bar = 0.1 expected change on one nucleotide.