Fig. 2.6. Bayesian 50% majority rule LSU consensus tree containing representative *Mollisia* and allied taxa for gene genealogy comparison. Culture collection, GenBank or JB Tanney personal collection accession numbers (NB) follow the species name (type strains in bold). All branches have Bayesian posterior probability values of 1.0; values lower than 1.0 are presented at nodes. The tree was rooted to *Pyrenopeziza dextrinospora* and bars indicate expected changes per site per branch.