



Maximum likelihood tree inferred from 110 18S, 5.8S, ITS1 and ITS2 rDNA sequences. Numbers at the nodes show the maximum likelihood bootstrap values, Bayesian posterior probabilities and concordance factors inferred from Bucky. Asterisks represent full support. The main morphological traits including position of ostiole-pore, rhizoids, heterotrichous thalli, crustose or tuft thalli, and lichenized or free-living of every strain are displayed and represented by circles, asterisks, ticks, triangles and rectangles respectively.