



Fig. 6-5. (a) Majority-rule consensus tree of the analyzed species of the MYRIOPUS and EUPLOCA clade, computed from the 112 most parsimonious trees of the ITS1 dataset ($l=332$ steps, $CI=0.723$, $RI=0.803$, $HI=0.277$). Important clades are indicated. The numbers above the branches are bootstrap percentages. Percentages $<50\%$ are not shown. The numbers below the branches are majority percentages $<100\%$. (b) Corresponding neighbor-joining tree. Important clades are indicated. The numbers above the branches are bootstrap percentages (1000 replicates, percentages $<50\%$ are not shown, scale bar 10% distance).