



Fig. 6-7. (a) Majority-rule consensus tree of the analyzed species of the HELIOTROPIUM II clade, computed from the 84 most parsimonious trees of the combined *trnL* and ITS1 datasets ( $l=373$  steps,  $CI=0.751$ ,  $RI=0.748$ ,  $HI=0.249$ ). 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).