

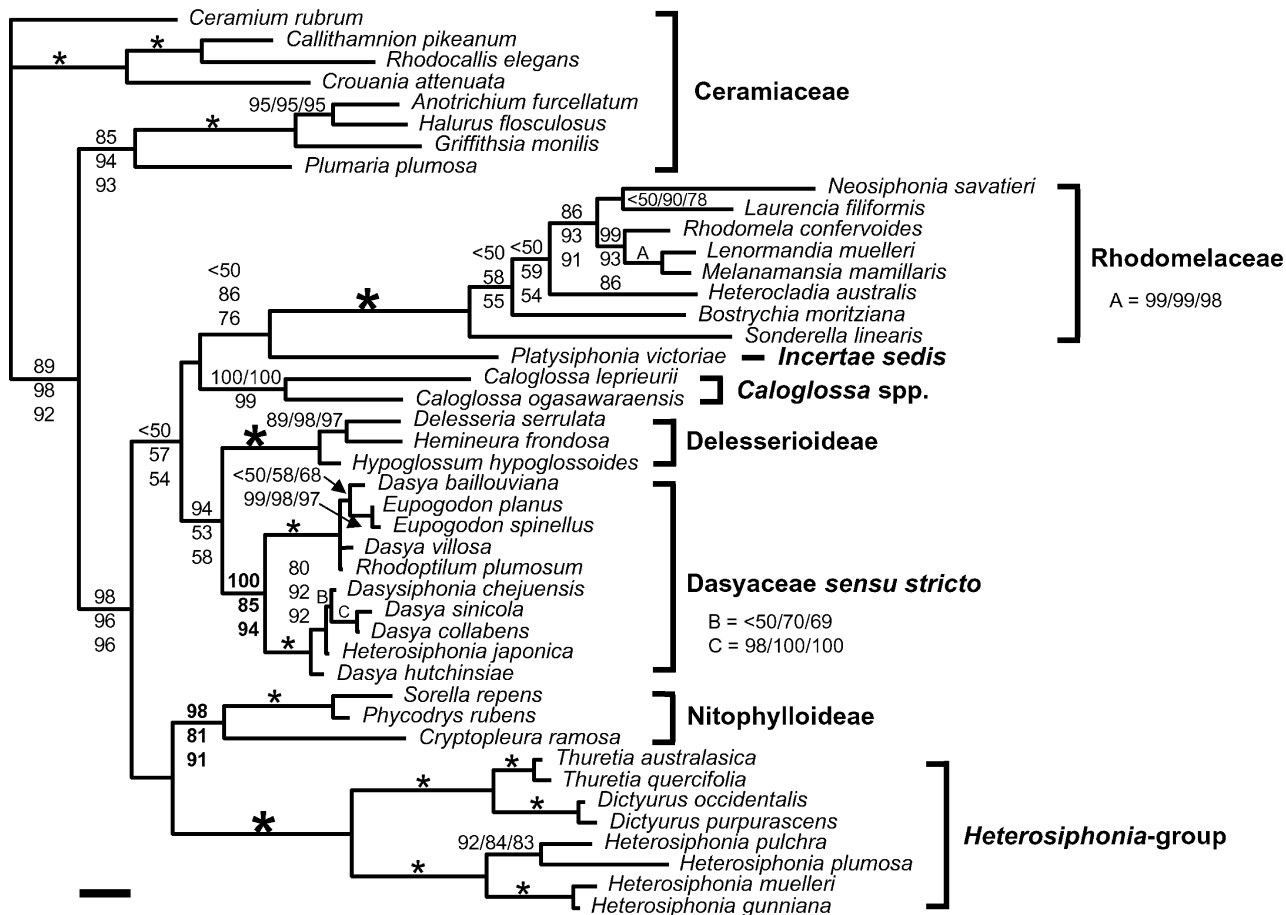


Fig. 1. Tree constructed with maximum likelihood for the SSU alignment excluding *Halodictyon mirabile*. Values at branches represent percentage of 2000 bootstrap replicates for distance analysis (top value) and of 1000 bootstrap replicates for 'transversion' (middle value) and unweighted parsimony (bottom value) analyses. Bold numbers and large asterisks are bootstrap values for five of the six major lineages within the Dasyaceae/Delesseriaceae/Rhodomelaceae complex. Branches marked with an asterisk received 100% support in all three analyses whereas those lacking values received less than 50% support. Scale bar represents 0.01 substitutions per site.