



Fig. 1. Maximum likelihood tree. Numbers above the branches represent clade credibility values; posterior probabilities in red, bootstrap values in a maximum parsimony framework in black, and bootstrap values in a maximum likelihood framework are in green. Monophyletic species with all their accessions grouping together are in black. Species represented by only one accession and only one sequence are colored in green. Species with only one accession and two alleles grouping together are in bold green. Species with only one accession and two alleles grouped two different clades are in bold black. Species with several accessions with some accessions or alleles in different clades are in colors other than green and black. Polyploid species are enclosed in boxes. Letters after accession numbers represent allelic variants.