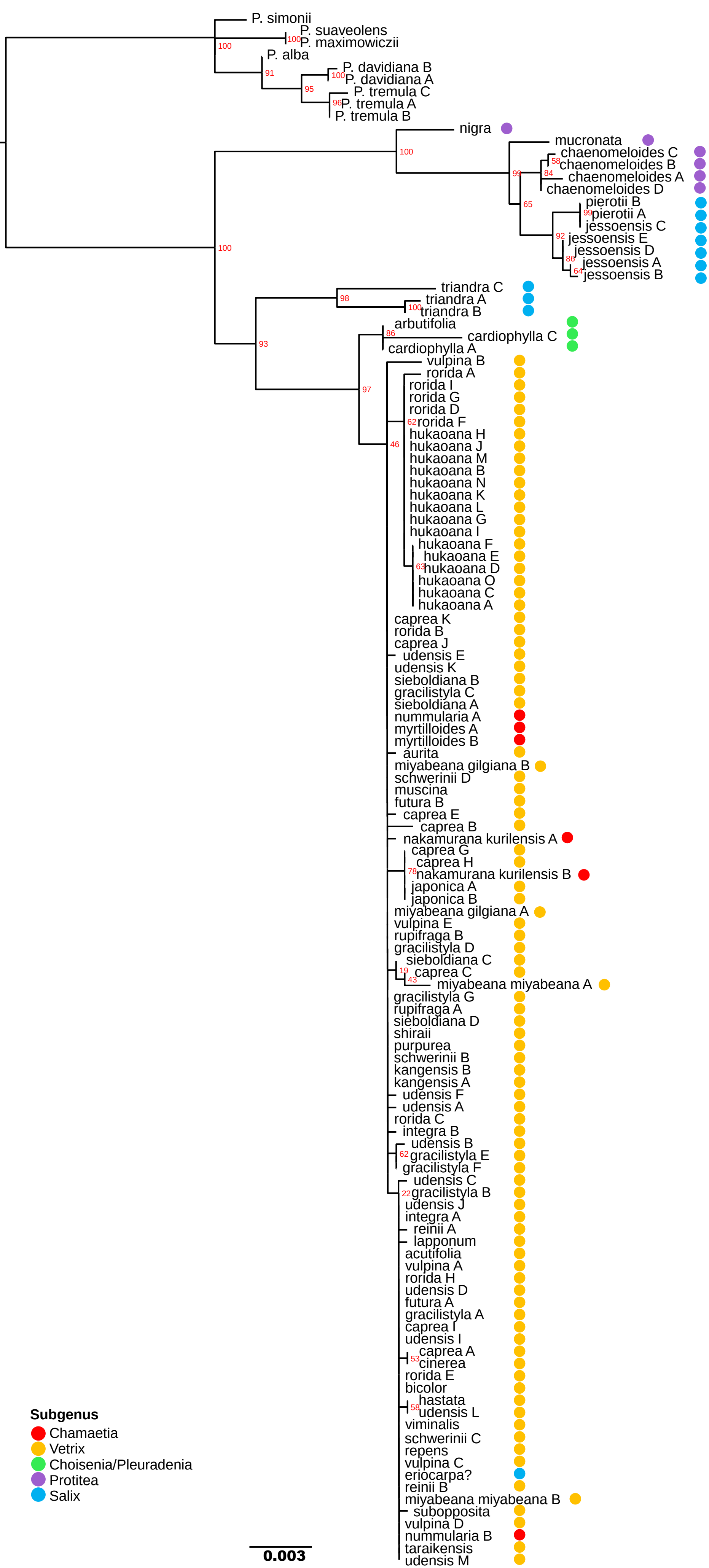


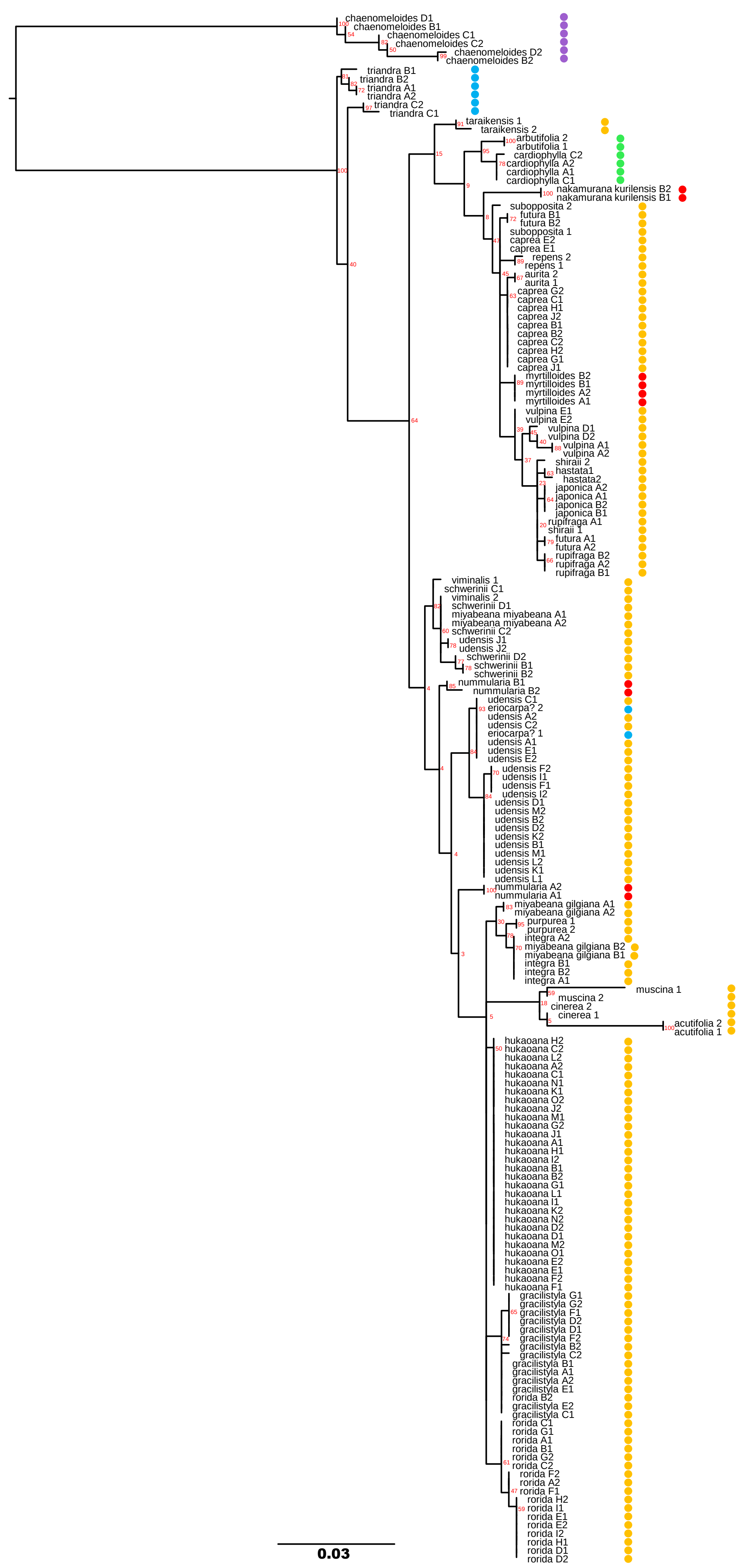
a Chloroplast



Online Resource 2

Phylogenetic trees (gene trees) based on (a) chloroplast, (b) nuclear *6PG*, (c) *PGI*, and (d) *ncpGS* gene sequences as reconstructed using the maximum likelihood (ML) method. The numbers at each node refer to the bootstrap values.

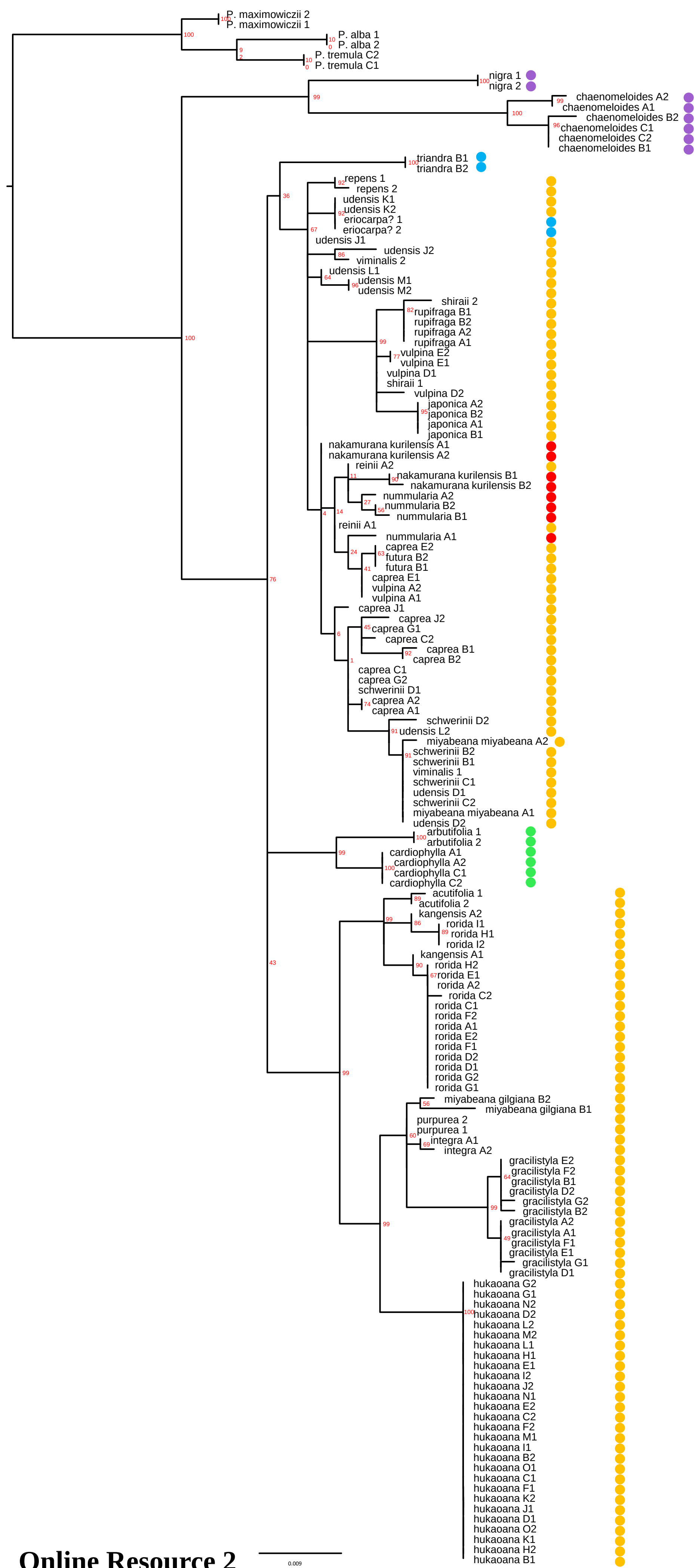
b ncpGS



Online Resource 2

Phylogenetic trees (gene trees) based on (a) chloroplast, (b) nuclear *6PG*, (c) *PGI*, and (d) *ncpGS* gene sequences as reconstructed using the maximum likelihood (ML) method. The numbers at each node refer to the bootstrap values.

c PGI

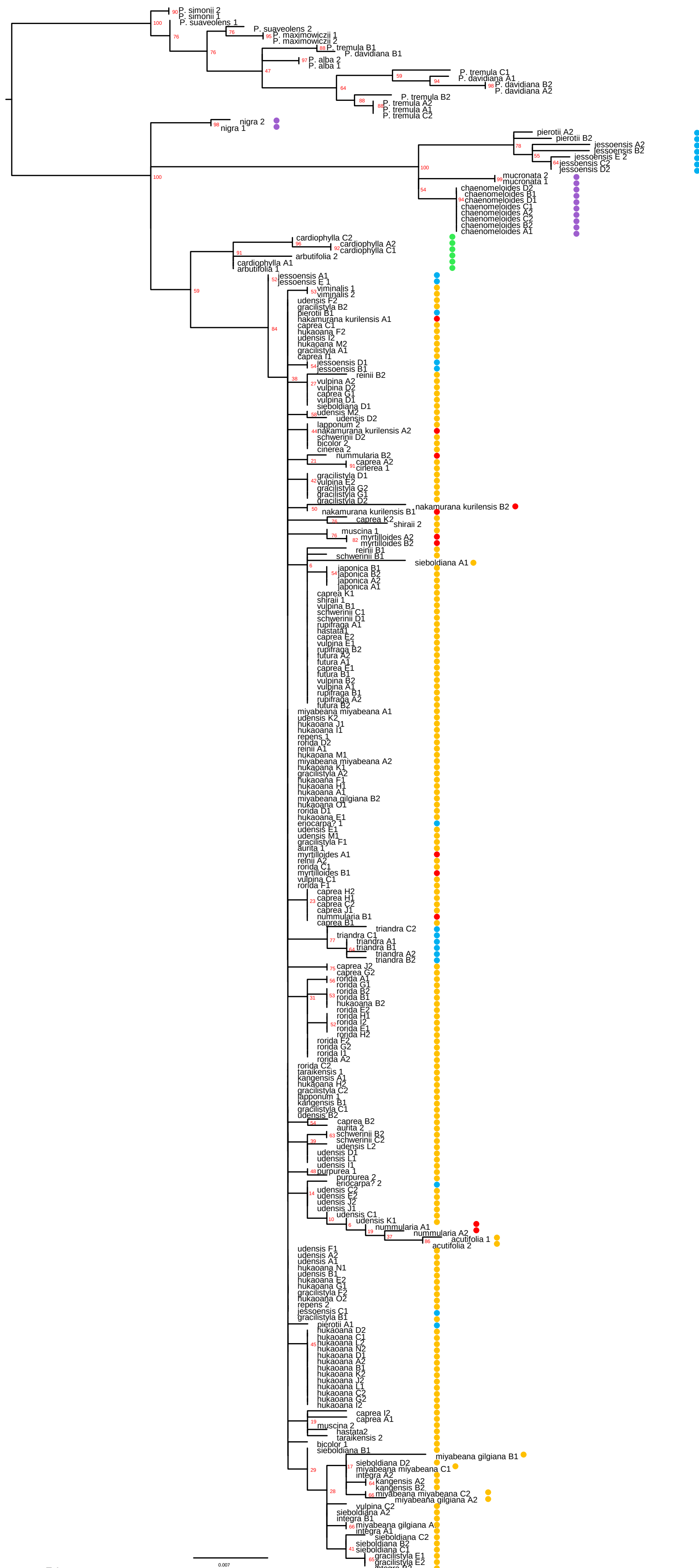


Online Resource 2

Phylogenetic trees (gene trees) based on (a) chloroplast, (b) nuclear *6PG*, (c) *PGI*, and (d) *ncpGS* gene sequences as reconstructed using the maximum likelihood (ML) method. The numbers at each node refer to the bootstrap values.

Kikuchi S, Setsuko S, Nagamitsu T & Suzuki W. Molecular phylogenetic analyses identify the process of speciation of endemic willow species in the Japanese Archipelago. *Journal of Plant Research*. Corresponding author: Kikuchi S, Forestry and Forest Products Institute, kikusato@affrc.go.jp

d 6pg



Online Resource 2

Phylogenetic trees (gene trees) based on (a) chloroplast, (b) nuclear *6PG*, (c) *PGI*, and (d) *ncpGS* gene sequences as reconstructed using the maximum likelihood (ML) method. The numbers at each node refer to the bootstrap values.