

Exemplos de mapeamento de caracteres químicos
sob árvores filogenéticas baseadas em dados
moleculares

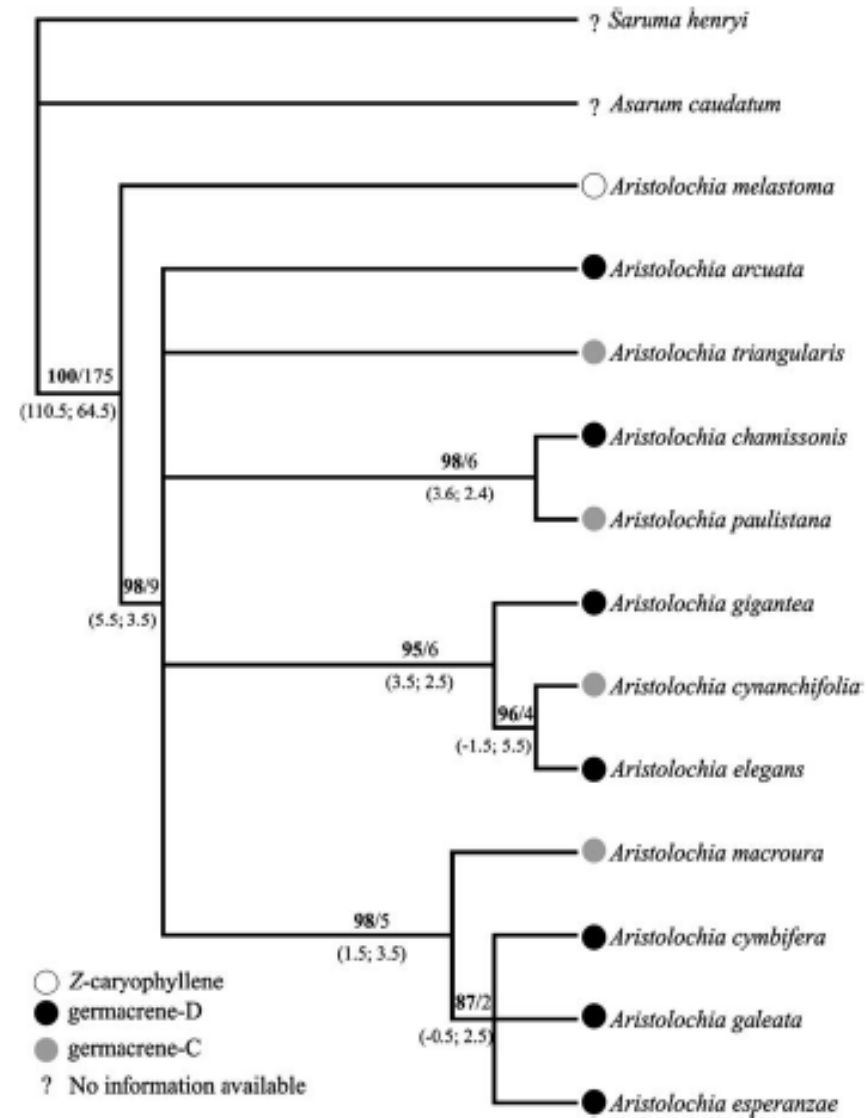


Fig. 1. Phylogenetic relationships hypothesis among *Aristolochia* species. Strict consensus tree of 24 equally parsimonious trees based on combined data analysis (477 steps). The numbers above the branches indicate the bootstrap values from 1000 replications and the Bremer support, respectively. Numbers below the branches are the partitioned Bremer support values, which indicate the contribution of *matK* and the region between *trnL* and *trnF*, respectively, to the Bremer support value of the combined analysis.

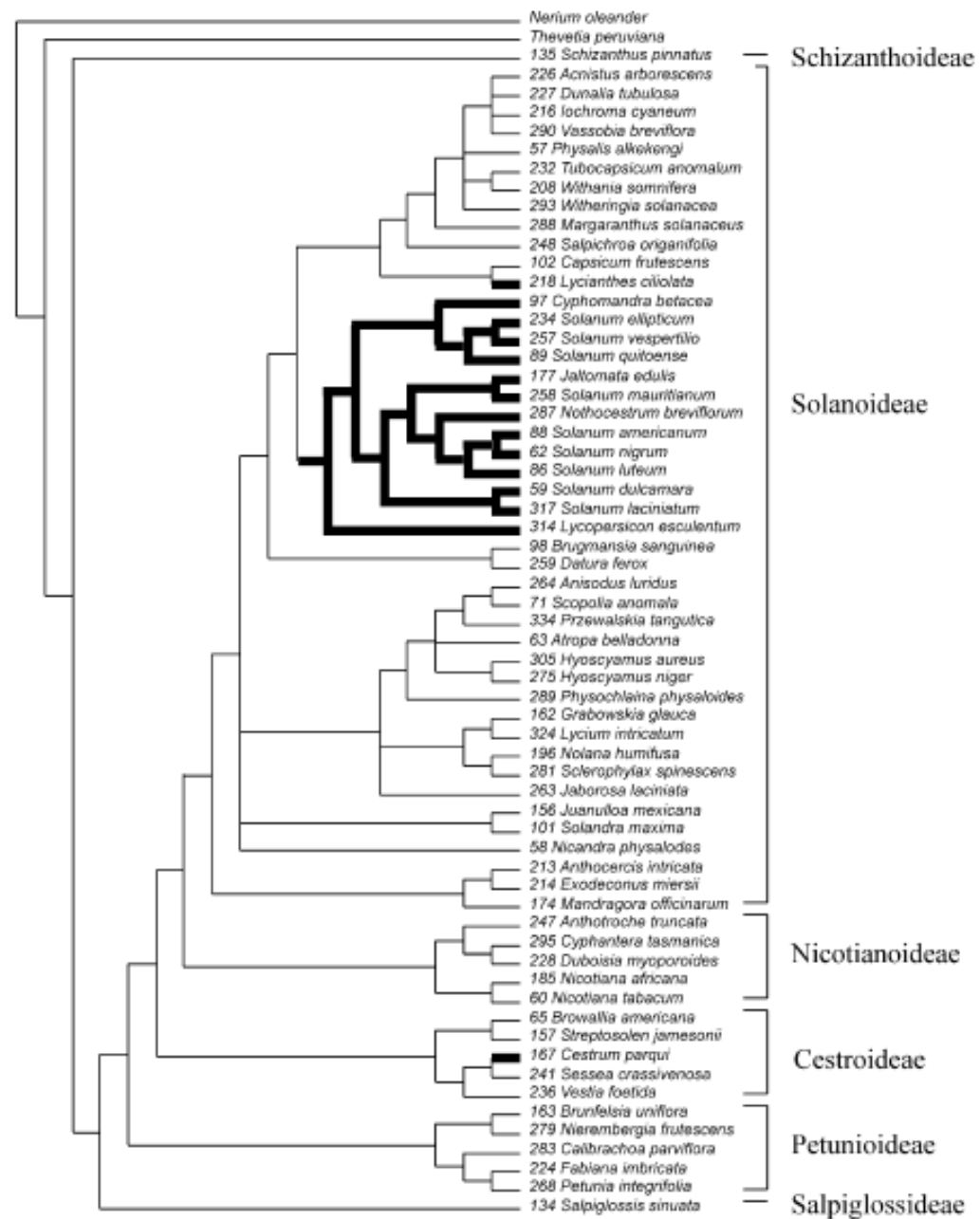


Fig. 4. Distribution of steroid alkaloids in Solanaceae.

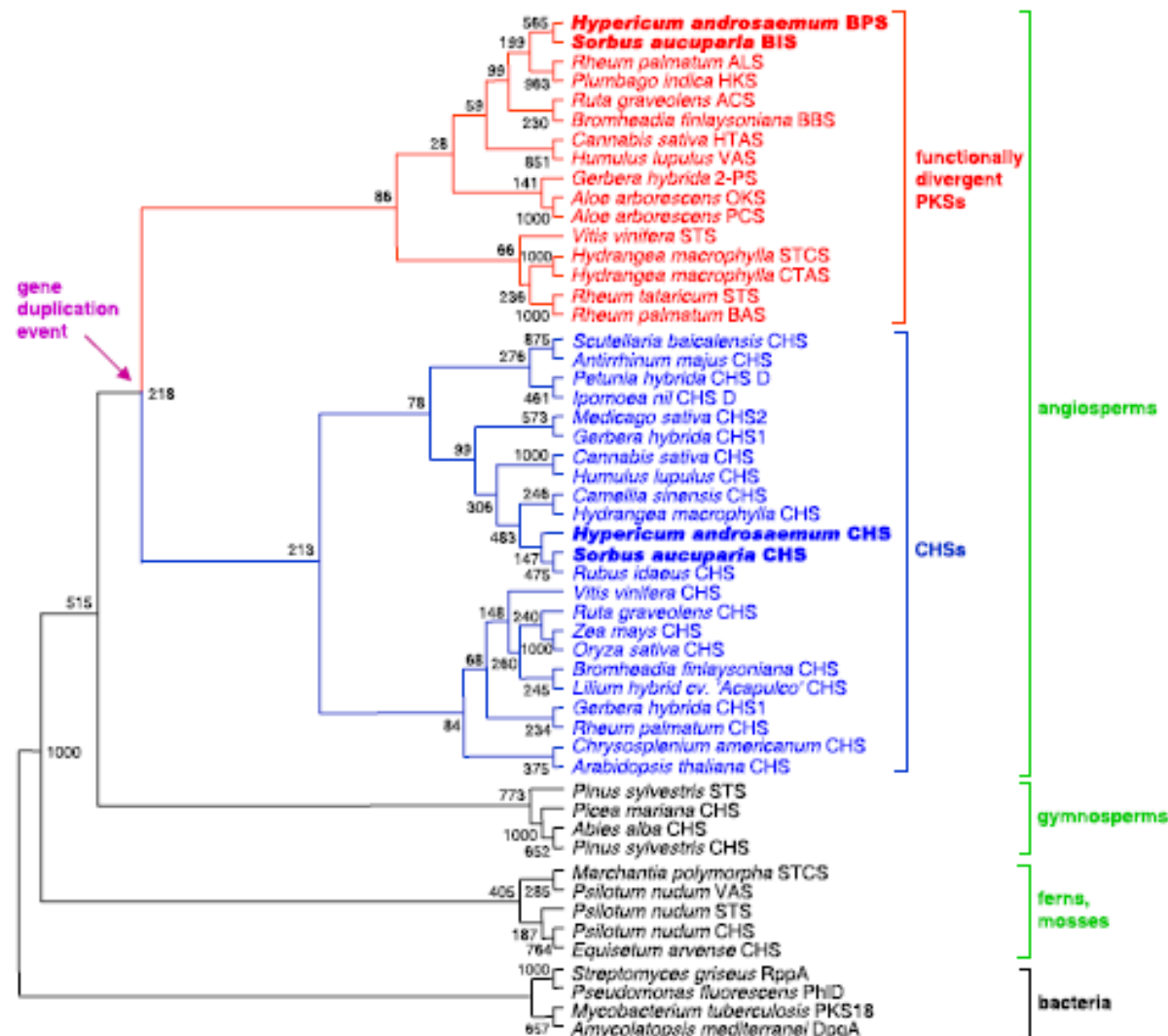


Fig. 3. Neighbour-joining tree of type III PKSs. CHSs (blue) and non-CHSs (red) from angiosperms divide into two clusters which originate from a gene duplication event (pink arrow) prior to the speciation of the angiosperms. Four functionally studied bacterial type III PKSs were used to root the tree. Numbers at the forks are bootstrap values from 1000 replicates. ACS, acridone synthase; ALS, aloesone synthase; BAS, benzalacetone synthase; BBS, bibenzyl synthase; BIS, biphenyl synthase; BPS, benzophenone synthase; CHS, chalcone synthase; CTAS, 4-coumaroyl triacetic acid lactone synthase; DpgA, 3,5-dihydroxyphenylacetate synthase; HKS, hexaketide synthase; HTAS, hexanoyl triacetic acid lactone synthase; OKS, octaketide synthase; PCS, pentaketide chromone synthase; PhID, acetylphloroglucinol synthase; 2-PS, 2-pyrone synthase; RppA, 1,3,6,8-tetrahydroxynaphthalene synthase; STS, stilbene synthase; STCS, stilbene carboxylate synthase; VAS, valerophenone synthase (Liu et al., 2003, 2007).

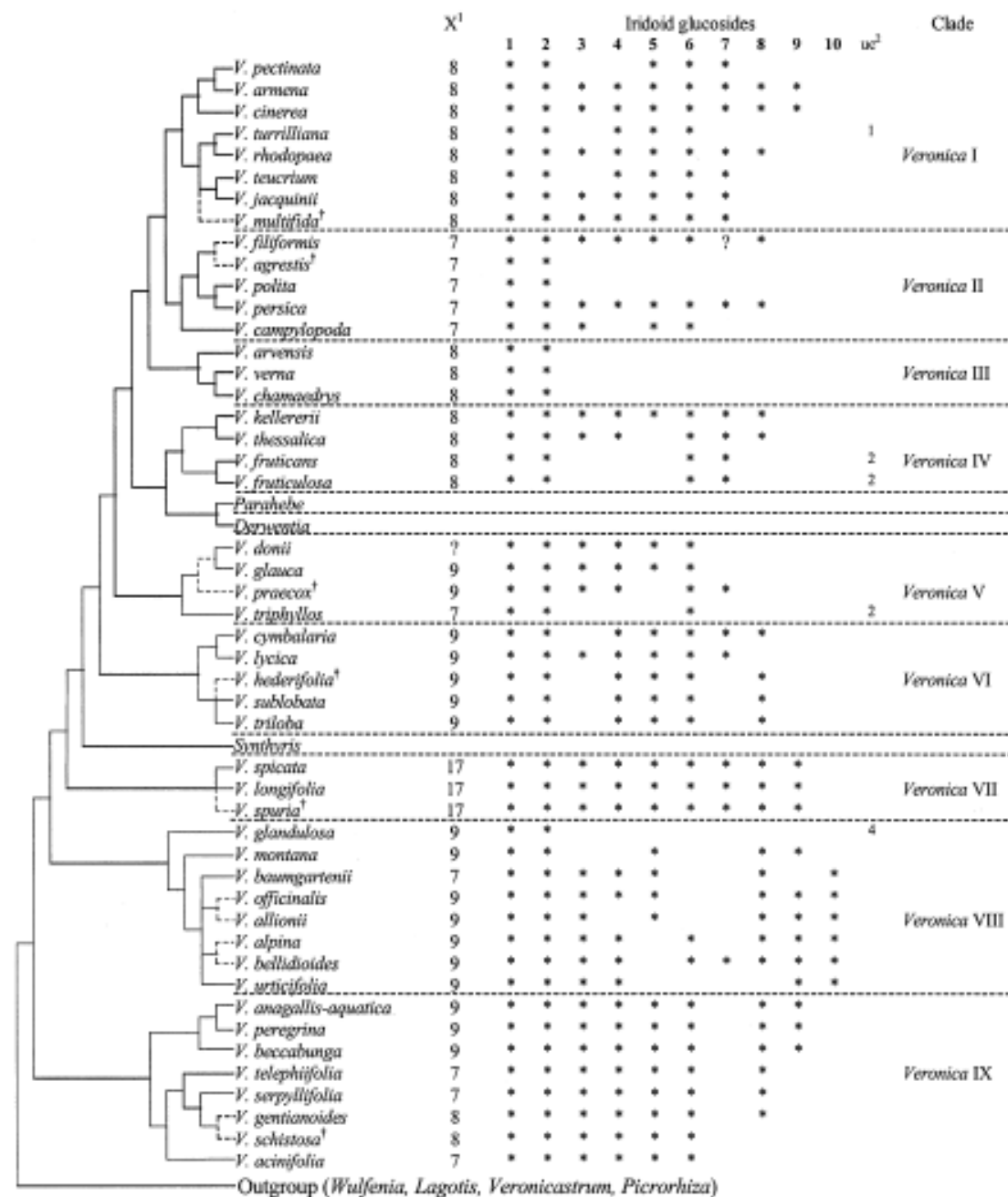


Fig. 3 Cladogram based on the ITS sequences, chromosome numbers, and iridoid composition of *Veronica* s.str.