

Capsi-conundrum: Resolving Relationships within Capsiceae (Solanaceae)

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Capsicum annuum



Capsicum eximium

Lycianthes moziniana



Lycianthes pringlei

Introduction

Capsicum - the plant genus that includes spicy peppers and their non-pungent relatives - constitutes a multi-billion-dollar industry. Their pungency is imparted by unique chemical compounds called capsaicinoids. Its members are found only in the Americas, principally in the tropics. The sister genus to *Capsicum*, *Lycianthes*, is more speciose but poorly understood. Together they make up the tribe Capsiceae.

Evolutionary relationships in the tribe Capsiceae remain unresolved

Until recently, phylogenetic analyses of Capsiceae based on several chloroplast and nuclear genes produced a poorly supported backbone with *Lycianthes* paraphyletic and *Capsicum* nested within it (Särkinen et al. 2013; Carrizo-García et al. 2016; Fig. 2). Genome-wide sequencing provides orders of magnitude more data for phylogenetic analysis. Additionally, genome-wide data allow for analytical techniques beyond concatenation, which ignores the problem of phylogenetic discordance (Larget et al., 2010; Fig. 3). Here, we present three phylogenetic trees for comparison, including a species tree based on concordance of individual gene trees that most accurately represents the evolutionary history of the clade (Fig. 4).

Chr	# Genes	# Probes
Chr 1	183	1628
Chr 2	136	1192
Chr 3	182	1588
Chr 4	123	1076
Chr 5	137	1217
Chr 6	148	1252
Chr 7	137	1215
Chr 8	108	899
Chr 9	157	1322
Chr 10	126	1048
Chr 11	155	1316
Chr 12	134	1136

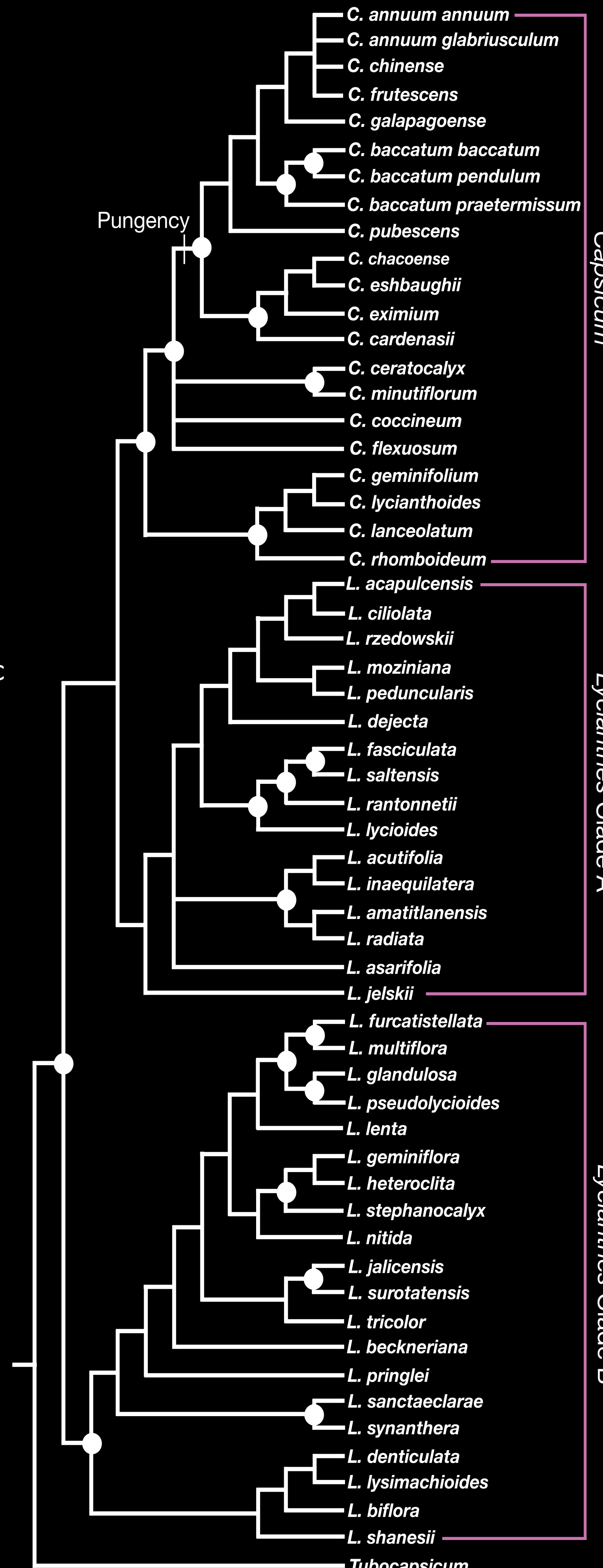


Fig 2. Four gene tree: strict consensus of 30 most parsimonious trees for 54 Solanaceae species constructed using data from nuclear (ITS, *waxy*) and chloroplast (*ndhF* and *trnT-F*) genes. Dots indicate nodes with 100% bootstrap support.

Results

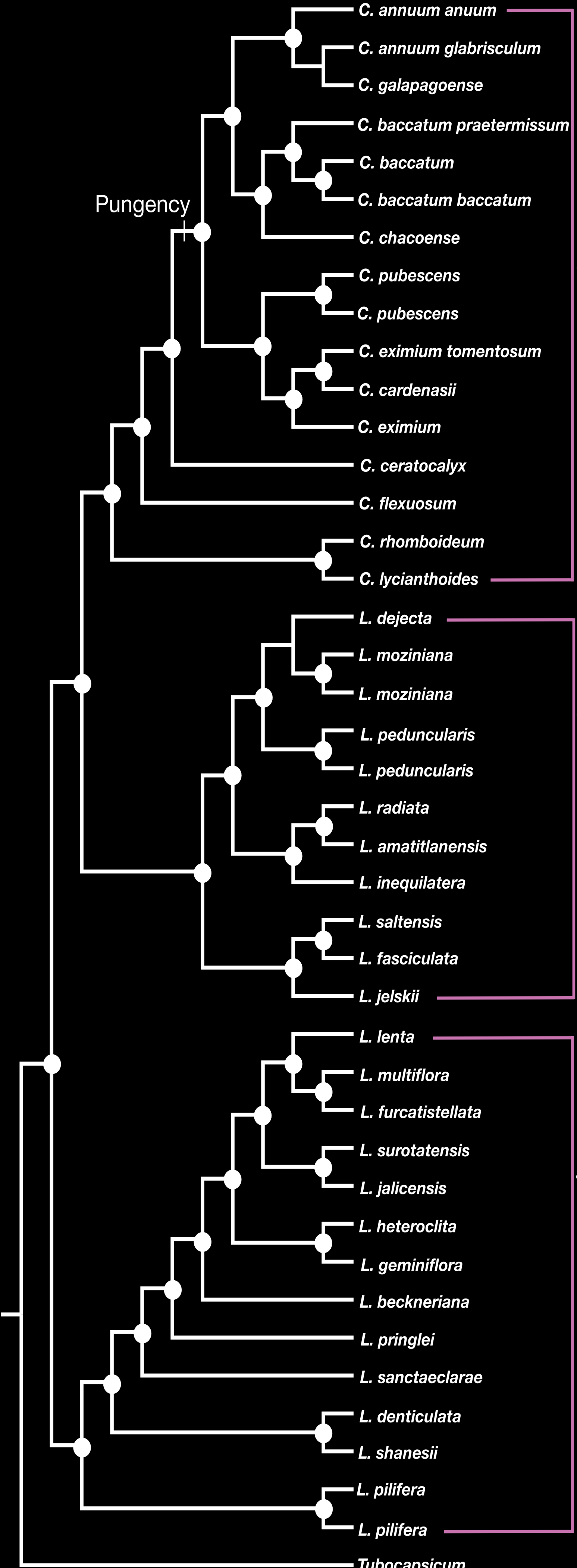


Fig 3. Concatenated tree: maximum likelihood tree of 42 taxa built from concatenated alignment of 1467 genes in RAxML. Dots indicate nodes with 100% bootstrap support.

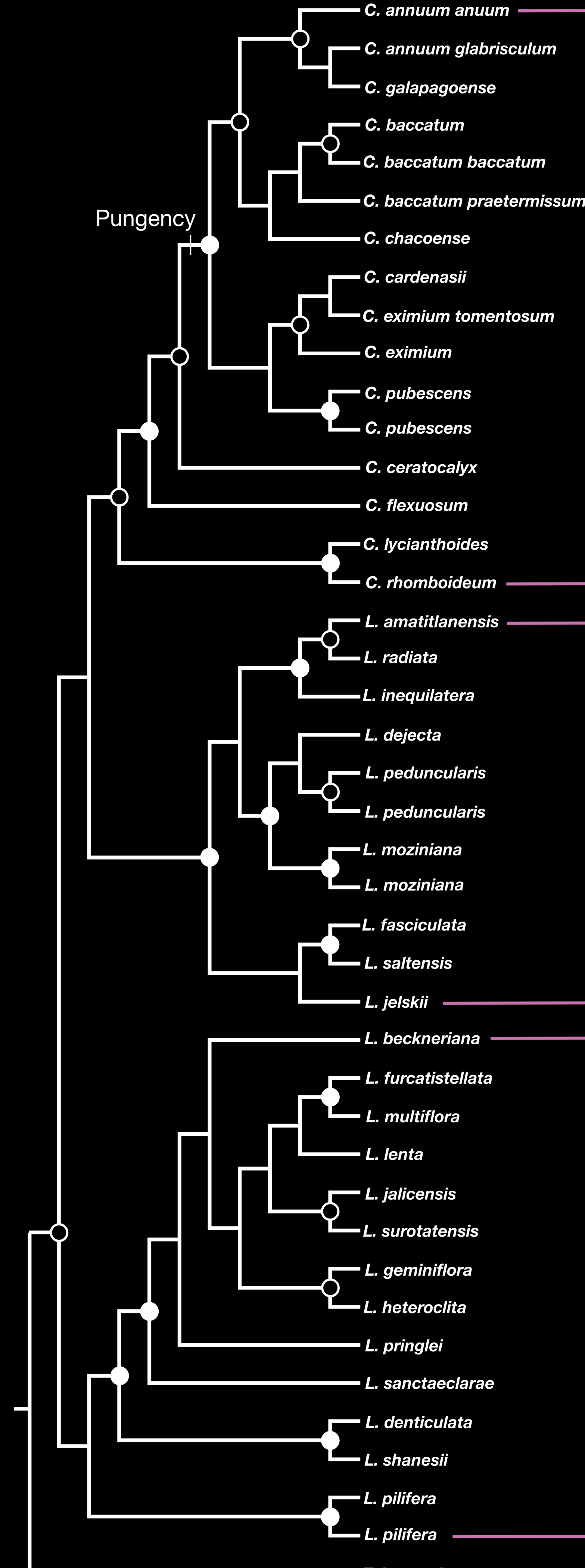
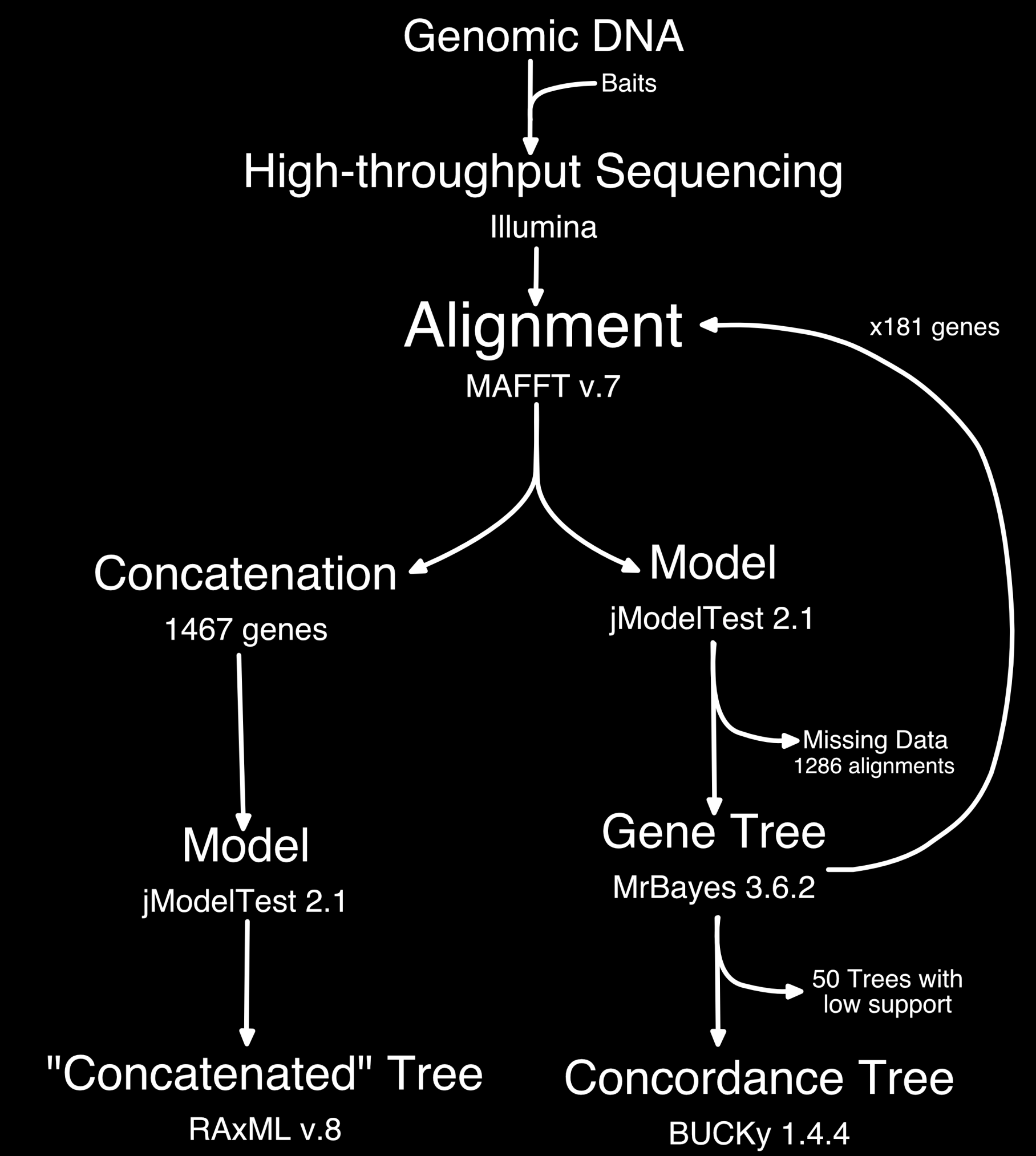


Fig 4. Concordance tree developed from 131 gene trees of 42 taxa using BUCKY, a program which analyzes multi-locus data sets with Bayesian Concordance Analysis. Concordance factors, which indicate the proportion of gene trees that support a given clade, are represented by dots: ● 0.75-1 ○ 0.5-0.74

Methods

We used targeted enrichment to sequence coding regions of the genome that are shared among *Capsicum*, *Lycianthes*, and outgroups (Fig. 1). Baits are presented in Spalink et al. (in press).



Discussion

The concatenated tree provides much more resolution and support than the 4-gene tree because it has orders of magnitude more data.

All three trees have the same fundamental topology, but the concordance tree highlights areas of discordance between gene trees - a signal that is obscured by concatenation. Low concordance factors do not imply low support, but imply that the clade has a complex evolutionary history. The dominant topology reflects a paraphyletic *Lycianthes*. Our results provide the means to update the taxonomy of *Lycianthes* to accurately reflect evolutionary relationships.

Future analyses should seek to determine the cause(s) of discordance, which genes are involved, and the implications thereof for understanding the evolution of species in the clade and important traits like pungency.