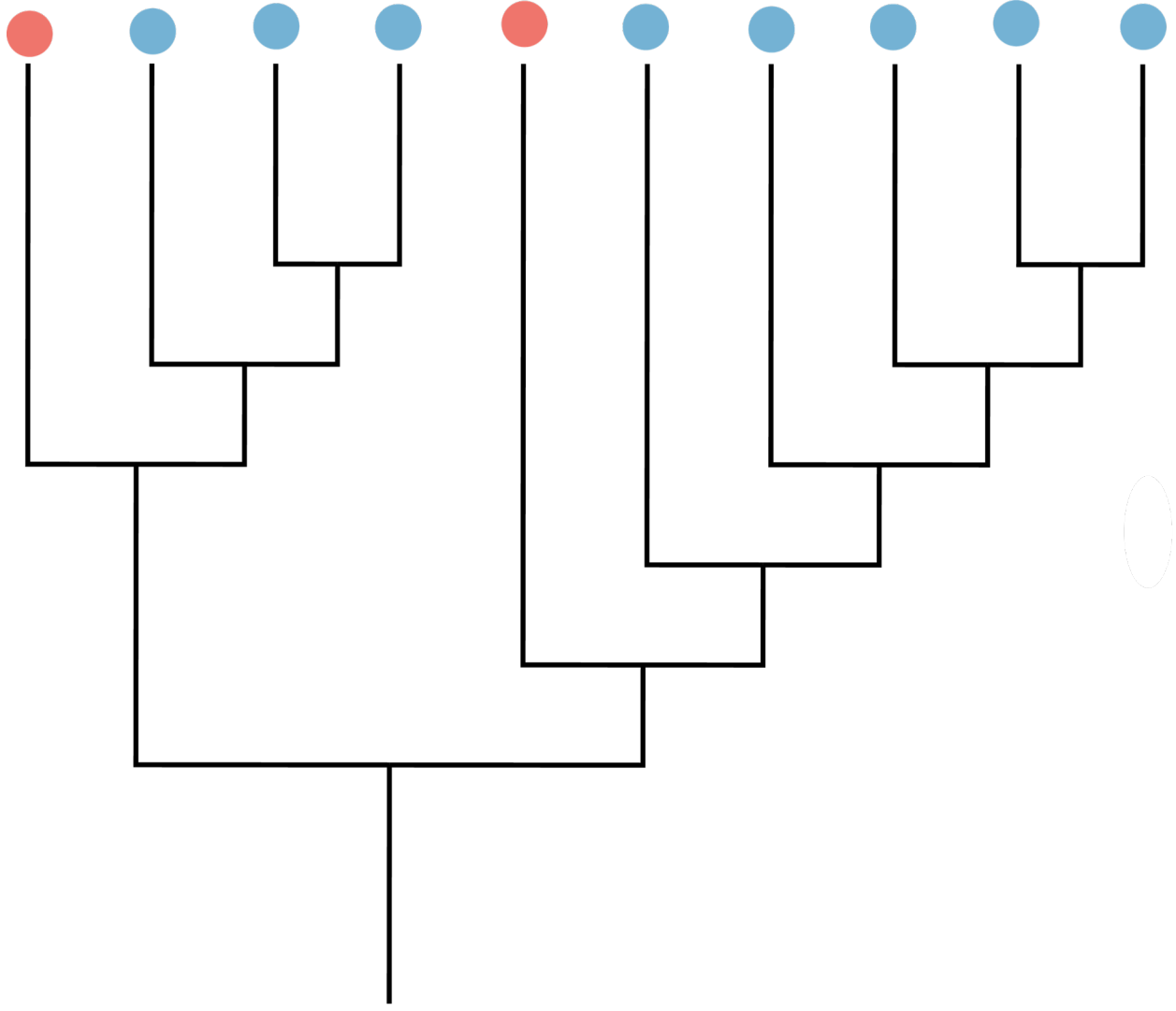
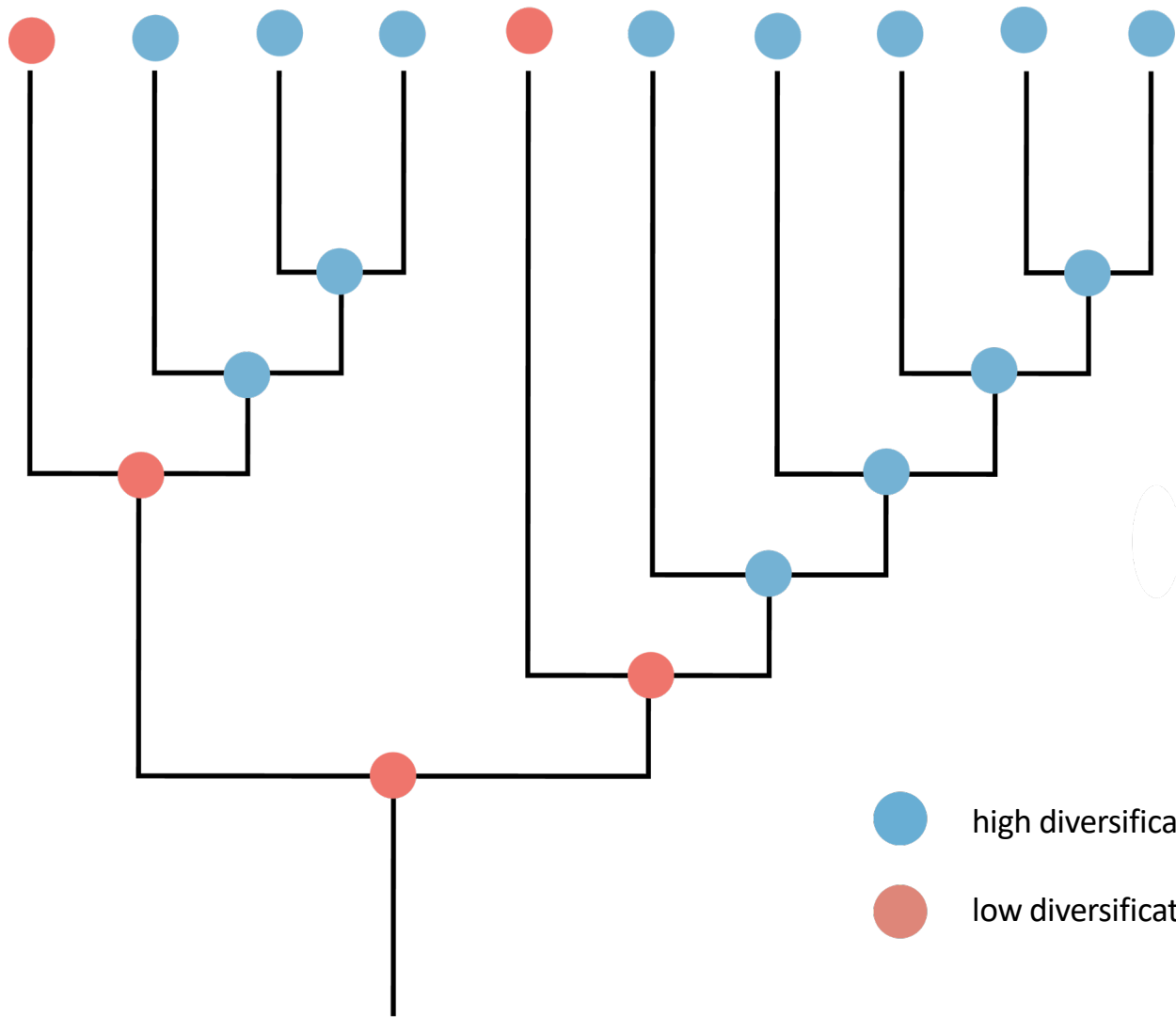
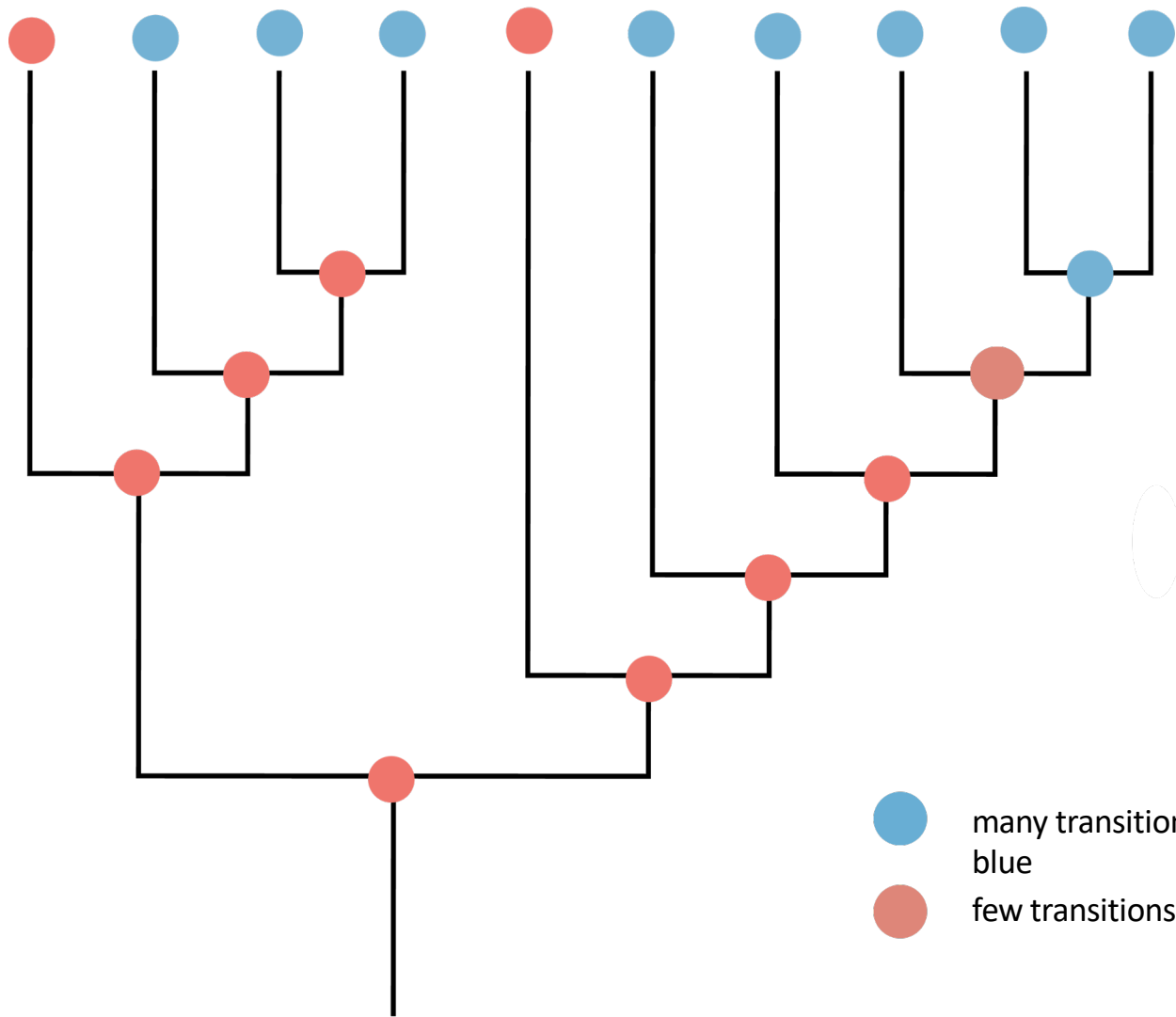


Introduction to Binary State dependent Speciation and Extinction (BiSSE)





● high diversification
● low diversification



● many transitions to blue
● few transitions to red

BRIEF COMMUNICATIONS

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CONFOUNDING ASYMMETRIES IN EVOLUTIONARY DIVERSIFICATION AND CHARACTER CHANGE

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Abstract.—Studies of character evolution often assume that a phylogeny's shape is determined independently of the characters, which then evolve as mere passengers along the tree's branches. However, if the characters help shape the tree, but this is not considered, biased inferences can result. Simulations of asymmetrical speciation (i.e., one character state conferring a higher rate of speciation than another) result in data that are interpreted to show a higher rate of change toward the diversification-enhancing state, even though the rates to and from this state were in fact equal. Conversely, simulations of asymmetrical character change yield data that could be misinterpreted as showing asymmetrical rates of speciation. Studies of biased diversification and biased character change need to be unified by joint models and estimation methods, although how successfully the two processes can be teased apart remains to be seen.

Key words.—Diversification, evolutionary dead-end, extinction, irreversibility, phylogeny, speciation.

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Estimating a Binary Character's Effect on Speciation and Extinction

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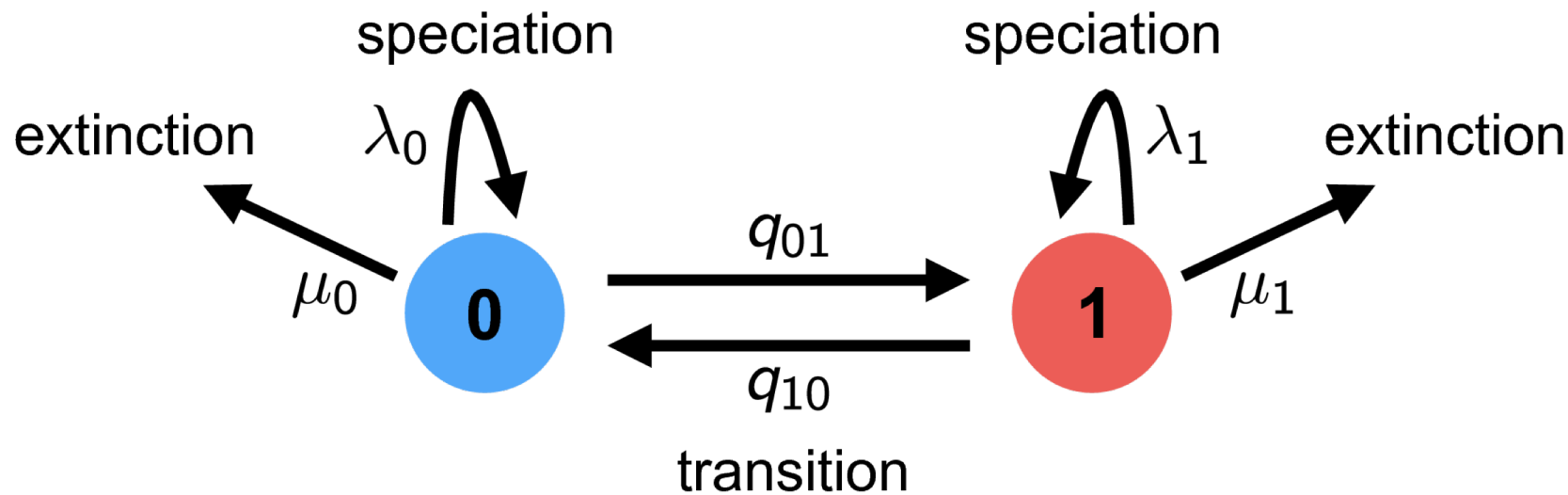
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Abstract.—Determining whether speciation and extinction rates depend on the state of a particular character has been of long-standing interest to evolutionary biologists. To assess the effect of a character on diversification rates using likelihood methods requires that we be able to calculate the probability that a group of extant species would have evolved as observed, given a particular model of the character's effect. Here we describe how to calculate this probability for a phylogenetic tree and a two-state (binary) character under a simple model of evolution (the "BiSSE" model, binary-state speciation and extinction). The model involves six parameters, specifying two speciation rates (rate when the lineage is in state 0; rate when in state 1), two extinction rates (when in state 0; when in state 1), and two rates of character state change (from 0 to 1, and from 1 to 0). Using these probability calculations, we can do maximum likelihood inference to estimate the model's parameters and perform hypothesis tests (e.g., is the rate of speciation elevated for one character state over the other?). We demonstrate the application of the method using simulated data with known parameter values. [Birth-death process; branching process; cladogenesis; extinction; key innovation; macroevolution; phylogeny; speciation; speciose; statistical inference.]





Species Selection Maintains Self-Incompatibility

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Identifying traits that affect rates of speciation and extinction and, hence, explain differences in species diversity among clades is a major goal of evolutionary biology. Detecting such traits is especially difficult when they undergo frequent transitions between states. Self-incompatibility, the ability of hermaphrodites to enforce outcrossing, is frequently lost in flowering plants, enabling self-fertilization. We show, however, that in the nightshade plant family (Solanaceae), species with functional self-incompatibility diversify at a significantly higher rate than those without it. The apparent short-term advantages of potentially self-fertilizing individuals are therefore offset by strong species selection, which favors obligate outcrossing.

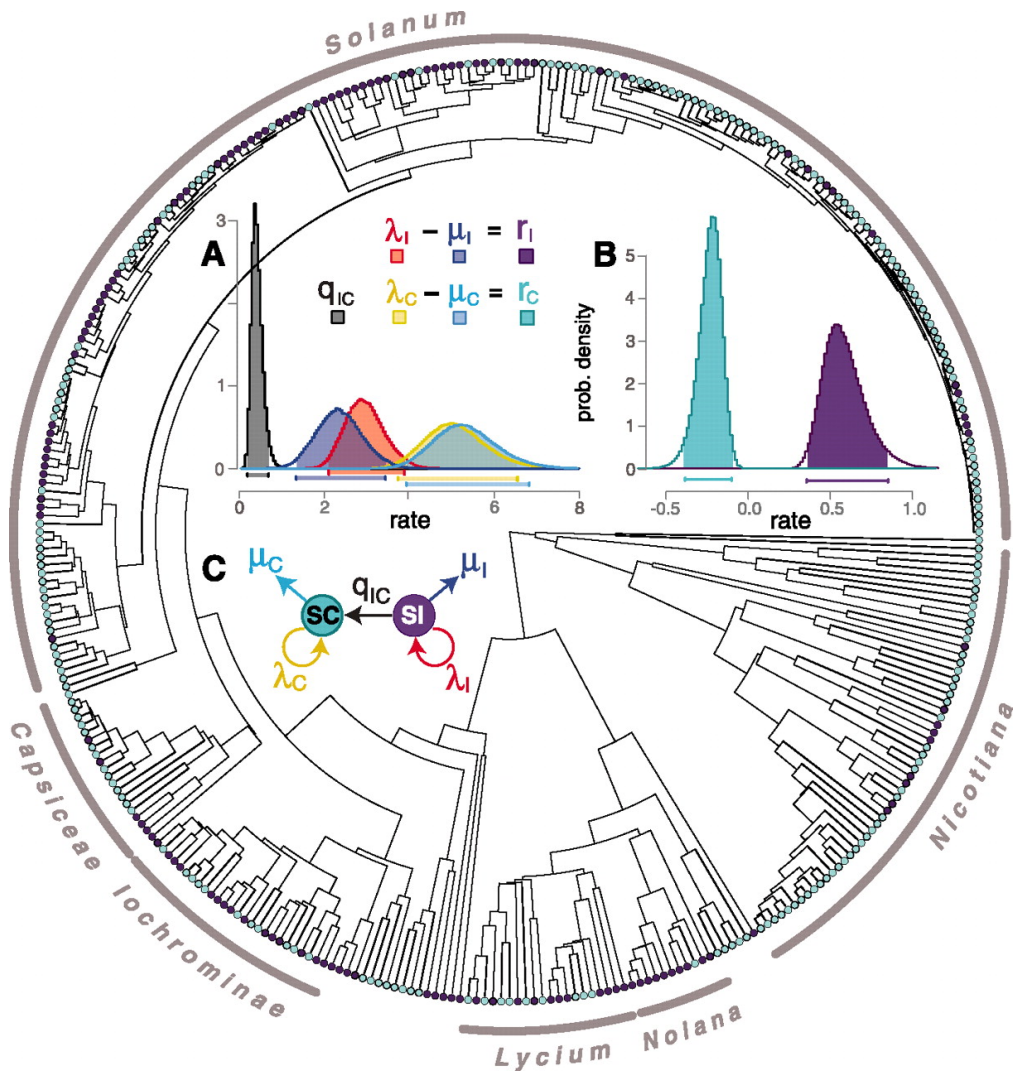


Fig. 1: Maximum likelihood tree of phylogenetic relationships among 356 species of Solanaceae. Higher ranks are indicated around the perimeter of the tree. Purple and turquoise tip colors denote SI and SC extant species, respectively. The root age is 36 million years. Inset panels display posterior probability distributions and 95% credibility intervals of reconstructed rates of character evolution (the time unit is millions of years). (A) BiSSE estimates of transition, speciation, and extinction parameters ($q_{IC} \ll \mu_I < \lambda_I \ll \lambda_C < \mu_C$). (B) Net diversification rate—the difference between speciation and extinction rates—associated with each state. (C) Schematic summary of estimated rate parameters. For methods, species names, character states, and further results, see (19).