# Breeding System Distribution in the Legumes

Lucy E. Delaney, Karolis Ramanauskas, and Boris Igić
Department of Biological Sciences, University of Illinois at Chicago

## Introduction

Despite the prevalence of hermaphroditism in angiosperms, nearly half are self-incompatible (SI)—they cannot set seed from their own pollen.

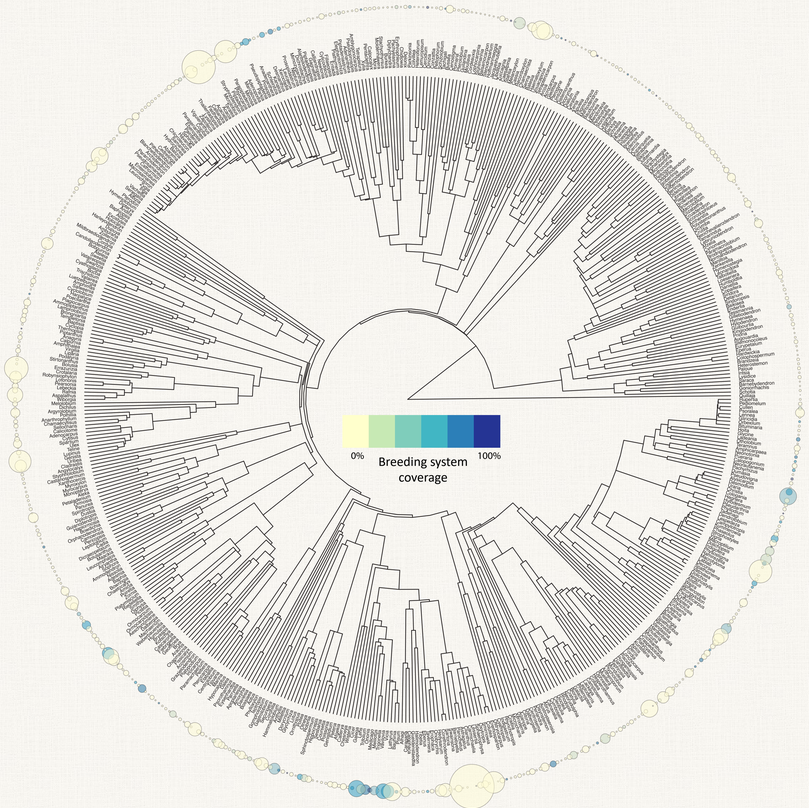
While many independently-evolved molecular mechanisms underpin self-incompatibility across flowering plants, they share some important features, including a key role in shaping the genetic structure of populations and frequent transitions to self-compatibility (SC).

Gains and persistence of many such mechanisms suggest a strong role of natural selection, but how this role ultimately shapes patterns of plant diversity is still an open question. Surprisingly little is known about the distribution of SI systems and their genetic and molecular bases in some of the largest angiosperm families, limiting the potential to answer questions about how and why these systems evolve and inform expectations for future study.

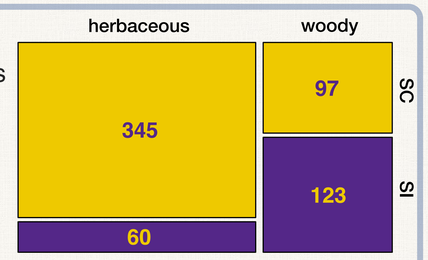
Here, we present a preliminary analysis of the distribution of breeding systems in Fabaceae (Leguminosae).

## Methods

- Conduct a wide literature survey for recorded information on breeding systems and other traits of interest (chromosome counts, life history traits)
- Verify data quality (e.g. reported crosses vs. unverified claims) and discard or assign quality scores to each entry
- Score data from pollination experiments with selfed and outcrossed fruit set to calculate Index of Self-incompatibility (ISI)
- Synonymize species names for all binomials in trait and phylogenetic datasets and collate (when multiple studies performed on the same species)
- Map phylogenetic distribution of breeding systems within the family and calculate summary statistics. (No *SSE or other reconstructions performed—low coverage and unclear if trait data are homologous.)




The negative correlation between selfing and size of an adult plant has long been recognized [2]. Several hypotheses have sought to explain it, often focusing on the effects of inbreeding depression in large-statured plants [5].

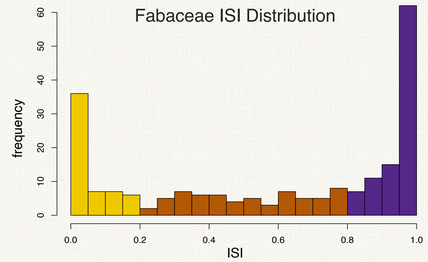



Below, we show the distribution of woody stem composition and SI across the family. This relationship was noted by Arroyo [1], leading her to suggest the overall trend from woody and SI to herbaceous and SC still observed in the family.


## Results

The above phylogeny [6] shows the coverage of breeding system data by indicating genus-level sampling, as well as the size of each genus.

The family shows an uneven distribution of SI from, for example, high SI and woody stem composition in the Caesalpinioid clade to the opposite pattern in Papilionoids. ISI distribution is largely bimodal, as in other angiosperms [4].




| | Caesalpinioideae | Cercidoideae | Detarioideae | Dialioideae | Papilionoideae |
|---|---|---|---|---|---|
| *Ambiguous* | 2 | 0 | 0 | 0 | 25 |
| *Dichogamy* | 0 | 0 | 0 | 0 | 1 |
| *Dioecy* | 8 | 0 | 0 | 0 | 0 |
| *Heterostyly* | 2 | 0 | 0 | 0 | 0 |
| *Self–compatibility* | 98 | 3 | 1 | 2 | 614 |
| *Self–incompatibility* | 100 | 8 | 2 | 1 | 123 |

## The Legumes

Fabaceae are comprised of three large subfamilies, characterized by notable differences in growth habit and floral morphology, including trends towards increasingly specialized pollinators (but see LPWG 2017 [ref. 3] for updated classifications). Previous work has indicated the presence of a gametophytic SI system, where rejection is determined by the haploid genotype of the pollen parent. It remains unclear whether this is the same GSI system found in the closely-related Rosaceae.

Caesalpinioideae

Mimosoideae

Papilionoideae

## Citations

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