



Supporting Online Material for

Plant Speciation

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Supporting Material

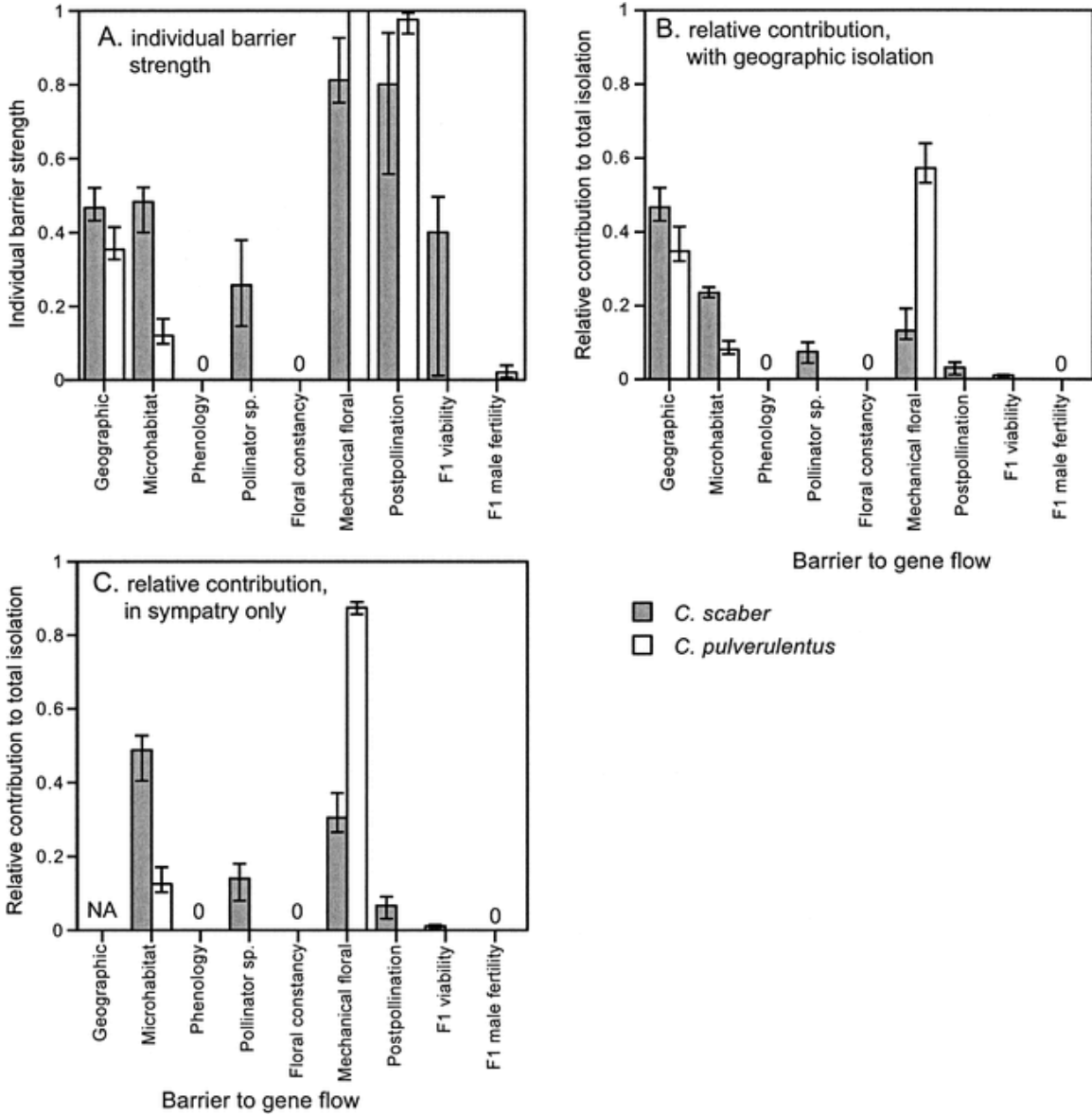


Fig. S1 Components of reproductive isolation calculated separately for two hummingbird-pollinated neotropical species of ginger (*Costus*). Total reproductive isolation was calculated as the product of individual reproductive barriers. The strength of isolation for each barrier was estimated independently, and the absolute contribution of that barrier is the proportional reduction in gene flow not eliminated by earlier acting barriers. **(A)** The strengths of individual isolating mechanisms calculated separately. **(B)** The relative contribution of each mechanism to total reproductive isolation, including geographic isolation. **(C)** The relative contribution of each mechanism in sympatry, without geographic isolation. All error bars represent 95% confidence intervals of the means. Reproduced with permission from (S11).

Table S1. Studies of plant speciation that support points made in the text.

Topic	Taxa studied	Conclusions	Ref.
Adaptive radiation	Hawaiian silversword alliance	The 28 Hawaiian-endemic species in silversword alliance include trees, shrubs, mat-plants, rosette plants, cushion plants, and vines; all have arisen in past 5.2 million years	S1
	Andean <i>Lupinus</i>	Eighty species have arisen in last 1.2-1.8 Myr. Life forms include trees, shrubs, prostrate perennial herbs, annual herbs, and rosettes	S2
Asexual taxa	<i>Antennaria</i> , <i>Crataegus</i> , <i>Poa</i>	Hybrid asexual taxa blur distinctness of otherwise discrete sexual species	S3-5
Interspecific gene flow	<i>Helianthus annuus</i> × <i>H. petiolaris</i>	Interspecific gene flow detected across much of genome despite strong intrinsic postzygotic barriers	S6
	<i>Populus fremontii</i> × <i>P. angustifolia</i>	Most of genome prohibited from introgression, but some markers introgressed over large geographic distances	S7
	<i>Iris fulva</i> × <i>I. hexagona</i>	Introgression confirmed by detection of markers from alternate species in allopatric populations	S8
Complete estimates of reproductive isolation	<i>Mimulus lewisii</i> and <i>M. cardinalis</i>	Ecogeographic and pollinator isolation contribute most to total isolation, despite substantial postzygotic barriers	S9
	<i>Mimulus guttatus</i> and <i>M. nasutus</i>	Mating system isolation most important reproductive barrier, despite very strong intrinsic postzygotic barriers	S10
	<i>Costus pulverulentus</i> and <i>C. scaber</i>	Ecogeographic and pollinator isolation contribute most to total isolation. Hybrids fertile but exhibit reduced viability	S11
	Diploid and tetraploid <i>Chamerion angustifolium</i>	Ecogeographic and pollinator isolation contribute most to total isolation, despite very strong intrinsic postzygotic barrier	S12
Ecological barriers arise first	<i>Wikstroemia</i> , <i>Schiedea</i> , <i>Tetramolopium</i>	Ecological isolation precedes evolution of intrinsic reproductive barriers	S13-16
Ecogeographic isolation	<i>Mimulus lewisii</i> and <i>M. cardinalis</i>	Both species exhibit greatest fitness at elevations central within range, reduced fitness at range margin, and near-zero fitness beyond present range limits	S17

	<i>Iris douglasiana</i> and <i>Iris innominata</i>	Each species survives best in own habitat. Additional differences in perianth-tube length and flowering time not developed into significant isolating factors	S18
Intrinsic postzygotic barriers arise first	<i>Ranunculus adoneus</i>	Autotetraploid species intersterile with diploid progenitor, but not ecologically differentiated	S19-20
Contemporary evolution: speciation in action	<i>Anthoxanthum odoratum</i>	Populations experiencing different fertilizer treatments now partially isolated due to shifts in flowering time and differential survivorship	S21-22
	<i>Agrostis tenuis</i> and <i>Anthoxanthum odoratum</i>	Populations of both species that occur on mine tailings and adjacent non-toxic pasture have diverged in flowering time	S23-24
Reinforcement	<i>Phlox</i>	Selection against unfit hybrids stimulus for divergence in floral color in sympatric populations of several species	S25-26
	<i>Gilia</i>	Sympatric species less cross-compatible than allopatric species, apparently due to selection against sterile hybrids	S27
	<i>Geraniaceae</i> , <i>Iridaceae</i> , <i>Orchidaceae</i>	Pollination system shifts in 41 pairs of sister taxa associated with edapic shifts in sympatric, but not allopatric pairs	S28
Sympatric Speciation	<i>Stephanomeria malheurensis</i>	Geographically restricted selfing species sympatric with widespread, outcrossing progenitor. Reproductive isolation maintained by differences in mating system and karyotype	S29
	<i>Howea belmoreana</i> and <i>H. forsteriana</i>	Sister species diverged on small oceanic island where geographic isolation unlikely, but island larger earlier in its ontogeny, possibly providing spatial separation	S30-31
	<i>Tolmiea menziesii</i>	Well-studied example of autopoloidy. Polyploidy most common type of sympatric speciation in plants	S32
Genetic studies of pollination syndromes	<i>Mimulus lewisii</i> and <i>M. cardinalis</i>	Nine of 12 floral traits differentiating species controlled by at least one major QTL (> 25% phenotypic variance explained)	S33
	<i>Petunia axillaris</i> and <i>P. integrifolia</i>	QTLs explaining > 30% of phenotypic variance underlie floral trait differences, but QTL magnitudes overestimated because of skewed phenotypic distribution in mapping population.	S34
	<i>Antirrhinum majus striatum</i> and	Major loci control flower color variation in wild snapdragon	S35-37

	<i>A. m. pseudomajus</i>	species. High-fitness ridge in floral-color adaptive landscape appears to connect color morphs, although possibility each morph adapted to own local environment not ruled out	
Genetics of mating system isolation	<i>Mimulus nasutus</i> and <i>M. guttatus</i>	Average of 13 QTLs detected for six floral traits, indicating polygenic basis for mating system isolation	S38
	<i>Leptosiphon bicolor</i> and <i>L. jepsonii</i>	Moderate effect size of QTLs underlying mating system isolation between <i>Leptosiphon</i> species	S39
Genetics of habitat isolation	<i>Silene vulgaris</i>	Serpentine adaptation controlled by major genes that have evolved under directional selection	S40
	<i>Helianthus paradoxus</i>	QTLs minimizing uptake of toxic mineral ions in salt marsh habitat of hybrid sunflower favored strongly enough to allow speciation in presence of gene flow	S41
	<i>Iris fulva</i> and <i>I. brevicaulis</i>	Major QTL from dry-adapted <i>I. brevicaulis</i> increases survivorship in flooded conditions favored by <i>I. fulva</i> .	S42
	<i>Mimulus guttatus</i>	Hybrid inviability associated with locus conferring tolerance to heavy metals, indicating hybrid incompatibilities may arise as byproduct of selection for habitat isolation.	S43
Self-incompatibility mechanisms	<i>Nicotiana</i>	Crosses among self-compatible species no longer succeed after transformation with S-RNase gene from self-incompatible species	S44
	<i>Lycopersicon</i>	One of three QTLs contributing interspecific incompatibility in tomato maps to S-locus	S45
	<i>Arabidopsis</i>	Glycine-rich oleosin proteins contributing to pollen coat proteome evolve rapidly due to positive selection	S46
Chromosomal rearrangements	<i>Helianthus annuus</i> and <i>H. petiolaris</i>	Nine of 11 hybrid sterility QTLs map to chromosomal breakpoints	S47
	Mediterranean orchids	Sympatric species pairs that share pollinators karyotypically more divergent than pairs with different pollinators	S48
BDM incompatibilities	<i>Lycopersicon hirsutum</i> and <i>L. esculentum</i>	Of 13 genomic regions associated with hybrid incompatibilities, four affect both male and female fertility,	S49

		five affect male fertility only, and four affect female fertility only	
	<i>Mimulus guttatus</i>	Widespread polymorphism of interacting alleles at loci underlying two distinct systems of hybrid lethality	S50
	<i>Mimulus nasutus</i> and <i>M. guttatus</i>	Hybrid sterility maps to two interacting loci, with the incompatibility allele at <i>hybrid male sterility 1</i> locus extremely restricted geographically	S51-52
Homoploid hybrid speciation	<i>Senecio squalidus</i>	New homoploid hybrid species arose in British Isles, following long-distance dispersal of hybrid material from hybrid zone on Mount Etna, Sicily, Italy	S53
	<i>Argyranthemum sundingii</i>	Multiply derived hybrid species occurs in ecologically intermediate habitat opened by deforestation following local hybridization in two valleys	S54
	<i>Helianthus anomalus</i> , <i>H. deserticola</i> , <i>H. paradoxus</i>	Greater than 50% increase in genome content in homoploid hybrid species due to proliferation of mobile genetic elements	S55
Polyploid speciation	<i>Asplenium</i>	Two allotetraploid species originated more than once	S56
	<i>Brassica napus</i>	Chromosomal rearrangement following polyploidization responsible for flowering time divergence among synthetic polyploid lineages	S57
	<i>Aegilops</i> and <i>Triticum</i>	Allopolyploidy-induced sequence elimination may restore diploid-like meiotic behavior of newly formed allopolyploids	S58
	<i>Senecio cambrensis</i>	Changes in gene expression following interspecific hybridization ameliorated by genome duplication	S59
Factors affecting species richness	Angiosperms	Bilaterally symmetric lineages more species rich than radially symmetrical sister lineages	S60
	Bulbophyllinae (Orchidaceae)	Twig epiphytism associated with species richness	S61
	Rosaceae	Polyploidy associated with species richness	S62
	Flowering plants	Environmental energy (evapotranspiration, temperature and UV radiation) associated with species richness	S63

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