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Giant leaps, not small steps

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The interplay between genes and the environment results in [adaptive evolution](#). Evolution of [biomolecules](#) was thought to occur by single, minor changes in the DNA sequence resulting in a gradual shift in function until a substantive change is selected for, but calculations of the time required for this to occur sometimes resulted in estimates longer than the age of the Earth. Current thinking suggests single changes causing major phenotypic effects to be at the root of adaptive evolution. In the November 13 [Nature](#), H.D. Bradshaw and Douglas Schemske at the [University of Washington](#) report the breeding of near-isogenic lines (NILs) of the *Mimulus* flower by backcrossing two species pollinated by two different means - one by the honeybee and the other by the hummingbird - so that a gene controlling flower color from one species was substituted into the other. Their analysis showed that the effective swapping of the flower color allele also resulted in the swapping of the pollinator, strongly suggesting that a single major mutation can cause an adaptive shift in response to a change in environment in plants in particular, with implications for adaptive evolution in general (*Nature* 2003, **426**:176-178).

Bradshaw and Schemske had previously shown that flower color controlled by the quantitative trait locus (QTL) *YELLOW UPPER (YUP)* in the two *Mimulus* species, *M. lewisii* and *M. cardinalis*, affected pollinator visitation. Repeated backcrosses resulted in NILs that closely mimicked the effect of a single major mutation in the *YUP* allele. Pollinator visitation rates were observed in the field, and comparison showed that the wildtype pink *M. lewisii* flower attracted >700 times more bees than hummingbirds, whereas the swapped 'mutant' only attracted 1.8 times more bees. In contrast, the wildtype red *M. cardinalis* attracted 1200 times more hummingbirds than bees, and the swapped 'mutant' only drew 15 times more. Results obtained from this study compared well with results obtained from a previous F₂ QTL mapping population study, suggesting that the two means are able to answer the same question.

"To understand in greater detail the dynamics of an adaptive pollinator shift, it will be necessary to more closely replicate the appearance of a new mutation... In addition, NILs could be developed carrying 1, 2,...*N* allele substitutions at major QTLs, in various combinations, to test alternative hypotheses for the trajectory of floral evolution and speciation in response to pollinator choice," the authors conclude.

References

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