

SPECIATION

Together apart

However choosy you are about who you mate with, it is unlikely that any mistake will have an appreciable impact on the course of human evolution. In the same situation, a female *Drosophila pseudoobscura* has a more onerous decision to take. Because this species coexists in some regions with the related *Drosophila persimilis*, and mating between the two gives rise to sterile males, the female's decision makes the difference between propagating the line and an evolutionary dead end. The genetics of reproductive isolation between the two species is well known; now, Daniel Ortiz-Barrientos and colleagues reveal how this behavioural discrimination is strengthened by natural selection. Their high-resolution genetic analysis is the first to examine the nitty gritty of the final stages of speciation, so filling one of several experimental gaps in the study of adaptation.

D. persimilis and *D. pseudoobscura* mate in the wild but, because of the sterility of the male offspring, females of both species (but not males) select mates primarily from their own species. How is this behaviour

reinforced by natural selection, such that the discriminatory mating behaviour survives in the face of gene flow? *D. pseudoobscura* females sampled from regions in which the two fly species overlap (in 'sympatry') are much choosier than those that do not live alongside *D. persimilis* (in 'allopatry'), and the authors show that this 'reinforced mating discrimination' trait is inherited from the female in a dominant manner. Backcrossing the progeny of a sympatric × allopatric cross into an allopatric background identified strong candidate regions for the trait on the X and fourth chromosomes, which were mapped in more detail to three QTL intervals by using 70 microsatellite markers. One of the candidate regions contains as few as five genes, and both the *D. pseudoobscura* genome sequence and information from *Drosophila melanogaster* mutants indicate the involvement of the olfactory response.

As with many studies of adaptation, theories abound over experiments. An exciting aspect of the work was to find that the genetic architecture of reinforcement traits within species differs from the basal level of mating discrimination seen between species, which is what some theories would predict.

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 **References and links**

ORIGINAL RESEARCH PAPER Ortiz-Barrientos, D. *et al.* The genetics of speciation by reinforcement. *PLoS Biol.* **2**, e416 (2004)

FURTHER READING

Coyne, J. A. & Orr, H. A. *Speciation* (Sinauer Associates Inc., Sunderland, Massachusetts, 2004)

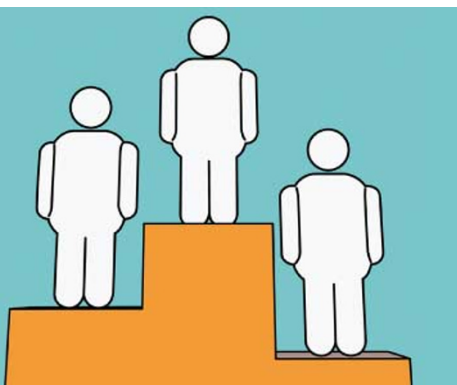
WEB SITE

Mohamed Noor's laboratory:

<http://www.biology.lsu.edu/webfac/mnoor/Noorlab.html>

FUNCTIONAL GENOMICS

A comparative success



Assigning a biological function to a string of DNA bases is the hardest and arguably the most important part of any genome-sequencing effort, as without knowing where genes are, we cannot say anything about their biological importance and evolutionary history. Tried and tested methods for genome annotation have their merits, but there is ample scope for developing new

approaches. Dario Boffelli and colleagues have now successfully risen to this challenge: by using the sea squirt *Ciona intestinalis*, they show that intraspecies sequence comparisons can be effective for identifying functional sequences — and that other organisms, including humans, might also benefit from the same strategy.

The most effective means of annotating genomes has been to compare the sequences among organisms at varying evolutionary distances, on the premise that less divergent sequences will be functionally important. However, using different species restricts the analysis to genes that are common to the species compared. Intraspecies comparisons have always posed a theoretical way out of this limitation, but until now, the high costs of sequencing many individuals prevented this method from being put into practice. However, with resequencing costs now becoming ever cheaper, it remains only to decide where to start.

Boffelli and colleagues settled on *C. intestinalis*, an excellent experimental system that also benefits from a high level of allelic polymorphism and a sequenced genome. The authors collected 140 individuals from 4 locations around the world, then using PCR, they amplified 4 defined stretches of coding and 5' upstream sequences (a total of ~16 kb) from

each organism. Although sequences were not obtained from all individuals, those that were available were used to infer the phylogenetic relationships, both among the four geographical populations and within the individuals collected at each location.

Crucially, the same intra-population sequence comparisons also told the authors which nucleotide sites were mutating more slowly than others, and these were then used to detect functional DNA regions. Several exons of *collagen* and *patched* were predicted in this way. 5' gene-control elements — five for the *forkhead* and two for the *snail* developmental genes — were also predicted computationally, and then verified by using *in vivo* reporter studies.

Intraspecies comparisons are unlikely to supplant the more conventional interspecies approaches. However, they come into their own when investigating species-specific sequences (including those that occur in humans), new species or those that lack relatives at a convenient phylogenetic distance.

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 **References and links**

ORIGINAL RESEARCH PAPER Boffelli, D. *et al.* Intraspecies sequence comparisons for annotating genomes. *Genome Res.* **15** November 2004 (doi:10.1101/gr.3199704)

WEB SITE

Eddy Rubin's laboratory: <http://www-gsd.lbl.gov/rubin>