tal approaches of developmental biology to the study of variation between closely related species. Developmental biologists typically work out the normal function of genes by examining the physical consequences of experimentally induced mutations within those genes. Evolutionary geneticists, by comparison, focus on the natural genetic variation found within and between species. Natural genetic variation normally causes more subtle phenotypic differences than the mutations studied in developmental biology. But it is becoming clear that researchers in these two fields have been studying different kinds of variation at the same genes[5–8].

The work of Kopp *et al.*[1] illustrates how developmental biology can help to identify the source of heritable phenotypic variations. The authors have used a model experimental organism — *D. melanogaster* — to gain a detailed genetic understanding of a phenotypic trait that varies between fruitfly species, and have determined whether variations in this gene between species correlate with phenotypic variations.

Kopp *et al.* first show that differential regulation of the *bric-a-brac* (*bab*) gene, which codes for a putative transcription factor, is required for the development of the sex-specific abdominal pigmentation patterns in *D. melanogaster*. In females, *bab* is expressed in all abdominal segments, repressing pigmentation. In males, *bab* is not expressed in the most posterior segments, leading to pigmented posterior abdomens (see Fig. 1 on page 553). The authors discovered that the *bab* gene integrates inputs from the sex-determination pathway, which limits repression of *bab* to males, and from the Hox genes, which limit *bab* repression to the posterior abdominal segments.

The authors then show that this sexually 'dimorphic' regulation of *bab* sometimes correlates with sex-specific pigmentation patterns in other *Drosophila* species. The implication is that the evolution of the regulation of *bab* was important in the evolution of this sexually dimorphic feature. However, in some species of the *montium* subgroup, *bab* is repressed in the posterior abdominal segments of males even though the species do not have sex-specific pigmentation. So, the genetic circuitry linking *bab* to pigmentation has also evolved, presumably as a result of alterations in the regulatory regions of genes downstream of *bab*. This link was probably either lost in the *montium* subgroup, or gained in the other subgroups.

Kopp *et al.* also examined other sexually dimorphic characteristics in *D. melanogaster*, such as the shape of abdominal segments and the patterns of bristles and of small projections of the cuticle called trichomes. They find that sexual dimorphism in these features also depends on the regulation of *bab*. In addition, in those species most closely related to *D. melanogaster*, male-specific expression of these characters correlates with the repression of *bab*. In contrast, species of the *ananassae* and *montium* subgroups have diverse bristle and trichome patterns that vary independently of *bab* expression patterns. In these lineages, there may have been evolutionary changes in unidentified genes that in *D. melanogaster* are regulated by *bab*, the sex-determination pathway and the Hox genes.

Finally, the authors have investigated the role of pigmentation patterns in sexual behaviour. They find that *D. melanogaster* females do not prefer males with a normal pigmentation pattern over males with a mutant, unpigmented posterior abdomen. Males, however, do discriminate against females with a 'male' pigmentation pattern. So males — but not females — may use pigmentation cues to discriminate between the sexes. Kopp *et al.*'s use of mutations within *D. melanogaster* to study sexual behaviour is innovative, and potentially links selection acting on mating systems to the molecular mechanisms underlying phenotypic evolution. But it is not yet clear whether these results are relevant to sexual behaviour in flies with natural variations in pigmentation.

This difference between the variation generated in the lab and that seen in natural populations illustrates one historical difference between developmental and evolutionary biology[9]. But Kopp *et al.*'s work[1] shows how these two fields can be brought closer together. No doubt more progress will come from further recognition that both fields are interested in studying the same genes, and from the identification of the specific genetic changes that cause natural phenotypic variations. ■

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Nanotechnology

Pinning on impact

When it comes to investigating phenomena at the nanometre scale, clusters are all the rage. These are minute particles, containing anything from tens of atoms to a few thousand, which exhibit size-dependent electrical, optical, catalytic and mechanical properties.

To study the behaviour of clusters, so-called 'nanoislands' — isolated clusters of nanometre dimensions on a supporting substrate — are often used. One approach is to form the clusters in a gas phase and then deposit them on the substrate. The trouble is getting the resulting nanoislands to stick. R. E. Palmer and colleagues have looked into the problem of pinning them down and have devised a system that involves smashing clusters of silver into a graphite substrate (*J. Chem. Phys.* **113,** 7723–7727; 2000).

Palmer's group use a beam of charged and size-selected silver clusters, accelerated in an electric field and directed onto the graphite surface. The simulation snapshots shown here illustrate the process for a silver cluster containing 147 atoms. When accelerated in an electric field to an energy of 1,500 electron volts (**a**), the cluster simply flattens on impact without penetrating the graphite surface. But at 2,000 electron volts (**b**), the cluster disrupts the carbon lattice of the graphite, and silver atoms implant into the surface. The onset of pinning — defined as one or more carbon atoms being displaced from their lattice site — occurs between 1,625 and 1,750 electron volts.

Similar behaviour is observed with clusters of 50 to 200 atoms in both molecular dynamics simulations and experiments using scanning tunnelling microscopy. The pinning threshold increases linearly with cluster size, suggesting that the energy required to remove one carbon atom from the lattice is transferred in the initial elastic collision. Pinning through the creation of defects beneath the incident cluster is particularly effective in this system; whether the approach might be applied to creating practically useful nanostructures remains to be seen. **Magdalena Helmer**