

WEB WATCH

Reactome

• <http://www.reactome.org/>
Not so long ago, anything you needed to know about the molecular interactions that took place in living systems could be found between the covers of *Molecular Biology of the Cell*. Now, with thousands of proteins and other metabolites continually being described, biologists need access to a comprehensive, up-to-date and accessible representation of cellular pathways. Reactome — a curated online database of human biological pathways that was released on 2nd June, 2004 — has been created to fulfil that need.

Jointly funded by Cold Spring Harbor Laboratory and the EMBL (European Molecular Biology Laboratory) European Bioinformatics Institute (EBI), Reactome, a swanky reincarnation of The Genome Knowledgebase, provides a clear, integrated view of many core cellular pathways and reactions. Along with a description of the selected process — the mitotic cycle, say — is a diagram of the pathway and links through to all the molecules (not only human ones) known to participate in it. You can decide between viewing the entire process or any of its subcategories (the G1 phase, for example). The site is easy to navigate and the 'starry sky' representation of each molecular reaction highlights links between pathways.

Named experts contribute the information, which is peer-reviewed and cross-referenced to several literature and biological databases, including Gene Ontology (GO). The data are searchable, citable and free. Reactome is therefore more than just an online textbook and it aptly responds to the current desire for a 'systems biology' view of molecular life.

Releases will occur quarterly, and will probably include additional processes and an expansion of its repertoire of interactions to include intercellular pathways.

Tanita Casci

POPULATION GENETICS

A breed apart

Long before humans got too lazy to fetch their own slippers, they were shaping the appearance and behaviour of dogs to suit their taste and practical requirements. Until recently, assigning a dog to one of the 150-or-so breeds that we have today depended on having a trained eye or a catalogue of each breed's vital statistics. Now, Heidi Parker and colleagues have shown that genetic information can be just as reliable — not only for telling breeds apart, but also for describing their genetic history.

Dog breeding is serious business and the strict standards imposed by kennel clubs mean that the gene pools of different breeds never mix. This is a boon to geneticists, who can use genetic markers to define the structure of dog populations and, from a medical perspective, to find the genes that underlie canine models of human disease.

Parker and colleagues concentrated on 85 domestic dog breeds, and genotyped 414 dogs at 96 microsatellite loci — these being the most useful genetic markers for characterizing recent populations. The history of genetic isolation among breeds showed up clearly in the analysis: dogs within breeds were genetically much more similar than dogs from different breeds. Indeed, 30% of total variation is accounted for by among-breed differences, which is among the highest of all domestic animals. This strong genetic differentiation allowed breed membership to be predicted from the dog genotype: with the exception of four breeds, dogs were consistently assigned to the same breed when they were clustered on the basis of similar microsatellite genotype (using the Structure statistical program). Microsatellite data also assigned each dog to its own breed in 99% of cases.

Having established the genetic pattern of modern breeds, the authors turned to some phylogenetic history. Using the



wolf to root the tree, a combination of the neighbour-joining method and the Structure algorithm was used to reconstruct the genetic relationship among breeds. Four main clusters appeared: an ancient one corresponding to a mixture of African and Asian breeds, and three more modern clusters of European origin that each contained breeds of similar morphology and behaviour. As well as confirming genetically what our eyes and historical records had already suspected, this study also reminds us to be wary of judging by appearances. For example, modern-day Norwegian Elkhounds, which were thought to be direct descendants of Arctic breeds that existed 5,000 years ago, have in fact been recreated more recently from more modern breeds.

Dog breeding is an ongoing evolutionary experiment that we can use to our advantage, and knowing the dog's population-genetic structure makes it simpler to map important dog genes — whether it be those that underlie the 350 inherited models of human disorders or those that make the Pekingeses 50 times lighter than the Irish Wolfhound.

Tanita Casci

 **References and links**

ORIGINAL RESEARCH PAPER Parker, H. G. *et al.* Genetic structure of the purebred domestic dog. *Science* **304**, 1160–1164 (2004)

WEB SITES

Dog Genome Project:
<http://mendel.berkeley.edu/dog.html>

Elaïne Ostrander's laboratory:
<http://www.gs.washington.edu/faculty/ostrander.htm>

Leonid Kruglyak's laboratory:
<http://www.fhrc.org/labs/kruglyak/>