EVOLUTION

Equus — how it all began

> "There is nothing so good for the inside of a man as the outside of a horse!"
>
> *Mark Twain*

For several thousand years, the destinies of horses and humans have been inextricably linked. In transport, nutrition, warfare and sport, the horse has played its part. But how did the relationship begin? Was the horse domesticated just once, or many times, and from how many founders did the modern breeds of horse descend? Some valuable insights into these questions have been provided in a population genetics study by Vilà and colleagues.

The authors assessed the variation in mitochondrial DNA (mtDNA) from modern horse breeds and compared this with mtDNA from the remains of wild horses dating back 12,000–28,000 years. They then used phylogenetic methods to analyse the data, and to make inferences about the evolutionary origins of modern breeds. The genetic data indicate that modern breeds are genetically highly diverse, and can be divided into distinct clades — groups of animals or breeds descended from a single ancestor. By estimating the rate of sequence divergence, the origin of the clades can be dated at over 100,000 years ago.

However, according to archaeological evidence, the horse was domesticated around 6,000 years ago in a broad region of the Eurasian Steppe, where wild horses would have been captured and selectively bred for desirable characteristics. The diversity found in the genetic analysis can be explained if there were many genetically diverse founders of modern horses, implying that domestication occurred independently on multiple occasions at this time.

Using data from microsatellite markers, the authors suggest that females have contributed more to the genetic diversity of horse breeds than males, perhaps because of a bias towards females in trade and breeding. This is consistent with traditional breeding practices in which a single male is bred with multiple females.

The picture that emerges from the combination of genetic and archaeological data is that, around 6,000 years ago, the technical know-how required for the domestication of horses spread rapidly from one region to the next. Founders would have been captured and bred by communities in different regions, thus accounting for the genetic diversity seen in modern horses, and initiating a relationship that has lasted to the present day.

Mark Patterson

References and links

ORIGINAL RESEARCH PAPER Vilà, C. *et al.* Widespread origins of domestic horse lineages. *Science* **291**, 474–477 (2001)
FURTHER READING Pennisi, E. Horses domesticated multiple times. *Science* **291**, 412 (2001)
WEB SITE Hans Ellegren's lab | Horse genome project

IN BRIEF

MULTIFACTORIAL GENETICS

Genetic mapping of quantitative trait loci governing longevity of *Caenorhabditis elegans* in recombination-inbred progeny of a Bergerac-BO x RC301 interstrain cross.

Ayyadevara, S. *et al. Genetics* **157**, 655–666 (2001)

This paper goes some way towards uncovering the natural polymorphisms that contribute to variation in longevity between two worm strains, *C. elegans* RC301 and Bergerac-BO. Seven highly significant quantitative trait loci (QTL) were identified from the progeny of these two strains, which were tested for QTL associations with lifespan after seven generations of inbreeding. All seven loci, which were identified using single-marker analysis, were confirmed and mapped more precisely by nonparametric interval mapping. Furthermore, making animals that were congenic for two candidate QTL had a significant impact on their survival.

CANCER GENETICS

A candidate prostate cancer susceptibility gene at chromosome 17p.

Tavitagan, S. V. *et al. Nature Genet.* **27**, 172–180 (2001)

Pten and p27KIP1 cooperate in prostate cancer tumor suppression in the mouse.

Di Cristafano, A. *et al. Nature Genet.* **27**, 222–224 (2001)

Previous mapping studies have failed to reveal highly penetrant alleles to account for prostate cancer in high-risk families. But now Tavitagan *et al.* report the cloning of a putative prostate cancer susceptibility gene, *ELAC2*, from a genome-wide screen of several such families. This screen led to a locus on chromosome 17p, from which the researchers positionally cloned *ELAC2*. Mutation analysis identified a frameshift and a non-conservative substitution in *ELAC2* in two independent prostate cancer families, but the gene's association with the disease was not clear cut — not all male family members with the frameshift mutation have prostate cancer and the substitution was present in some but not all individuals with the disease. Whether these non-carriers are sporadic cases remains to be resolved, as does the role of *ELAC2* in DNA repair and prostate cancer susceptibility. In the second paper, Di Cristafano *et al.* report on the cooperation between Pten and one of its targets, p27KIP1 (encoded by *Cdkn1b*), in suppressing prostate cancer. $Pten^{+/-}$ mice die of cancer by ~51 weeks of age. This survival rate rapidly decreases with the loss of one or both alleles of *Cdkn1b*. By the age of three months, all $Pten^{+/-}/Cdkn1b^{-/-}$ mice develop prostate cancer that histologically and pathologically resembles the human disease. Cell proliferation, but not cell survival, is increased in these mice, indicating that Pten and p27KIP1 cooperate to suppress tumour formation through the control of cell-cycle progression.