

Canine genome sequence is completed

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Harvard scientists say they have finished compiling the genome sequence of the dog -- *Canis familiaris*.

The accomplishment brings researchers a step closer to identifying differences among breeds, and potentially providing insight into the genetic causes of common mammalian diseases.

Researchers said the genomic data was supplied by Tasha, a female Boxer -- a breed nominated by breeding clubs and veterinary schools as the most inbred dog in the world.

Scientists said Tasha's high level of inbreeding means she has fewer differences between her chromosome pairs, allowing for quicker and easier sequencing.

Geneticists led by Harvard University's Kerstin Lindblad-Toh sequenced the 2.4 billion letters of the dog's DNA, representing 39 chromosome pairs. Since she is a female, researchers did not get any Y-chromosome data.

The researchers took DNA samples from 10 other breeds in an effort to spot genetic differences among them. They also compiled a catalogue of 2.5 million "single-nucleotide polymorphisms" -- sites where single-letter changes occur in the DNA sequence. That is aimed at helping identify the mechanisms underlying complex traits, such as behavior, as well as congenital diseases.

The research appears in this week's issue of the journal Nature.

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