

Researchers Decode DNA of Dogs

Genome sequence analysis could help eradicate disease and improve health in purebred dogs.

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Breakthroughs in the mapping of the canine genome will help researchers understand and intervene in many genetic diseases canine and human. A detailed analysis of the canine genome published by an international team of researchers describes the potential for improving health and eradicating disease in the future.

Researchers, who sequenced 99 percent of the genome of a female boxer named Tasha, also examined the DNA from 10 different dog breeds and other related canine species including the gray wolf and coyote. By comparing these dogs, the researchers were able to pinpoint about 2.5 million individual genetic differences among breeds.

"Of the more than 5,500 mammals living today, dogs are arguably the most remarkable," says senior study author Eric Lander, director of leading research partner the Broad Institute, and professor of biology at MIT and systems biology at Harvard Medical School. "The incredible physical and behavioral diversity of dogs from Chihuahuas to great Danes is encoded in their genomes. It can uniquely help us understand embryonic development, neurobiology, human diseases and the basis of evolution."

Modern dog breeds developed through selective breeding practices that aimed to preserve certain desirable traits, but this breeding method also predisposed many breeds to genetic disorders including heart disease, cancer, blindness, cataracts, epilepsy, hip dysplasia and deafness, reports the National Human Genome Research Institute.

"Using the dog genome sequence in combination with the human genome sequence will help researchers to narrow their search for many more of the genetic contributors underlying cancer and other major diseases," says Elaine Ostrander, Ph.D., chief of the NHGRI's Cancer Genetics Branch.

According to Francis Collins, M.D., Ph.D., director of NHGRI, continuity is what separates this genome sequence from that of the previously published genome.

When a researcher wants to compare genes in genomes, it is easier to do so if it's known where the gene is located in the sequence. "It's the difference between having single pages of a book in no particular order and having a book with chapters and page numbers," says Collins.

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