

CORNELLCHRONICLE

June 19, 2017

Science, Tech & Medicine

Arts & Humanities

Business, Law & Society

Campus Life

Global Outreach

Archive

Search Chronicle

[Bookmarks](#)

Jan. 28, 2016

Largest dog genetic study informs human diseases

By *Krishna Ramanujan*

Cornell researchers have completed the largest genetic study of dogs to date, comprising the genetic analysis of 4,200 dogs.



J.J. Hayward/Provided

Dog breeds display very different degrees of morphological traits, including shedding. In the study, the researchers identified a novel area on chromosome 1 that is significantly associated with shedding, as well as loci affecting other complex traits and diseases in dogs.

The study investigated 180,000 genetic markers, DNA sequences with a known physical location on a chromosome. Such markers can help link an inherited disease with the responsible gene.

The study, published Jan. 22 in the journal *Nature Communications*, is a big

step toward efficiently mapping genes responsible for complex diseases in dogs, most of which are very similar in humans, thereby accelerating our understanding of human genetic diseases. By identifying important genes and proteins in dogs for diseases and traits, researchers may then test those homologous genes in humans.

There is increased interest in dogs as a model for studying human diseases because dogs share more than 350 diseases with humans – from hip dysplasia to lymphoma – and similar pathways and genes often underlie these shared diseases, according to the paper.

“The more we know about the genetic basis of diseases, the better we are at keeping pure-bred dog populations genetically healthy,” said Adam Boyko, assistant professor of biomedical sciences at Cornell’s College of Veterinary Medicine and the paper’s senior author. Jessica Hayward, a postdoctoral research associate in Boyko’s lab, and Marta Castelhana, director of the Cornell Veterinary Biobank, are co-lead authors of the paper.

But genetics in dogs is far simpler than in humans, and since dogs are diagnosed with many of the same diseases as humans, studying dog genetics is a “useful and underused way to understand genetic diseases from a human perspective,” Boyko said. For complex diseases, the researchers identified areas on the genome that are associated with hip dysplasia, elbow dysplasia, idiopathic epilepsy, lymphoma, mast cell tumor and granulomatous colitis. The researchers also identified genes that influence such traits as body size, fur length and shedding.

“We found 17 genes for body size in dogs, and by looking at those genes we can predict a dog’s size with 90 percent accuracy,” said Boyko. He added that identifying such genes is much easier in dogs than in humans, where hundreds of genes contribute to body size.

TRENDING

EDITOR'S PICKS MOST EMAILED MOST READ

Kate Walsh named dean of School of Hotel Administration

VP for infrastructure, properties and planning appointed

Cornell CubeSat wins ride into space with NASA in 2019

Index highlights innovation advances in Europe, Africa

RELATED INFORMATION

Complex disease and phenotype mapping in the domestic dog

RELATED STORIES

Central Asian village dogs closest to original dogs

SHARE

[Facebook](#)

[LinkedIn](#)

[Reddit](#)

[StumbleUpon](#)

[Twitter](#)

[G+1](#) 2

[Printer-friendly version](#)

[Send by email](#)

[Bookmark](#)

STORY CONTACTS

Cornell Chronicle
Krishna Ramanujan
607-255-3290
ksr32@cornell.edu

Media Contact
Melissa Osgood
607-255-9451
mmo59@cornell.edu

Human disease-mapping studies generally include genotyping tens of thousands of individuals and looking at 1 million markers across the genome. In this study, the researchers conducted simulations to show that “in dogs, we expect to be able to identify genetic risk factors for most major diseases with 1000 individual dogs and 1000 controls,” Boyko said.

The study was made possible due to samples of more than 150 breeds, 170 mixed-breed dogs and 350 free-ranging village dogs from the Cornell Veterinary Biobank; the project represents the culmination of several years of work by the biobank to collect samples and secure funding.

The study was funded by Zoetis Animal Health, [the Cornell University Center for Advanced Technology in Life Science Enterprise](#), the National Geographic Society, National Institutes of Health, The American Kennel Club and the Cornell University College of Veterinary Medicine.