



Press release

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Canine hip dysplasia genes identified

TiHo scientists unravel genes responsible for canine hip dysplasia.

Canine hip dysplasia (CHD) plays a central role in the selection of breeding animals ever since modern dog breeding began. This inherited condition is common in all dog breeds as well as in mongrels. Researchers at the Institute for Animal Breeding and Genetics at the University of Veterinary Medicine Hannover Foundation (TiHo), has identified important genetic variants and their interrelated pathways for the pathogenesis of CHD in German Shepherds. The scientists genotyped more than 1000 German Shepherds and screened a large number of single nucleotide polymorphisms (SNPs) for their association with CHD. Professor Dr. Ottmar Distl and his doctoral student Lena Fels have published their research results in the international online journal PLOS ONE (dx.plos.org/10.1371/journal.pone.0096618).

CHD is caused by a malformation and instability of the hip joints. The first attempts to breed against CHD started at the end of the 1960s due to the severity of this disease and its general significance for the health of dogs. The sole basis of the breeding programs was X-rays of both hip joints. Dogs with significant and severe changes were excluded from breeding. Systematic preventative programs have been established by most dog breeding associations and have become an integral part of the selection programs in purebred dog breeding.

The genetic mechanisms responsible for CHD involve the formation of cartilage and bone. The metabolic pathways show significant similarities with osteoarthritis and chondrodysplasia in humans. Research of CHD is of fundamental importance in terms of understanding the processes that can lead to osteoarthritis in humans, says Distl, head of the Institute for Animal Breeding and Genetics at TiHo.

Dog breeding will significantly benefit from the research. Despite the use of estimated breeding values (EBVs) for CHD, dogs affected with CHD are not uncommon and often unexpected according to the parental EBVs. This presents large problems for dog breeders. Handling of CHD-affected dogs is often difficult and dogs frequently suffer from the painful condition, says Fels. Using these new results, CHD can be prevented much more effectively. Simulation studies using real population parameters and the new approach have demonstrated its superiority over traditional methods.

The genome-wide CHD-test is now available at the Institute for Animal Breeding and Genetics at TiHo and can be provided to all breeders and owners of German Shepherds. Further details can be found on the homepage of the Institute for Animal Breeding and Genetics (www.tiho-hannover.de/kliniken-institute/institute/institut-fuer-tierzucht-und-vererbungs-forschung/). Similar genome-wide tests have already been developed for Bernese Mountain dogs. The research on Bernese Mountain dogs was published in December 2012 at PLOS ONE (dx.plos.org/10.1371/journal.pone.0049782).

Future work by TiHo geneticists will focus on genome-wide, next-generation sequencing of dog samples. The objective is to sequence the entire genome for a large number of dogs of different breeds in order to detect polymorphisms and structural variants. This will enable us to compare CHD-affected dogs with dogs free of any signs of CHD and that show a very low risk for CHD in their progeny. Using this approach, we will be in the position to map the CHD-associated mutations and provide new insights into the pathogenesis of CHD. As such, our research will be able to be extended to include many more different dog breeds, says Distl.

The original publication

Identification and validation of quantitative trait loci (QTL) for canine hip dysplasia (CHD) in German Shepherd Dogs

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