Investigation of potential genetic interactions behind dilated cardiomyopathy (DCM) in dogs via a genome-wide association study (GWAS)

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Veterinary cardiologists have observed a concerning increase in the number and variety of dilated cardiomyopathy (DCM) cases, including in younger dogs and atypical breeds[1-3]. Although genetic mutations associated with DCM have been discovered in some dog breeds, many more likely exist; for example, >50 genetic loci have been identified in humans[4-13]. It is also possible that in some dogs, the development of DCM is polygenic in nature where multiple genes interact collectively or additively with environment or dietary factors that have yet to be elucidated. DCM has an incomplete penetrance in both humans and dogs (ie, not all dogs with the same mutation will develop DCM)[1,4]. Furthermore, not all dogs with the same genetic mutation will respond the same way to clinical interventions such as a change in nutrition and drug therapy. Therefore, a better understanding of genetic risk factors and intersecting environmental factors may be of help in the prevention and treatment of DCM and understanding of the current cases of DCM.

Because researchers at Hill's Pet Nutrition have previously utilized genomics approaches to understand gene-nutrient interactions[14,15], Hill's Pet Nutrition and Embark Veterinary have launched a partnership to recruit 1000 dogs diagnosed with DCM in the largest study of its kind to date. Independent review of complete clinical data, specifically an echocardiogram confirming DCM diagnosis, any current or past drug therapy, and medical and nutritional history, is required for a dog to qualify. Qualifying participants receive a simple cheek swab to collect the DNA sample from their dog. Once there are enough subjects in the study, a genome-wide association study analysis will be conducted using Embarks' customized SNP (single nucleotide polymorphism) microarray developed in partnership with Cornell University College of Veterinary Medicine using the latest genotyping platform. The DNA of the dogs diagnosed with DCM will be compared with the DNA of a healthy control cohort. In this genome-wide association study (GWAS), statistical associations will determine how strongly either single or multiple genotypes are associated for this focal phenotype. The study therefore will aim to determine possible links between DCM and several factors (eg, spay/neuter status, medical history, medications, food choice). We will provide an update on the recruitment status along with demographic analysis of the currently enrolled dogs.

This study may provide information about potential genetic risk factors, gene-nutrient interactions, and/or interactions with other environmental factors not yet recognized in the development of DCM. This information could lead to an understanding of the links between food choices and development of DCM, genetic tests for identifying dogs at risk of developing DCM, and new solutions to support recovery of affected pets, all of which may have a positive impact on the health of dogs.

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