**Novel Locus Associated with Symmetrical Lupoid Onychodystrophy in the Bearded Collie**

Symmetrical lupoid onychodystrophy (SLO) is characterized by inflammation of the nail beds and subsequent nail sloughing that can cause affected dogs considerable pain and discomfort. Although the cause of the disease remains unclear, SLO appears to be an autoimmune condition. According to literature, SLO is uncommon in the general dog population, although German Shepherds, Gordon and English Setters, Giant Schnauzers and Bearded Collies appear to be predisposed. Health surveys conducted by the Bearded Collie Foundation for Health indicate an increasing prevalence of SLO over the years, affecting 3.6% of surveyed dogs in 2019.

Recently, a study conducted by the Oberbauer laboratory the University of California, Davis, has confirmed association of the major histocompatibility complex (MHC) class II genes with SLO in Bearded Collies. These immune genes play an important role in distinguishing between an individual’s own healthy tissue and what is pathogenic or diseased. Failure in identifying one’s own tissue as self may result in autoimmunity, which is the destruction of one’s own healthy tissue by their immune system. In the dog, the MHC is called the dog leukocyte antigen (DLA). For canine disease studies, it is most informative to characterize the genotypes of three MHC class II genes (designated DLA-DRB1, DLA-DQA1 and DLA-DQB1) and generate three-locus haplotypes. Haplotypes are the genotypes of a group of genes that are inherited together from the parent. Two DLA class II haplotypes have been associated with increased risk for developing SLO in Bearded Collies. However, SLO appears to be inherited as a complex trait (i.e. involving multiple genes as well as environmental factors) and DLA class II risk haplotypes are not able to completely explain disease development in this breed. Therefore, the research team sought to characterize additional genetic markers underlying SLO in Bearded Collies by exploring the genetic characteristics of individuals that carried these DLA class II risk haplotypes for SLO.

A genome-wide association study allows researchers to explore the natural genetic variation seen between individuals within a dog breed and determine if any particular variant (or genetic marker) is more frequently found among dogs that have a particular disease when compared to dogs that do not have a disease. This study can be used to identify regions of the genome that are associated with developing a particular disease. In this case, the study was conducted on 101 Bearded Collies (38 with SLO and 68 who were at least 8 years old and never developed SLO). The study revealed two regions of association on different canine chromosomes, both of which contain genes that may be involved with SLO disease development. One of the regions also corresponds to the location of the DLA class II genes, which supports the initial observation of particular DLA class II haplotypes being strongly associated with SLO. However, given their close proximity to other genes, at this time, it remains unclear whether the DLA class II genes are solely responsible for SLO disease development in Bearded Collies or whether they are simply mirroring variation in nearby genes that are actually causing the disease. These findings offer progress towards understanding the genetic components underlying SLO disease development in Bearded Collies, although further research is necessary to determine causation and identify genetic markers that can be effectively used to predict the likelihood of developing SLO.