RESEARCH PROGRESS REPORT SUMMARY

Grant 01937-B: Evaluating the Complex Genetic Basis of Bloat

Principal Investigator: Elizabeth Rozanski, DVM
Research Institution: Tufts University
Grant Amount: $251,097.00
Start Date: 1/1/2014 **End Date:** 12/31/2018
Progress Report: Mid-Year 5
Report Due: 6/30/2018 **Report Received:** 7/29/2018

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Original Project Description:

Gastric dilatation volvulus (GDV), or bloat, is a common condition in large and giant breed dogs with an unacceptably high morbidity and mortality rate. Due to the importance of GDV in many dog breeds, several previous studies have investigated potential risk factors for the development of GDV. It is known that there is no single cause for GDV, rather its occurrence is multifactorial, with both genetic and environmental factors likely contributing. This study will allow for further investigation of how these risk factors cause GDV through the application of genomic and molecular methods. Samples from purebred dogs with GDV will be analyzed and compared to control dogs of similar age and breed that have not developed GDV. A genome wide association study (GWAS) will help to identify differences in the genetic makeup of dogs with GDV, and see which genes are turned on and off in GDV (epigenomics). The study will also determine if dogs with GDV have different types or amounts of proteins, hormones and other molecules in their blood and tissues (transcriptomics, proteomics and metabolomics). The investigators hypothesize that only when all of this information is considered together (genomic, epigenomic, transcriptomic, proteomic and metabolomic) will we truly understand what causes GDV, and guide more effective preventive and treatment strategies.

Publications:

Bell, J. S. (2014). Inherited and predisposing factors in the development of gastric dilatation volvulus in dogs. Top Companion Anim Med, 29(3), 60-63. doi:10.1053/j.tcam.2014.09.002

Sharp, C. R., & Rozanski, E. A. (2014). Cardiovascular and systemic effects of gastric dilatation and volvulus in dogs. Top Companion Anim Med, 29(3), 67-70. doi:10.1053/j.tcam.2014.09.007

The follow manuscripts have been submitted:

a) Wiley E, Rozanski E, Oura T, Huynh TT, and Jennings S. Breed variability in Gastrohepatic ligament length in dogs. Manuscript in preparation for submission to Veterinary Surgery. – submitted 12/17 *in re-review
b) CR Sharp, EA Rozanski, E Finn, EJ Borrego.The pattern of mortality in dogs with gastric dilatation and volvulus. Manuscript in preparation for submission to Journal of Veterinary Emergency and Critical Care-submitted 11/17; Accepted April 2018.

Presentations:

Dr. attended the Briard Specialty in St. Charles IL in August, 2017; this club has provided significant support for the study. http://briardmedicaltrust.org/bmt/ additionally, she will be attending the IW and BMD shows this spring.

We have presented one poster at the Merial-NIH National Veterinary Scholars Symposium in August 2014 (abstract included in Mid-year report), and have just recently published numerous manuscripts regarding GDV.

Two of the investigators (Sharp CR and Rozanski EA), were co-guest-editors of a special issue of the journal Topics in Companion Animal Medicine to cover the topic of Gastric dilatation and volvulus in dogs. This will was published in September 2014. Dr Jerry Bell (Co-I) has written one of the manuscripts for this publication regarding genetic predispositions to bloat. Drs Sharp and Rozanski have also written a review article to contribute to this special issue. Additionally, Dr Laura Nelson (recipient of the other AKC-CHF Bloat Initiative grant) also contributed a manuscript to this special issue.

Dr. Rozanski attended IW and BMD specialty shows this spring in Sturbridge and Boxborough MA, where she discussed the study as well as bloat in dogs.

Report to Grant Sponsor from Investigator:

This study has been progressing slowly. After a variety of challenges, we have secured a new group to collaborate with, TGEN in Arizona. We will initially focus on GSD, as this breed is the most commonly affected. All the samples are currently with our new collaborators (TGEN) and we expect genomic sequencing this fall. As soon as this data is obtained, it will be analyzed. This data promises to open new doors for a better understanding of GDV. Additionally, we have one paper accepted and another in revisions.