RESEARCH PROGRESS REPORT SUMMARY

Grant 02606: The Genetic Background of Lumbosacral Transitional Vertebrae in Dogs

Principal Investigator:	Hannes Lohi, PhD
Research Institution:	The Folkhälsan Institute of Genetics
Grant Amount:	$59,320
Start Date: 4/1/2019	**End Date:** 3/31/2020
Progress Report:	Mid-Year 1
Report Due: 9/30/2019	**Report Received:** 9/30/2019

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Original Project Description:

Dogs of medium and large size or breed can suffer from a condition called lumbosacral transitional vertebrae (LTV), which means that the dog has a malformed vertebra in the caudal end of the spinal cord. Different types of LTV exist and radiographic screening is used to determine the form of LTV in dogs. The disorder can be seen right after birth and it is hereditary. However, it is not known how the disease is inherited, or what genes may contribute to this abnormal development of the spinal vertebrae. LTV is common in German Shepherd Dogs and the disorder predisposes the dogs to cauda equina syndrome. Affected dogs may become increasingly painful or may develop paralysis of the hind legs. There is a need to clarify the genetic background of LTV. The investigators plan to use genetic analyses to identify and confirm genetic risk factors that bring about LTV in dogs. The researchers will both search for regions in the dog genome that associate with the disease and will also investigate the possible contribution of known LTV candidate genes discovered in other species.

Publications:

No peer reviewed publications yet. Several breed club newsletters (~10) to inform the ongoing project in Finland.

Presentations:

Several oral presentations (5) to different breed clubs to inform the ongoing projects in Finland.

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Page 1 of 2

Report to Grant Sponsor from Investigator:

Our goal is to map the LTV locus in German Shepherds (GS), identify the candidate causal gene and compare the results across breeds with LTV-affected dogs. Towards this objective, we proposed to recruit more dogs in the study for more powerful genetic analyses. We have recruited about half of the aimed number of dogs, genotyped the samples and performed a new analysis, which revealed a suggestive marker within an excellent functional candidate gene. The next steps include additional recruitments and more careful analyses to validate the preliminary new results.

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Page 2 of 2