

# Molecular genetics of ectopic ureters in Entlebucher Mountain Dogs

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## Key words

Entlebucher Mountain Dog, Ureteral Ectopia, Molecular Genetics

## Aim of the study

Entlebucher Mountain Dogs have a much higher risk of ureteral ectopia, compared to other dog breeds. The aim of this study was to collect data (phenotypes and genotypes) in order to identify potentially functional genetic variants associated with ureteral ectopia in Entlebucher Mountain Dogs.

## Material and methods

400 Entlebucher Mountain Dogs and 15 Appenzeller Mountain Dogs were phenotyped by abdominal ultrasound. Thus, data from a total of now 1026 Entlebucher and 115 Appenzeller Mountain dogs are available. Another 96 dogs were genotyped with the Illumina CanineHD (173k) BeadChip. Together with the previous genotyping experiments, we know the genotypes of a total of 285 dogs. The data from these 285 dogs were analyzed using the MQLS statistics-program.

To identify potentially functional genetic variants, we also resequenced the genomes of 4 affected and 4 non-affected Entlebucher Mountain Dogs.

## Results and significance

The results of the MQLS analysis show that ureteral ectopia in the Entlebucher Mountain Dog is associated with the chromosomes 3, 8 and 13. There are also signs that chromosome 11 might be associated with the genotype.

With a Bonferroni correction for 72150 markers and a probability of error of  $\alpha=0.05$  per marker, the conservative threshold of significance lies at 6.16. In our study, the most strongly associated markers show values of  $\log(1/\text{MQLS})$  between 4 and 5, and do not yet reach the threshold of significance. As more dogs are needed to obtain statistically significant results, the project is ongoing.

The analysis of the resequenced genomes showed no non-synonymous variations, for which all other dog breeds, as well as the non-affected Entlebucher Mountain Dogs, were homozygous wild type (0/0) and all affected Entlebucher Mountain Dogs were either homozygous mutated (1/1) or heterozygous (0/1). Furthermore, no non-synonymous variations were found, for which all other dog breeds, as well as the non-affected Entlebucher Mountain Dogs, were homozygous wild type (0/0) or heterozygous (0/1), while all affected Entlebucher Mountain Dogs were homozygous mutated (1/1).

We consider it possible that the intergenic and intron-regions, that were excluded from the first analysis, could potentially harbor functionally important regulatory variants. Additionally, the filters used (all cases were required to carry a certain variant allele) were possibly too strict, considering the assumption, that ureteral ectopia is most probably a trait with a complex mode of inheritance.

## Publications, posters and presentations

Sugiarto, S. (2013) Talk at the lab seminar at the Vetsuisse-Faculty Bern: Molecular genetics of the ureteral ectopia in the Entlebucher mountain dog.

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