

Provisional Book of Abstract

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Exploring the genomic basis of dental agenesis in Labrador Retrievers

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Dental anomalies, which frequently have a genetic basis, are well-studied in humans but remain largely unexplored in dogs. Among these, tooth agenesis or hypodontia -the congenital absence of one or more teeth- is particularly common and is considered a fault by several -but not all- breed standards. In humans, non-syndromic tooth agenesis is associated with mutations in genes such as *MSX1*, *PAX9*, and *WNT10A*. In dogs, studies on this topic are scarce: research on the Kerry Blue Terrier confirmed a genetic basis for tooth agenesis, though no genomic studies have identified the associated regions in this species. This study aimed to investigate the genomic basis of tooth agenesis in the Labrador Retriever, whose standard requires full dentition. We analysed 23 Labrador Retrievers, including 21 from a three-generation family. Of these, 12 had complete dentition, and 11 exhibited dental agenesis, primarily on the superior arch (n = 8), involving the first, third, and/or fourth premolars. DNA was genotyped using the Canine SNPchip 230K (Illumina), and the groups were compared with multiple analyses: Wright's F_{st} (top 1% SNPs retained), XP-EHH (top 1% SNPs retained), runs of homozygosity (top 1% delta between groups retained), and logistic regression incorporating the results of a principal component analysis as covariates to account for family structure. Genomic analyses identified multiple candidate regions, though none overlapped with the genes most commonly associated with non-syndromic familial tooth agenesis in other species. However, some genes mapped within these regions are linked to syndromes involving dental anomalies in humans or with key roles in odontogenesis. Notably, two genes were highlighted across three analytical approaches. Among these, one is a coactivator of *NOTCH1* and a tooth-specific target of *RUNX2*, a gene critical for dental development and previously associated with tooth agenesis in other species. This study offers the first genomic insights into dental agenesis in dogs, identifying candidate genes and regions that deserve further investigation. Expanding this research to larger cohorts and additional breeds will be crucial for more accurately identifying the genomic regions involved in hypodontia in dogs, thereby improving our understanding of its pathogenesis and mode of inheritance.