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The genomic signature of dog domestication reveals adaptation to a starch-rich diet

Erik Axelsson, Abhirami Ratnakumar, Maja-Louise Arendt, Khurram Maqbool, Matthew T. Webster, Michele Perloski, Olof Liberg, Jon M. Arnemo, Åke Hedhammar & Kerstin Lindblad-Toh

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The domestication of dogs was an important episode in the development of human civilization. The precise timing and location of this event is debated^{1, 2, 3, 4, 5} and little is known about the genetic changes that accompanied the transformation of ancient wolves into domestic dogs. Here we conduct whole-genome resequencing of dogs and wolves to identify 3.8 million genetic variants used to identify 36 genomic regions that probably represent targets for selection during dog domestication. Nineteen of these regions contain genes important in brain function, eight of which belong to nervous system development pathways and potentially underlie behavioural changes central to dog domestication⁶. Ten genes with key roles in starch digestion and fat metabolism also show signals of selection. We identify candidate mutations in key genes and provide functional support for an increased starch digestion in dogs relative to wolves. Our results indicate that novel adaptations allowing the early ancestors of modern dogs to thrive on a diet rich in starch, relative to the carnivorous diet of wolves, constituted a crucial step in the early domestication of dogs.

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Author information

Affiliations

**Science for Life Laboratory, Department of Medical Biochemistry
and Microbiology, Uppsala University, 75237 Uppsala, Sweden**

Erik Axelsson, Abhirami Ratnakumar, Maja-Louise Arendt, Khurram
Maqbool, Matthew T. Webster & Kerstin Lindblad-Toh

**Broad Institute of Massachusetts Institute of Technology and
Harvard, Cambridge, Massachusetts 02139, USA**

Michele Perloski & Kerstin Lindblad-Toh

**Grimsö Wildlife Research Station, Department of Ecology,
Swedish University of Agricultural Sciences, 73091 Riddarhyttan,
Sweden**

Olof Liberg

**Department of Forestry and Wildlife Management, Faculty of
Applied Ecology and Agricultural Sciences, Hedmark University
College, Campus Evenstad, NO-2418 Elverum, Norway**

Jon M. Arnemo

Department of Wildlife, Fish and Environmental Studies, Faculty of Forest Sciences, Swedish University of Agricultural Sciences, 901 83 Umeå, Sweden
Jon M. Arnemo

Science for Life Laboratory, Department of Clinical Sciences, Swedish University of Agricultural Sciences, 75651 Uppsala, Sweden
Åke Hedhammar

Contributions

K.L.-T. and Å.H. designed the study. K.L.-T. and E.A. oversaw the study. M.-L.A. coordinated and performed the majority of the sample collecting and O.L. and J.M.A. provided samples of critical importance. E.A. performed the SNP detection and selection analyses; A.R. identified candidate causative mutations and analysed haplotypes in CDRs; K.M. detected CNVs bioinformatically; M.T.W. performed phylogenetic analysis and analysed the Canine HD-array data; A.R. performed the maltase activity assay; M.-L.A. validated CNVs and quantified mRNA expression of candidate genes; M.P. performed validation SNP genotyping; E.A., A.R., M.-L.A. and K.L.-T. interpreted the data; E.A. and K.L.-T. wrote the paper with input from the other authors.

Competing financial interests

The authors declare no competing financial interests.

Corresponding authors

Correspondence to: Erik Axelsson or Kerstin Lindblad-Toh

Sequence reads are available under the accession number SRA061854 (NCBI Sequence Read Archive).

Supplementary information

PDF files

1. Supplementary Information (6.4M)
This file contains Supplementary Discussions sections 1-9, Supplementary references, Supplementary Figures 1-24 and Supplementary Tables 1-25.

Zip files

1. Supplementary Data 1 (3.4M)
This zipped file lists the position of short indels in the canine genome.
2. Supplementary Data 2 (257K)
This zipped file lists the position of CNVs in the canine genome.

Comments

2013-01-28 05:19 AM

Elzi Volk said: A shame that *C. latrans* was not included in this analyses.

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