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NATURE | LETTER

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

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*Nature* (2013) doi:10.1038/nature11837

Received 01 July 2012 Accepted 11 December 2012 Published online 23 January 2013


The domestication of dogs was an important episode in the development of human civilization. The precise timing and location of this event is debated<sup>1, 2, 3, 4, 5</sup> 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 domestication<sup>6</sup>. 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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## Accession codes

### Primary accessions

Sequence Read Archive

SRA061854

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### **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.

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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.

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## 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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**Nature** ISSN 0028-0836 EISSN 1476-4687

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