

## Title: Arctic-Adapted Dogs Emerged at the Pleistocene-Holocene Transition

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**Abstract:** We used a palaeogenomic approach to investigate the spatiotemporal emergence of sled dogs. We sequenced the genomes of ten modern Greenland sled dogs, a ~9500 year old Siberian dog associated with archaeological evidence for sled technology, and a ~33,000 year old Siberian wolf. We found significant genetic similarity between the ancient dog and modern sled dogs. We detect gene flow from Pleistocene Siberian, but not modern American wolves, to present-day sled dogs. The results indicate that the major ancestry of modern sled dogs traces back to Siberia, where sled dog specific haplotypes of genes that potentially relate to Arctic adaptation were already established by 9500 years ago.

**One Sentence Summary:** Specialized Arctic sled dogs form an evolutionarily distinct lineage that was established in Northeast Asia at least 9500 years ago.

**Manuscript:** In Siberia, late Upper Paleolithic artifacts of carved bone, antler and ivory, similar to tools used by modern Inuit for securing dog harness straps, suggest ancient origins of dog sledding (1). Furthermore, archeological findings from Zhokhov Island provide evidence of sled technology and dogs by the Sumnagin Mesolithic Culture ~9-8000 years ago (1–3) (Fig. S1), offering an opportunity to use genomics to further our understanding of early dog domestication and the origin of sled dogs.

We generated nuclear genomes from a dog mandible present at this site (“Zhokhov”, 9.6x coverage), dated to 9524 cal years before present (YBP) (Fig. 1A and Fig. S2) and a Siberian Pleistocene wolf mandible (“Yana”, 4.7x coverage), dated to 33,019.5 cal YBP (Fig. 1A and Fig. S3). In addition, we sequenced 10 modern Greenland sled dog genomes, a dog best described as an indigenous landrace breed, used for hunting and sledging by Inuit. Samples consist of two individuals from each of five geographically diverse localities (Fig. 1A), thus providing a broad representation of the indigenous dog diversity.

We analysed our data alongside genomes from 114 geographically and genetically diverse canids (Table S1), using whole-genome pairwise distances, principal component analysis (PCA), Treemix (4) admixture graphs and *D*-statistics (Fig. 1). Zhokhov was found most closely related to American pre-European-contact dogs (PCDs) and modern sled dogs (Greenland sled dogs, Alaskan Malamutes, Alaskan and Siberian huskies), while Yana appeared alongside wolves (Figs. 1B and 1C). Unsupervised clustering analyses with NGSadmix (4) (Fig. S6) grouped modern domestic dogs into four clusters: African, European, Asian, and sled dogs including Zhokhov. These relationships were confirmed by an admixture graph, where Yana was more closely related to a Pleistocene wolf from Taimyr Peninsula than to modern wolves,

whereas Zhokhov represents a lineage that diverged from the ancestor of present-day sled dogs (Figs. 1C and S8-S9). This suggests genetic continuity in Arctic dog breeds for at least the past ~9500 years, setting a lower bound on the origin of the sled dog lineage.

Next,  $D$ -statistics indicated an excess of allele sharing between both Yana/Taimyr and PCDs/Zhokhov/sled dogs (Figs. 1D and S14), corroborating previous reports (3, 5). Importantly, this suggests the admixture occurred between Pleistocene wolves and the ancestor of PCDs, sled dogs and Zhokhov.

Previous studies have demonstrated an association between Canine Transmissible Venereal Tumour (CTVT), sled dogs and especially PCDs (3). Here, we evaluated the relationship between Zhokhov, two CTVT genomes (Table S1), dogs and wolves using  $f_3$  statistics and phylogenetic analysis. Recent analyses of exome data suggest that CTVT expanded across Eurasia ~6000 years ago (6), thus reducing the likelihood that this transmissible cancer originated in the Americas. In our study, both the phylogenetic analysis (Fig. S9) and  $f_3$  statistics (Fig. S10) placed the CTVT genomes closer to PCDs than to sled dogs or Zhokhov. These results imply that (i) the basal dog lineage that led to PCDs (3) occurred in Eurasia ~6000 years ago, and/or (ii) multiple introductions of PCD-like dogs to the Americas.

We employed NGSadmix, admixture analyses and  $D$ -statistics (Fig. S6-S8, S11-S15) to evaluate gene flow and shared ancestry between Zhokhov, modern dogs and wolves. We found no significant gene flow between any sled dog (including Zhokhov) and modern American-Arctic wolf populations when compared to the Eurasian wolf (Fig. S15), thus suggesting that gene flow from modern wolves has not contributed to the sled dog gene pool within the past 9500 years. This result was surprising given genetic evidence for post

domestication admixture between other wolves and dog breeds (5, 7). Furthermore, ethnographic evidence from Greenland indicates that, at least historically, dog-wolf matings were not uncommon (8). If true, the lack of gene flow from modern American-Arctic wolves into sled dogs implies selection against hybrids.

The clustering and admixture results show gene flow between some sled dogs and other modern dog breeds (Fig. 1C, Fig. S6-S8). We further explored this by comparing pairs of sled dogs to Zhokhov using  $D$ -statistics (Fig. 2A). While pairs of Greenland sled dogs are symmetrically related to Zhokhov ( $D \sim 0$ ) indicating a lack of admixture, comparisons involving non-Greenland sled dogs were not always consistent with the null hypothesis of no admixture.  $D$ -statistics and admixture analyses (Figs. 2B and S13) indicated that non-Greenland sled dogs carry ancestry from non-sled dogs and that Greenland sled dogs are the least admixed. These results imply that Greenland sled dogs (i) have largely been kept isolated from contact with other dog breeds, and (ii) that their lineage traces more genomic ancestry to Zhokhov-like dogs relative to other dog breeds. Isolation of the Greenland sled dogs was supported by inference of their historical effective population size (Fig. S16), which showed Greenland sled dogs had a relatively stable population size until a severe bottleneck ~850 years ago. The timing of the bottleneck is consistent with the colonization of Greenland by Inuit (9), suggesting isolation in Greenland ever since.

Numerous generations in the Arctic environment and as draft animals may have provided a unique selection pressure on sled dogs. To detect putative signals of positive selection, we used Population Branch Statistics (PBS) (4), to scan for genomic regions highly differentiated in modern sled dogs relative to non-sled dogs (hereafter, other dogs) and wolves. We computed

these statistics on modern genomes of 17 sled dogs, 61 other dogs and 30 wolves (Table S1). A sliding window analysis revealed several genomic regions with high PBS values, hinting at selection in sled dogs (Fig. 3A). We took an outlier approach and focused on the most extreme values of the empirical distribution (above 99.95<sup>th</sup> percentile). For each of these outlier regions (Table S4), we identified overlapping genes and compared haplotypes across samples.

Enrichment analysis (4) on genomic regions with high PBS values (above 99.95<sup>th</sup> percentile) identified three gene ontology terms that were overrepresented (Table S6), two of them relating to ion transport across the cell membrane. To investigate further, we focused on eight genomic regions that are highly differentiated in sled dogs, and three where other dogs differ from sled dogs and wolves (Figs. 3A and S18), and validated the autosomal regions with a cross-population composite likelihood ratio statistic (5) (Fig. S21). In the differentiated regions, we focused on two sets of genes, (i) genes where Zhokhov carries the same haplotype as the modern sled dogs and (ii) genes involved in adaptation to different diets.

*TRPC4* is highly differentiated in sled dogs and the putatively selected haplotype bears a striking similarity to Zhokhov (Figs. 3A and C). *TRPC4* is a transient receptor potential (TRP) channel protein that plays an important role in vasorelaxation and lung microvascular permeability (10). It is also involved in a temperature sensitivity pathway (11, 12), where it interacts with *TRPV2*, which is also highly differentiated in sled dogs (99.8<sup>th</sup> PBS percentile, Table S4 and Fig. S19A), and codes for temperature and potentially pain receptors (13). Several related thermo-TRP sensors in the same pathway - calcium ion transmembrane transport - have been previously reported to be under selection in cold-adapted woolly mammoths (14), which suggests convergent evolution in Arctic adaptation.

Another highly differentiated gene in sled dogs, *CACNA1A* (Fig. 3A and B), is a calcium channel subunit that plays an essential role in skeletal muscle contraction (15). Further, *CACNA1A* has been reported to be under positive selection in humans - the Bajau sea nomads (16), where it is involved in hypoxia adaptation (17), indicating a possible role managing exercise-induced hypoxia in sled dogs. Altogether, we hypothesize that the *TRPC4*, *TRPV2* and *CACNA1A* genes are involved in functions beneficial to physical activity in the Arctic. If so, given that the differentiated haplotypes are also found in Zhokhov (Figs. 3A, B and S19A), any advantages they confer would have been important to dogs in the Arctic ~9500 YBP.

Most domestic dogs are adapted to starch-rich diets via significant increases in *AMY2B* copy numbers and strong positive selection for a dog-specific *MGAM* haplotype (18). Consistent with previous findings (19), we observed that sled dogs carry substantially fewer *AMY2B* copies than other dog breeds (Fig. S20). Interestingly, we also found that *MGAM* and *AMY2B* are the regions of the genome with lowest PBS, suggesting high differentiation of other dogs relative to sled dogs and wolves (Fig. 3A). Because negative PBS can arise under different demographic scenarios, we confirmed these observations by computing PBS with other dogs as the focal population (Fig. S18). Indeed, modern sled dogs and Zhokhov are among the only dogs in our dataset that carry the ancestral *MGAM* haplotype found at high frequency in wolves (Figs. 3C and S18). Therefore, our observations suggest sled dogs do not carry the genetic adaptations to starch rich diets seen in other dog breeds.

In contrast, sled dogs harbor unique haplotypes of genes involved in coping with high intake of fatty acids. *SLC25A40*, a mitochondrial carrier protein involved in clearing triglycerides from the blood (20), and *APOO*, an Apolipoprotein gene involved in regulating high levels of fat

and fatty acid metabolism (21), are both highly differentiated in sled dogs (Figs. 3A). Interestingly, the derived haplotypes of both genes are absent in Zhokhov, indicating the haplotypes are unique to modern sled dogs and post-date their common ancestry with Zhokhov (Figs. S19B and S19E). As another example of convergent evolution, another gene of the Apolipoprotein family, *APOB*, is reported to be under selection in polar bears, possibly as a result of adaptation to fat rich diets and clearance of cholesterol from the blood (22). Overall, similar adaptations to high intake of fatty acids have been described in the Inuit (9), thus our observations suggest that sled dogs co-adapted to a fat rich, starch poor diet alongside the Arctic human cultures they co-existed with.

Bone composition of polar bears and reindeer consumed at the Zhokhov site indicate an extensive hunting range and transport of large body parts back to camp (23). Further, abundant obsidian tools found at the Zhokhov site reveal movement of obsidian across ~1500 km to the site (3). Together, they indicate significant long-distance travel and transportation of resources, in which dog sledding would have been highly advantageous if not necessary. Putative sled remains and our genomic analyses of a 9500 years old dog from the Zhokhov site indicate that tradition and key genomic variation that define modern sled dogs, were established in the Northeast Asian Arctic over 9500 years ago. Our results imply that the combination of these dogs with the innovation of sled technology facilitated human subsistence since the earliest Holocene in the Arctic.

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M.-H.S.S., S.G., J.R.-M., M.d.M.M., and M.T.P.G. conceived of the project and designed the research; V.V.P., E.Y.P., P.A.N., A.K.K., V.V.I., and E.W provided archaeological work, logistics and/or ancient collected samples; M.-H.S.S., M.F., S.E.W., M.P.H.-J., R.D., and C.S. coordinated logistics of - and/or provided – modern samples; C.C and M.-H.S.S. conducted the laboratory work; S.G., J.R.-M., M.d.M.M., L.K., L.A.F.F., F.G.V., J.N. and J.A.S.C. conducted the analyses of data with considerable input from M.-H.S.S., B.P., T.S.-P., T.M.-B., A.J.H. and M.T.P.G.; S.G., J.R.-M., M.d.M.M., L.K., L.A.F.F., F.G.V., J.N., J.A.S.C., P.S., M.-H.S.S., T.M.-B., A.J.H. and M.T.P.G interpreted results with considerable input from B.P., T.S.-P., V.V.P., T.R.F., E.U.A.-R., P.D.J., M.M., L.D., G.L., L.B., and Ø.W.; M.-H.S.S., S.G., J.R.-M., M.d.M.M., and M.T.P.G. wrote the paper with input from all other authors. **Competing interests:** Authors declare no competing interests. **Data and materials availability:** Raw sequencing data can be accessed at NCBI Short Read Archive with project number PRJNA608847.

### Supplementary Materials:

Materials and Methods

Figs. S1 to S26

Tables S1-S6

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**Fig. 1. Geographic location of the samples and overall genetic affinities.** (A) Identity by State pairwise distances between Zhokhov and present-day dogs (Table S1), geographic affiliation of dogs and archaeological sites. Color scale indicates genetic distance between Zhokhov and each sample. Circles and triangles represent modern and ancient dogs, respectively. Stars show Zhokhov and Yana sites. (B) Principal Component Analysis using whole-genome data (2,200,623 transversion sites) on all samples. (C) Treemix admixture graph built using whole genome data (766,082 transversion sites) on a dataset consisting of 66 canids merged into 15 groups according to their geographic location and admixture profile (Table S1 and Fig. S6). Colors indicate main groups as in panel B. Arrows show inferred admixture edges colored by migration weight. (D)  $D$ -statistic of the form  $D(H1, \text{Boxer dog}; \text{Taimyr/Yana}, \text{Andean fox})$  testing for Pleistocene wolf gene flow in ancient and modern dogs, testing whether samples share more alleles with Taimyr (x-axis) or Yana (y-axis) wolves when compared to the boxer dog. Color indicates the type of sample in  $H1$ . Points show the  $D$ -statistic, while horizontal and vertical lines show 3 standard errors for the test with the Taimyr (x-axis) and Yana (y-axis), respectively. The results obtained from both ancient wolves fall along the diagonal, suggesting they are symmetrically related to all dogs.

**Fig. 2. Relationships between Zhokhov and present-day sled dogs (sled dogs).** (A)  $D$ -statistics testing the relationships between pairs of sled dogs and Zhokhov. Cell colors indicate

the Z-scores obtained from the test  $D(\text{dog1}, \text{dog2}; \text{Zhokhov}, \text{Andean fox})$ , where dog1 and dog2 are all possible pairs of sled dogs. Comparisons involving pairs of Greenland sled dogs and non-Greenland sled dogs resulted in significant deviations from  $H_0$  ( $|Z| > 3$ ). **(B)**  $D$ -statistics showing that sled dogs that are significantly further from Zhokhov compared to Greenland sled dog Aasiaat 2 (y-axis:  $D(\text{Greenland sled dog Aasiaat 2}, H_2; \text{Zhokhov}, \text{Andean fox})$ ) also show evidence of significant gene flow from other dogs (x-axis:  $D(\text{Greenland sled dog Aasiaat 2}, H_2; \text{German shepherd dog}, \text{Andean fox})$ ). Points indicate the  $D$ -statistic, while horizontal and vertical lines indicate 3 standard errors for the x- and y-axis, respectively. We considered the test to be significant for gene-flow when these lines do not overlap with the dotted line ( $|Z| > 3$ ).

**Fig. 3. Adaptation.** **(A)** Manhattan plot of the PBS values (y-axis) in windows of 100 kilo-base pairs (kb) using a 20 kb slide across chromosomes (x-axis). Data points between the 20<sup>th</sup> and 80<sup>th</sup> percentile of the empirical distribution are not plotted and dashed red lines show the 99.95<sup>th</sup> and 0.05<sup>th</sup> percentiles. Names of genes within the highest peaks are shown, with asterisks representing no overlap with genes. We note that other genes not displayed in the figure can overlap the outlier regions, a full list can be found in Table S4-5. Haplotype structures for CACNA1A **(B)**, TRPC4 **(C)** and MGAM **(D)**. Rows represent individuals, columns polymorphic positions in the dog genome. Cells are colored by genotype: dark gray (alternative allele homozygous), light gray (heterozygous) and white (reference allele homozygous). The row height for ancient individuals was increased to facilitate visualization. Zhokhov is highlighted with a red asterisk. SDs is used as an acronym for sled dogs.