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Breed-Specific Ancestry Studies and Genome-Wide Association Analysis Highlight an Association Between the *MYH9* Gene and Heat Tolerance in Alaskan Sprint Racing Sled Dogs

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Abstract

Alaskan sled dogs are a genetically distinct population shaped by generations of selective interbreeding with purebred dogs to create a group of high performance athletes. As a result of selective breeding strategies, sled dogs present a unique opportunity to employ admixture-mapping techniques to investigate how breed composition and trait selection impact genomic structure. We used admixture mapping to investigate genetic ancestry across the genomes of two classes of sled dogs, sprint and long distance racers, and combined that with genome wide association studies (GWAS) to identify regions correlating with performance enhancing traits. The sled dog genome is enhanced by differential contributions from four non-admixed breeds (Alaskan Malamute, Siberian Husky, German Shorthaired Pointer, and Borzoi). A principle components analysis (PCA) of 115,000 genome-wide SNPs clearly resolved the sprint and distance populations as distinct genetic groups, with longer blocks of linkage disequilibrium (LD) observed in the distance versus sprint dogs (7.5–10 and 2.5–3.75 kb, respectively). Further, we identified eight regions with the genomic signal either from a selective sweep or an association analysis, corroborated by an excess of ancestry when comparing sprint and distance dogs. A comparison of elite and poor performing sled dogs identified a single region significantly association with heat tolerance. Within the region we identified seven SNPs within the myosin heavy chain 9 gene (*MYH9)* that were significantly associated with heat tolerance in sprint dogs, two of which correspond to conserved promoter and enhancer regions in the human ortholog.

Keywords

canine; admixture; attributes; GWAS

Introduction

The Alaskan sled dog has evolved over the past century from a working dog, originally developed to haul cargo sleds over snow-covered terrain (Collins 1991; Rennick 1987; Vaudrin 1977), to an elite modern-day athlete. Their dominating presence in polar exploration and the boom of the Alaskan Gold Rush gave rise to the “Era of the Sled Dog”

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from approximately the late 1800s to the early 1900s (Wendt 1999). The incorporation of modern transportation methods forced the sled dog into retirement from its necessary role of working dog, transitioning, instead, to a sport-racing dog. Though not recognized by the American Kennel Club (AKC) (AKC, 1998) and not developed to meet a physical standard, Alaskan sled dogs are bred for climate-specific athletic performance attributes, which has resulted in a level of genetic distinctiveness comparable to that of AKC-recognized breeds (Huson et al. 2010). Performance selection has given these dogs a common athletic phenotype: a quick and efficient gait, superior pulling strength, and increased endurance. Overall body weight and coat type, however, can vary depending upon racing style, geographic location, lineage, and cross breeding to purebred lines.

Sled dog racing can be divided into two distinct styles based upon the mileage teams' travel. Long distance racing covers approximately 1,000 miles over multiple days with moderate racing speeds (13–19 km/h) (*e.g.*, Iditarod and Yukon Quest) (Iditarod 2011; Quest 2011), while sprint racing is comprised of multiple events or classes defined by the number of dogs in the team (4–20), faster racing speeds (29–40 km/H) and shorter distances (~6–38 km). The extreme differences in racing style has led to divergent selection of Alaskan sled dogs for either endurance or speed, resulting in two distinct populations (Figure 1) (Huson et al. 2010).

As a result of interbreeding practices, the modern sled dog genome is a mosaic of purebred dog ancestry that represents a unique opportunity to document the acquisition of athletic performance traits through both a selection scan and admixture mapping. Admixture mapping has successfully been implemented for genetic variants and disease phenotypes in human populations with mixed ancestry (Patterson et al. 2004; Buerkle and Lexer 2008; Winkler et al. 2010; Seldin et al. 2011). The method scans through a mosaic genome and identifies the ancestry for each chromosomal fragment, provided that parental genomes are defined. The frequency and size of these fragments is influenced by the frequency and direction of interbreeding duration, as well as trait selection. Written pedigrees as well as genetic investigation (Huson et al. 2010) reveal that the Alaskan Malamute, Siberian Husky, Pointer (English and German Shorthaired), Saluki, Borzoi, Irish Setter, Weimaraner, German Shepherd, and Anatolian Shepherd were utilized in generating the Alaskan sled dog (ADMA 2011; Huson et al. 2010). Here, we have utilized two genome-wide panels consisting of 115,425 and 27,416 SNPs to assess population structure and conduct both admixture mapping and a genome-wide association study to explore the genetics of endurance and heat tolerance in Alaskan sled dogs.

Methods

Sample Collection and SNP Array Genotyping

DNA was extracted from blood samples provided by 150 Alaskan sled dogs, 65 from distance and 85 from sprint racing kennels (see Performance Ratings Section below), and 45 purebred dogs from four AKC-recognized domestic breeds (Alaskan Malamutes, AMAL n=10; Siberian Huskies, HUSK n=12; German Shorthaired Pointers, GSHP n=11; Borzois, BORZ n=12) (Huson et al., 2010; Boyko et al., 2010). All 45 purebred dogs were unrelated at the grandparent level, as well as 19 distance and 27 sprint sled dogs, selected from pedigree analysis. Prior to sample collection all owners provided informed consent, consistent with NHGRI Animal Care and Use Committee rules. Whole blood samples were collected from the cephalic vein into 3–5ml EDTA or ACD tubes. Sled dogs were sampled at their home kennels while purebred dog samples were obtained through clinics set up at large gatherings, such as conformation competitions, or through their local veterinarian. Samples were stored at 4°C prior to extraction and genomic DNA was isolated using standard proteinase K/phenol extraction methods by Health Gene (Toronto, Canada) or RX

Bioscience (Rockville, MD). DNA samples were stripped of identifiers, coded, and aliquoted for long-term storage at −80°C. Finally, detailed pedigrees were collected for each sampled individual.

A total of 150 Alaskan sled dogs were genotyped using the Illumina HD Canine SNP array (San Diego CA, USA). The 45 AKC-registered purebred dogs sampled to represent ancestral populations were previously genotyped for 48,716 SNPs (VonHoldt et al., 2010; Boyko et al., 2010) using the Affymetrix v2.0 Canine SNP array (Affymetrix, Santa Clara, USA). A total of 115,425 SNPS were retained from the sled dogs using the Illumina HD Canine SNP array after similar quality filtering. For both platforms, SNPS ≥93% genotype call rate, <10% missing genotypes and >10% minor allele frequency based on data from using Genome Studio (Illumina, San Diego, CA) and PLINK software (Purcell 2009; Purcell et al. 2007). We identified a set of 27,416 overlapping SNPs between the Illumina and Affymetrix panels to be used for population structure analyses.

Performance Ratings

Sled dogs were individually scored for their abilities related to speed, endurance, work ethic, mental stress tolerance, and heat tolerance. Distance dogs (n=65) were sampled from four kennels, all of which finished in the top 15% of competitors for the Yukon Quest or Iditarod races during two consecutive years (2007–2008) of sample collection. Sprint dogs (n=85) were also sampled from four kennels, each of which placed in the top 25% of the International Sled Dog Racing Association points-ranking medal program during the sampling years (2005–2007). All distance kennels maintained similar training regimes with regard to mileage (increasing up to ~322 kilometers) and speed (13–19km/h) as it related to fall training through winter racing season (September-March). Sprint kennels also had similar metrics with regard to mileage (increasing up to ~48 kilometers) and speed (24–40km/h) during the same time period. The study did not control for individual driver training style. The kennels sampled were located throughout the northern continental United States, including Alaska, as well as northern Canada with slight variations in weather and terrain. Sampled dogs competed in many of the same races, several of which were held in Alaska. Brand of dry dog food varied between kennels, but was comparable in total protein (~26–34%) and fat (~14–20%) content. Each kennel also supplemented diets with either raw meat or meat supplements, particularly during the winter racing season.

Criteria for each athletic attribute were defined and tested by one of us (H.J.H.) and reviewed by five professional sled dog drivers. Scorers independently rated a minimum of the same eight sled dogs after a single training run, and scores were reviewed for reliability and repeatability. Distance dogs were scored a single time to obtain their overall performance score for each phenotype (speed, endurance, work ethic, mental stress tolerance, and heat tolerance) during the peak racing season (~March). Individual sprint dogs were scored on a weekly basis for each phenotype beginning at fall training (~September/October) and continuing through the end of the peak-racing season (~March/April). Approximately 80% of the sprint dogs were scored for phenotype during consecutive years (2005–2007). To achieve a single score for the sprint dogs that was comparable to those obtained for distance dogs, the last weekly rating for each sprint dog during peak racing season was regarded as their performance score for that year. For each dog consecutive year ratings were obtained. If a dog's ranking for each attribute (speed, endurance, work ethic, heat tolerance, mental stress tolerance) did not change over consecutive years, that score was simply used as the dog's overall performance score. For this study, each athletic attribute was viewed independent of the other four. A dog that had different annual scores for any particular athletic attribute was not included for analysis of that trait. In order to obtain suitable numbers, sled dogs were not restricted by age, which ranged from one to six years at the time of sampling. A disparity in male versus females was

observed for sprint versus distance dogs. Sprint kennels had a higher percentage of females (60%) while distance kennels had a higher percentage of males (72%). Performance was investigated for sprint and distance dogs separately and no sex disparity was observed in elite versus poorly performing dogs.

Endurance was scored using the average mileage traversed in a race with dogs ranked one, two or three, based on their performance. Mileage requirements ranged from 13–48 km for sprint dogs and 1,595–1,850 km for distance dogs. A ranking of one was given to dogs completing the required mileage in good condition. Dogs that completed the mileage but struggled to do so were ranked two, and dogs unable to complete the mileage were ranked three.

Heat tolerance is a measure of whether a dog reaches or nears a state of heat exhaustion (inability to reduce body temperature) while running in warm temperatures (approximately −7 to 10° Celsius). The body temperature rise associated with heat exhaustion causes an increased heart rate, muscle weakness, dizziness or confusion, rapid breathing, nausea, and vomiting. Observational data for the dog's degree of heat exhaustion were substituted as a proxy for the physiological state. Dogs showing no change in their ability to perform were ranked as one. A two was given to dogs demonstrating a lower than normal performance when running in warm temperatures. Such dogs showed mild signs of heat exhaustion for two or more of the above symptoms. Dogs unable to complete the mileage and demonstrating considerable signs of heat exhaustion (collapse or near collapse) were scored as a three.

Ancestry Informative Marker (AIM) Identification

Phase was inferred using the program fastPHASE version 1.4.0 (Scheet and Stephens 2006) across the 27,416 SNP panel for all purebred and sled dogs with a 0.05 masking rate. We specified the number of haplotype clusters (K) to range from two to nine with an interval of one. We selected ancestory informative markers (AIMs) that highly differentiated the reference breeds, selecting one reference breed in comparison to a pool of the other three breeds (e.g. AMAL vs. HUSK/GSHP/BORZ). This allowed us to identify SNPs that were informative for the ancestry of each reference breed. Across all comparisons, the average genome-wide level of differentiation was moderate (F_{ST}=0.12). In order to retain as many SNPs as possible but not compromising the level of differentiation, we included SNPs with an F_{ST} at least 1 SD above the genome-wide mean (F_{ST} >0.35) but also required a genome-wide SNP spacing of ~300Kb. As a result, we then identified a subset of 7,644 AIMs that were diagnostic for the four reference (ancestry) breeds: AMAL, HUSK, GSHP and BORZ (Cheng et al. 2010; Rosenberg et al. 2010; Tang et al. 2006; Tian et al. 2006). Note that the (English) Pointer, identified in our previous microsatellite work (Huson et al. 2010), was substituted for the GSHP due to the availability of SNP data for that breed only. Both Pointer breeds have been documented as being interbred with Alaskan sled dogs (Parker et al., 2010).

Population Structure, Linkage Disequilibrium and Homozygosity Analysis

We conducted a PCA using the *smpartpca* function in the EIGENSTRAT package (Price et al. 2006; Shriner 2011) to assess population structure of the unrelated sled dogs (distance n=19; sprint n=27) as well as the entire dataset of sled dogs and the four AKC breed contributing most to the sled dog genome (AMAL, BORZ, GSHP, and HUSK). We additionally conducted a PCA with the panel of 7,644 AIM SNPs. This panel was used, specifically, to test the ability of the AIMs to distinguish individual populations. We obtained estimates of observed heterozygosity (H_O) per SNP using PLINK (Purcell et al. 2007), and Wright's genetic differentiation (F_{ST}) (Boyko et al. 2010) using the program

SCATTER (Vonholdt et al. 2010) using data from the 115,425 SNPs collected on all sled dogs. We calculated F_{ST} estimates (see AIMs section above) for the purebred dogs only using the set of 27,416 overlapping SNPs.

To measure the extent of linkage disequilibrium (LD) we estimated pairwise inter-marker genotypic associations (r^2), an estimate of LD using PLINK. We randomly subsampled 19 unrelated sprint dogs to match the sample size of the distance dogs as sample size differences will impact r^2 estimates. Using the panel of 27,416 overlapping SNPs and all unrelated dogs, r^2 scores were averaged for a set of inter-SNP distances (kb) binned into the following classes: 1.25, 2.5, 3.75, 5, 7.5, 10, 15, 20, 30, 40, 60, 80, 115, 150, 212.5, 275, 387.5, 500, 737.5, 975, and 1000 as described in Boyko et al., (2010). The distance to LD decay was defined as the distance bin in which the r^2 score dropped below the threshold of 0.5 for each population (Sutter et al. 2004). LD is expected to be more extensive in inbred as opposed to admixed populations (Boyko et al. 2010; Gaut and Long 2003; Gray et al. 2009; Pritchard and Przeworski 2001; Tang et al. 2006). Population distances were also calculated using an r^2 threshold of 0.2 providing a direct comparison to the study of Gray et al. (2009). Additionally, we determined the level of autozygosity within each population by surveying runs of homozygous genotypes (ROH) using the 27,416 SNP panel and PLINK. Homozygous tracks were required to be a minimum of 100 kb in length and to contain at least 25 SNPs as described by us previously (Boyko et al. 2010).

Selective Sweep

We conducted a selective sweep analysis in order to detect genomic regions that differentiated the two performance classes of sled dogs and potentially contained candidates genes linked to endurance and heat tolerance. Four independent criteria were used to distinguish the major areas of selective sweep within the sprint (n=27) and distance (n=19) populations using the full panel of 115,425 SNPs. Using the genome-wide estimates of H_O, we selected 9,362 SNPs from the lower fifth percentile (distance=0 H_O; sprint<0.0833 H_O). These SNPs demonstrate a loss of heterozygosity (LOH) defined as the observed heterozygosity being greater than one standard deviation below the genome average (H_O-1SD: distance=0.16; sprint=0.22). To reduce the number of sites for further investigation we required that at least one SNP per region be in the top fifth percentile of the greatest H_O difference between the sprint and distance populations (5,158 SNPs) and the top fifth percentile of F_{ST} scores (5,621 SNPs) as described in (Vonholdt, et al., 2010). Finally, regions were retained if SNPs were clustered (inter-SNP distance < 300 Kb), with each SNP in the cluster displaying high levels of LOH. This included 2145 regions had two consecutive snps <300kb apart. Sixty regions both consecutive snps and LOH.

Genome-Wide Association Studies

GWAS were run with the data set of 115,425 SNPs in the sled dogs using EMMAX (Kang 2010), which corrects for population stratification and relatedness. To identify SNPs associated with sled dog population differentiation, 27 sprint and 19 distance dogs were compared in a case/control analysis. GWAS were also performed to investigate the performance attributes of endurance and heat tolerance. Age and sex were not considered as covariates. All dogs were required to be unrelated through the second generation. Dogs that received scores of one were considered elite. Because less than 10% of dogs in this study scored a three for either endurance or heat tolerance, the dogs ranked as two or three were grouped together and considered as poor performers. Significance levels were generated using basic (adaptive) permutation testing in PLINK. SNPs demonstrating genome-wide association in EMMAX (Bonferroni correction equals a p-value $\leq 4\times10^{-7}$) were required to have a corrected p-value $\leq 1\times10^{-6}$ in PLINK.

Endurance was tested in sprint (poor n=20; elite n=21) and distance dogs (poor n=14; elite n=19) separately due to the considerable difference in performance requirements between the two groups, with poor performers (scores of two and three) assigned case status while so called “elite” performers (score of one) were controls. Heat tolerance was also tested independently within each sled dog population (sprint poor n=17 and elite n=21; distance poor n=10 and elite n=19). As environmental temperature conditions were comparable between the two groups, an additional GWAS for heat tolerance was conducted by combining the sprint and distance groups, comparing all elite versus all poor performers for this attribute (poor n=27, elite n=40).

Modeling Ancestry

SABER was utilized for modeling ancestry within the sprint and distance populations. An admixture mapping approach using this information was taken to identify regions of particular selection within the two sled dog populations (Tang et al. 2007; Tang et al. 2006). SABER delineates ancestry blocks in the admixed sled dog populations from the reference domestic breeds by implementing an extended Markov-Hidden Markov Model (MHMM) for inferring ancestry switches across the genome while accounting for background LD. We specified a 1.0 cM/Mb recombination rate (Boyko et al. 2010) and used a prior of ten generations from the initial admixture event ($\tau = 10$) for ancestry block assignments across all 38 autosomes.

SABER generates diploid ancestry block assignments for individual sled dogs. Using the four ancestor populations ten diploid ancestry states are produced; four states are homozygous for the individual ancestor breeds (AMAL, BORZ, GSHP, and HUSK) and six are heterozygous combinations of the breeds (AMAL/BORZ, AMAL/GSHP, AMAL/HUSK, BORZ/GSHP, BORZ/HUSK, and GSHP/HUSK). The sled dogs were grouped with respect to their racing style (distance n=19; sprint n=27) to identify the most frequent ancestry per SNP for each sled dog population. In order to estimate ancestry block frequency within each sled dog group, we used the randomly subsampled 19 unrelated sprint dogs for comparison to the 19 distance dogs. We filtered for ancestry blocks that had at least three contiguous SNPs with the same ancestry assignment in an effort to exclude potentially false ancestry blocks (due to random chance or lack of information). Ancestry blocks were deemed private to a single sled dog population if they had >20% frequency in that population to and <5% frequency in the opposing population. Regions showing excess or deficient selection (>1 SD from each ancestral frequency mean) towards a particular ancestor were identified within the distance and sprint sled dogs based upon the highest degree of differential ancestry at consecutive SNPs, defined as the difference between the two populations (Tang et al. 2007). The top 5% of AIMs (382 SNPs) which showed the highest degree of differentiation between the sprint and distance populations were used to identify genomic regions that had undergone the strongest selection. These regions were greater than two standard deviations from the mean ancestry frequency difference (Tang et al. 2007).

Sequencing of the HINT1 and MYH9 Genes

Two candidate genes were selected for sequencing based on GWAS results. The histidine triad nucleotide binding protein 1 *(HINT1)* gene, identified as a candidate due to a significant association with population variation between the sprint and distance dogs, is located on canine chromosome 11 (22,400,779–22,560,252; CanFam2.0) and consists of four exons that encompass 560bp. The myosin heavy chain 9 non-muscle type II class A *(MYH9)* gene is located on canine chromosome 10 (CFA10: 31,135,177–31,194,500) and consists of 40 exons, totaling 7,318 bp.

Nineteen distance dogs and 27 sprint dogs, eight GSHP and eight HUSK were sequenced across all exons of *HINT1*. Five amplicons, averaging 550bp, were necessary to cover the *HINT1* coding region. Forty-three amplicons, averaging 620bp in length, were sequenced to cover the *MYH9* exons, with an additional 11 amplicons included to cover highly conserved regions flanking the gene. Six elite and six poor performers for the heat tolerance attribute were initially sequenced for all 54 amplicons to identify SNPs. An additional set of 26 poor performers and 15 elite performers were genotyped for 16 *MYH9* SNPs demonstrating association in the initial 12 dogs. Eight GSHP and six AMAL were also genotyped for the 16 critical SNPs to provide a comparison to the sled dogs.

PCR amplification for both genes was performed in 10 μl volumes containing 10ng genomic DNA, 1 μl of 10x TaqGold Buffer, 0.05 μl of ABI TaqGold (Applied Biosystems, Carlsbad, CA), 1 μl of 1mM dNTPs, 0.3 μl of 50mM $MgCl_2$, 1 μl of both forward and reverse 2μM primers, and 4.65 μl water. Touchdown PCR was carried out as follows: 94°C for 10 min, followed by 20 cycles of 94°C for 30s, then decreasing by 0.5°C/cycle starting at 65°C down to 55°C during annealing for 30s, and 72°C for 45s, followed by another 20 cycles of 94°C for 30s, 55°C for 30s, and 72°C for 45s, with a final extension phase of 72°C for 10min. A small subset of amplicons within each gene required the following PCR protocol for successful amplification: 10 μl total volume containing 10ng genomic DNA, 5 μl of KOD Buffer, 0.2 μl of KOD (EMD Chemicals, Merck, Darmstadt, Germany), 1.6 μl of 2.5mM dNTPs, and 1.2 μl of both forward and reverse 2μM primers. The annealing temperature was also adjusted in the touchdown PCR decreasing by 0.5°C/cycle for the first 20 cycles from 67°C to 57°C and remaining at 57°C for the second 20 cycles.

PCR products were sequenced using Big Dye version 3.1 on an ABI 3730x1 capillary electrophoresis unit. Sequence reads were aligned and analyzed using Phred, Phrap, and Consed software (Bhangale et al. 2006; Ewing et al. 1998; Gordon et al. 1998). PolyPhred software was used to identify SNPs (Nickerson et al., 1997). All genetic variations, both SNPs and insertion/deletion polymorphisms, were then analyzed with Haploview 4.2 to assess LD structure, identify haplotypes and test for association (Barrett et al. 2005).

Results

Population Structure, Linkage Disequilibrium and Homozygosity Analysis

PCA of the Alaskan sled dogs identified two separate but closely related groups (sprint and distance) with PC1 accounting for 6% of the variation and PC2 through PC4 each accounting for 4% (Figure 2A). In a comparison of the domestic breeds and Alaskan sled dogs (Figure 2B), the first PC (PC1, 16%) separates the Northern breeds (AMAL and HUSK) from the BORZ and GSHP, with both sled dog populations falling between the breed extremities. PC2 (9.8%) separates the BORZ from the GSHP, while PC3 (6.1%) distinguishes the AMAL from the HUSK. PC4 (3.6%) separates all Alaskan sled dogs from all domestic breeds tested, while PC5 (1.9%) separates the sprint from distance sled dogs.

To assess inbreeding patterns associated with the Alaskan sled dog, we estimated the decay of LD and found that both sled dog populations had shorter distances to LD decay ($r^2_{0.5}$; sprint, 2.5–3.75Kb; distance, 7.5–10Kb) than any of the purebred groups (GSHP, 10–15Kb; HUSK, 15–20Kb; AMAL and BORZ, 20–30Kb) (Figure 3A). For the LD decay threshold of $r^2_{0.2}$, the AMAL, HUSK, BORZ, and distance sled dog populations had longer-range LD (>1Mb). LD at $r^2_{0.2}$ decayed at approximately 700 kb in GSP and 80 kb in sprint dogs, which is comparable with previously reported estimates (Gray et al. 2009). We also analyzed the genome-wide degree of autozygosity, or identity by descent, surveyed as the size distribution of homozygous tracts (runs of homozygosity, ROH) (Figure 3B) (Boyko et al. 2010). Trends were similar to that of LD decay, with domestic breeds having ROHs that

were of longer length (>2Mb) than the sled dogs, indicating a comparatively higher degree of inbreeding in the domestic breeds. However, the distance dogs had a slight inflation of ROHs of large size (~12Mb) compared to the sprint dogs, concordant with the previous inbreeding assessments reported for Alaskan sled dogs (Huson et al. 2010).

Selective Sweep

We identified 60 genomic regions with a selective sweep signature when comparing the sprint and distance populations using H_O and F_{ST} scans (Supplemental Table 1). Fifty-two (87%) of the regions showed a selective sweep in the distance dogs, while only eight were observed in the sprint dogs. The region of greatest H_O difference (0.833) was on canine chromosome 3 (CFA3) at 83,775,932 to 83,798,854 bp, and was observed in the distance dogs. The region is gene-poor, containing only two annotated genes within one Mb of the region boundaries, the most provocative of which is the ADP-ribosylation factor-like 2 binding protein *(ARL2BP)* gene, which is linked to mitochondrial activity in cardiac and skeletal muscle tissues (Sharer et al. 2002). The highest region of heterozygosity difference (0.75) within the sprint dogs was on CFA17 (8158751–8170123bp), but there are no obvious candidate genes ±1 Mb of the region boundaries (UCSC browser http://genome.ucsc.edu/).

Genome-Wide Association Study (GWAS)

Genome-wide association analyses were performed to identify loci associated with either population differentiation or the performance attributes of endurance or heat tolerance. Due to intense artificial selection for performance attributes in Alaskan sled dogs it was possible to utilize relatively small sample sizes of both cases and controls in comparison to human GWAS studies as exemplified by previous GWAS of humans and dogs (Hakonarson and Grant 2011; Parker et al. 2010). Six loci associated with sprint and distance population variation had p-values $< 4.68\times10^{-6}$ (permutated p-values $<3\times10^{-6}$) (Supplemental Table 2). SNP CFA3.82650187 had the most significant population association with a p-value of 1.03 $x10^{-7}$, and is located one Mb upstream from the selective sweep region containing *ARL2BP*. The next significantly associated region contained two SNPs in a gene-rich region (25 genes annotated in a ±1Mb window) on CFA11 (p-values of 1.00×10^{-6}). Of the 25 genes, the histidine triad nucleotide binding protein 1 *(HINT1)* gene, located approximately 70 and 600 kb (UCSC Browser, http://genome.ucsc.edu/), respectively, from these SNPs is the most interesting candidate for these studies. *HINT1* was previously associated with anxiety and stress coping behaviors in knockout mice (Barbier and Wang 2009; Varadarajulu et al. 2011)

Elite versus poorly performing dogs were assessed for each class of sled dog. While endurance in sprint sled dogs was associated with 15 loci, characterized by SNPs with p-values $< 1 \times 10^{-6}$, permutation testing proved all sites statistically unstable (p-values $>1 \times 10^{-4}$). Performance of the heat tolerance attribute in sprint dogs showed stronger association stability, delineating a region on CFA10 (31089847–31188654 bp) with four clustered SNPs (p-values 4.53×10^{-6} to 5.57×10^{-7}, and permuted p-values from 1.20×10^{-5} to 5×10^{-6}) (Figure 4 and Supplemental Table 2). The SNPs highlighting this region are either within or directly upstream of the myosin heavy chain 9 non-muscle type II class A *(MYH9)* gene. However, an additional 33 genes are annotated in a ±1Mb window around the critical SNPs, but these either do not have gene or protein function information or they have not demonstrated an association with heat tolerance. The *MYH9* gene makes for an intriguing candidate. It has been associated with muscle efficiency and differences in protein activity have been observed in an association with variation in muscle temperature (Burniston 2009; Gray et al. 2006; Ingalls et al. 1998).

Ancestry Modeling

A genome-wide ancestry profile was generated for the sprint and distance sled dogs to determine regions of ancestry selection based on the four reference breeds (AMAL, HUSK, GSHP, BORZ) (Huson et al. 2010). The genome has an overall mosaic structure in each of the sled dog populations (Figure 5). However on average the distance sled dog genome is composed of 32% AMAL, 26% HUSK, 23% GSHP and 19% BORZ, whereas the sprint sled dog genome is predominantly GSHP (33%), with 25% AMAL, 22% HUSK and 20% BORZ (Table 1; Figure 6A). Notably, GSHP was substantially higher in the sprint dogs, accounting for the largest proportion of ancestry (sprint, 33% and distance, 23%) (Figure 6A and Table 1). A genome-wide analysis of ancestry block frequencies demonstrated that the most frequent block in distance sled dogs was the AMAL (AMAL/AMAL, 13%; HUSK/AMAL, 13%; GSHP/AMAL, 13%; BORZ/AMAL, 11%) while it was the GSHP in sprint dogs (AMAL/GSHP, 16%; HUSK/GSHP, 13%; GSHP/GHSP, 13%; BORZ/GSHP, 12%) (Figure 6B and Table 1).

We identified 186 unique ancestry blocks in the Alaskan sled dogs that were private to either distance (n=97 unique blocks; median length: 1337Kb) or sprint (n=89 unique blocks; median length: 1137Kb) (Table 2). The most frequent of these blocks in distance dogs was AMAL/GSHP (18%, 80/447) and the longest ancestry block was a homozygous state of AMAL (2354Kb). Seventeen percent of the blocks private to the sprint dogs were of BORZ/GSHP ancestry, with the longest being of HUSK/HUSK ancestry (1891Kb) (Table 2).

We further identified 48 regions showing the substantial ancestry differences between the sprint and distance populations (Supplemental Table 3). The minimum ancestral frequency difference in these regions was 0.33, >2SD from the mean (mean = 0.095; 2SD = 0.26). The highest ancestral frequency difference was located on CFA 11 (18482294–23584745bp), a region that also had increased HUSK ancestry (frequency difference=0.510) in distance dogs. This 5Mb region contains two fibrillin genes (*FBN1*, *FBN2*) whose protein products are integral to the structure and function of connective tissue, as well as acyl-CoA synthetase long-chain family member 6 (*ACSL6*) and solute carrier family 27, member 6 (*SLC27A6*) genes which are important in fatty acid metabolism and transport respectively (UCSC Browser, http://genome.ucsc.edu/). Additionally *HINT1* is located within this region and corroborates our GWAS results (Barbier and Wang 2009; Varadarajulu et al. 2011). Overall, nineteen regions demonstrated a substantial excess of ancestry in sprint dogs, with two regions of excessive BORZ and 17 of excessive GSHP. The remaining 29 regions demonstrated an excess of ancestry in distance dogs, and include 15 AMAL, two BORZ, one GSHP, and 11 HUSK ancestry blocks.

We combined the results from the selective sweep, GWAS and ancestry analysis to tabulate the regions that have overlapping significant results for the sled dog populations. Here, we attempted to differentiate between random ancestry excess and non-random inheritance of variants due to the directional selection for functional phenotypes in the sled dog. Five selective sweep regions overlapped with four regions of ancestry selection and were located on CFA 3, 10, 16, and 28 (Table 3). CFA3 contains two selective sweeps in distance dogs that also contain a signal of positive selection for HUSK ancestry. This region includes the gene solute carrier family 2, member 9 (*SLC2A9*) gene, which is integral to glucose homeostasis as a glucose transporter (UCSC Browser http://genome.ucsc.edu/). CFA10 also had coinciding selective sweep and GSHP ancestry selection, but in different populations (Table 3). The nearest gene, methionine sulfoxide reductase B3 *(MSRB3)*, encodes a protein that performs crucial functions for cell protection against oxidative stress, which may be important for sled dogs that perform under extreme physiological and environmental conditions (Kwak et al. 2009).

Two distinct ancestry patterns occur in the selective sweep on CFA16. There is a large region of positive selection for GSHP ancestry (0.398 frequency difference, Supplemental Table 3) in sprint dogs, and a selective sweep with a 0.25 decrease in AMAL ancestry, coinciding with an increase of 0.25 for HUSK in distance dogs (Figure 7). Located within this region is the protein tyrosine phosphatase, receptor type, N polypeptide 2 *(PTPRN2)* gene, which functions in insulin binding and beta cell growth regulation within the insulin granule (Suckale and Solimena, 2010). CFA28 possessed a selective sweep (29046328–29143901bp) with an excess of AMAL (0.312 frequency difference) in distance dogs and a strong frequency difference for GSHP in sprint dogs (0.421). We identified attractin-like 1 (*ATRNL1*) as a candidate gene of interest in this region as it contributes to cognitive functionality, information processing, and distinct morphological characteristics (e.g. dysmorphic facial attributes and toe syndactyly) (Stark et al., 2010; Luciano et al.2011).

We further identified two regions, using both GWAS and ancestry analyses, on CFA 11 and 32 that significantly differentiated sprint and distance dogs (P-values $<1\times10^{-6}$) (Table 3). The CFA 11 locus was highlighted by two SNPs and provided independent confirmation of *HINT1* as a candidate gene (UCSC Browser, http://genome.ucsc.edu/) (Supplemental Table 3 and Index #18 & 19). The *MYH9* gene, investigated for its role in heat tolerance, also correlated with positive selection of the GSHP within sprint dogs (frequency difference 0.313). This region was not highlighted in our initial analysis because the frequency of ancestry fell below the 95th percentile threshold (frequency difference ≥0.333) (Supplemental Table 3). Overall, eight loci, identified by either GWAS or selective sweep, corresponded with an excess of one of the ancestral reference populations.

Fine-Mapping of the HINT1 and MYH9 Genes

Direct sequencing of the four *HINT1* exons and their surrounding region produced seven non-coding variants found in sprint and distance dogs. Six of the variants were found in GSHP and four were found within HUSK. None of the variants were found to be associated with the sprint or distance sled dogs.

GWAS identified two SNPs located within the *MYH9* gene with a significant association to heat tolerance, and two additional SNPs located 45Kb and 20Kb upstream of the 5′ end of the gene that were also significant. Direct sequencing of six elite and six poorly performing sprint dogs with regard to the heat tolerance attribute through the 40 *MYH9* exons and conserved flanking regions revealed 51 variants. Forty-three variants were within the *MYH9* gene, including five SNPs within exons, 43 SNPs within introns, and two indels within introns. An additional eight SNPs and two indels were found upstream of the 5′ end of the gene. Synonymous amino acid changes were found in exons 4 (31155024 bp), 9 (31161766 bp), 18 (31175229 bp), 24 (31181751 bp, and 29 (31184517bp).

We conducted a preliminary single-marker association analysis of 72 markers (indels and SNP) that compared six sprint dogs from each of the elite and poorly performing classes for heat tolerance. This analysis revealed 16 SNPs with raw p-values < 0.05 that were associated with poor heat tolerance. An additional 26 sprint dogs who are poor performers for the heat tolerance attribute and 15 sprint dogs who are high performers for the same attributes. Single marker analysis of these 16 SNPs comparing 32 (26+6) poor to 21 (15+6) elite sprint with regards to heat tolerance dogs yielded 14 SNPs with raw p-values < 0.05 (Table 4). Seven of these SNPs retained permutated p-values < 0.05, with the most significant SNP exhibiting a permutation p-value of 0.0001 (Table 4). A pairwise comparison of LD among these seven SNPs revealed substantial linkage (D′>0.90) for 65% of the pairwise comparisons, with the remaining 35% demonstrating moderate to strong LD (D′=0.6–0.9).

We also analyzed 16 SNPs from the *MYH9* gene using DNA collected from AMAL and GSHP, two breeds demonstrating excessive ancestry within the sprint dog genome. Three of the SNPs were found to be associated, demonstrating both raw and permutated p-values being < 0.05 (Table 5). SNPs CFA10.31115476 and CFA10.31123184 had similar allele frequencies between poorly performing (heat tolerance attribute) sprint dogs (p-value 2.02×10^{-6}, *G* allele 0.840; p-value 0.0024, *T* allele 0.553) and AMAL (p-value 4.92×10^{-5}, *G* allele 0.700; 6.00×10^{-4}, *T* allele 0.700). SNP CFA10.31156486, for which the *A* allele is associated with the Alaskan Malamute breed did not show a significant association to heat tolerance after permutation testing. Also, there were no significant differences in the allele frequency regarding poor (f_A=0.487) versus elite (f_A=0.310) sprint dogs with regard to heat tolerance.

Discussion

The Alaskan sled dog is the embodiment of a unique, genetically distinct breed developed solely by selection and breeding for athletic attributes (Huson et al. 2010). They possess a distinct admixed population structure, a consequence of crossing purebred dogs possessing desirable performance traits to what were at the time native Alaskan Sled dogs (Huson et al., 2010). The end result is two populations of modern Alaskan sled dogs, optimized for racing short (up to 48 kilometers) or long (~1,609 kilometers) distances. In this study we demonstrated that sprint and distance Alaskan sled dogs are genetically distinct, based upon results from two data, which corroborates our published findings done using microsatellite markers (Huson et al., 2010) in which microsatellite marker data was used to clustered dogs based on their racing style (Figure 2A).

We used a set of 7,644 AIM SNPs to model ancestry in sprint and distance sled dog populations with four known reference breeds: Alaskan Malamute, Siberian Husky, German Shorthaired Pointer, and Borzoi. The distance sled dogs had, on average, highest AMAL ancestry (32%) compared to sprint dogs whose highest ancestry was the GSHP (33%). As a result, the most frequent ancestry blocks contained at least one AMAL haplotype in the distance dogs and one GSHP haplotype in sprint dogs (Table 1). This distinct difference in ancestry is likely due to mating strategies that crossed closely related individuals together in order to retain desirable traits. It is likely, therefore, that there are selective advantages for a distance sled dog to have an excess of AMAL ancestry and for sprint dogs to retain GSHP ancestry. Other differences include the fact that distance dogs had a greater number of long (~12Mb) ROH, a length comparable to those found in purebred Siberian Huskies. Finally, when we compared the ancestry blocks unique to each population, we found that distance dogs have larger private blocks than sprint dogs (Table 2), a result that is concordant with previous microsatellite data and likely reflects the particular breeding strategies used to propagate the population (Huson et al. 2010).

Our ancestry analyses highlights 48 loci that demonstrated a substantial contribution to either the sprint or distance populations (Supplemental Table 3). Investigation of LOH produced sixty regions characterized by selective sweeps, with 87% of those occurring in distance dogs (Supplemental Table 1). While this may be indicative of complex genetic interactions with genes of small effect, we postulate that there are also more attributes under selection within distance dogs, therefore genomic variation should be, on average, more constrained. Some of these selective sweep regions may signify characteristics that are strictly maintained in distance dogs due to the extreme nature of their racing conditions (e.g. fur length, hair follicle density, hardiness of the toe pads). We utilized a unique approach that combined the ancestry results with selective sweep and GWAS methods to identify a subset of eight regions likely experiencing selective pressure within a sled dog population or due to their athletic performance. In all, five areas of selective sweep overlapped with four

regions of ancestry selection, with potentially interesting candidate genes located at several of the loci (Table 3). CFA3 displayed highly concordant results in the distance dogs. The remaining loci showed a more complex ancestry pattern where diversity derived from multiple breeds was obviously beneficial. Future research using a denser set of AIMs is required to understand how genes under selection are developed and maintained in breeds whose sole purpose is to perform. A denser set of SNPs is also needed to identify causative variants.

Genome-wide association analyses were used to identify loci associated with either population variation between sprint and distance dogs or the performance attributes of endurance or heat tolerance. Sampling sled dogs from high performing racing kennels compounded GWAS issues since there were few poorly performing (rank three) dogs for either endurance or heat tolerance. Therefore, it was necessary to pool dogs scoring a two and three for the GWAS, which decreased our ability to identify the desired loci. However this created a potential problem with differential relatedness among cases versus controls. In order to accommodate this problem, we closely matched cases and controls for analysis using EMMAX software, which corrects for both population relatedness and structure. The GWAS results overlapped with three loci that had an excess of ancestry (Table 3), with two of these regions (CFA11 and 32) related to sled dog population differentiation.

The *HINT1* gene on CFA 11 allowed us to explore the impact of differential ancestry on sprint versus distance dogs. We originally hypothesized that this gene may account for differences in stress coping abilities between the two groups. An excess of HUSK ancestry in distance dogs and GSHP in sprint dogs that overlapped the *HINT1* gene supported this idea, however no association was found with an *HINT1* variants and any population of dogs.

The remaining question of HUSK versus GSHP ancestry, however, is interesting. While the Siberian Husky has been characterized as “stubborn and easily bored” despite its hardy working dog nature, the German Short Hair Pointer breed is noted for its “ease of training and adaptability” along with its commitment to performing (AKC, 1998). Anecdotally, the “mental toughness” (ability to deal with stress) of Alaskan sled dogs crossed with German Shorthaired Pointers is a topic of debate among sled dog drivers with many feeling the cross has an increased desire to perform but may not handle stress as well as the non-Pointer crosses.

The heat tolerance attribute was associated with a cluster of four GWAS SNPs on CFA10, two of which were within the *MYH9* gene and demonstrated genome-wide significance (two highest SNPs had a P-value of 5.57×10^{-7}) (Figure 4 and Table 3). Previous research has associated an increase in myosin heavy chain production with increased cardiac output (Burniston 2009). Another study found a decrease in myosin heavy chain and actin within injured mouse extensor muscles accounts for approximately a 58% reduction in isometric titanic force output (Burniston 2009; Ingalls et al. 1998). Most notably, it has been reported that the percent increase of the myosin heavy chain type II class A within muscle tissue experiencing elevated temperatures (ET=37.5°C; Normal, N=34.2°C) correlates with the magnitude of increased power output. It is thought that slight temperature elevations improve muscle fiber power output through an increase in the rate of anaerobic ATP turnover and muscle fiber conduction velocity (Gray et al. 2006). However, the efficiency of muscle contraction actually decreased as temperature rose. Overall, Gray et al. (2006) has concluded that fibers with a high proportion of myosin heavy chain type II class A were the most sensitive to temperature fluctuations (Gray et al. 2006). We found that the *MYH9* gene overlapped with an excess of GSHP and AMAL ancestry in sprint sled dogs and our fine-mapping identified seven SNPs associated with heat tolerance (Table 4). The two most significantly associated (CFA10.31105851, 7.83×10^{-06}; CFA10.31115476, 2.02×10^{-06})

were 19Kb and 29 Kb upstream from the 5′ end of the *MYH9* gene and in nearly complete LD with the other four SNPs of note in this region (D′ ≥0.871). SNP CFA10.31105851 lies within a conserved region of the dog, human, and mouse genomes. In the human genome, chromatin profiling of human skeletal muscle myoblasts shows this region to be an active promoter site. At least seven other human cell types showed signs of having strong enhancers within this region. Likewise, a second SNP, CFA10.31121778, located in an additional conserved region upstream from the 5′end of the first region was also found to have a strong enhancer in the analogous region of the human genome (Ernst and Kellis 2010; Ernst et al. 2011). We postulate that variants within promoter and enhancer regulatory sites may be the means by which the canine *MYH9* gene potentially affects heat tolerance performance in sprint sled dogs, although functional studies remain to be done.

SNPs CFA10.31115476 and CFA10.31123184 differentiated significantly between the contributions of AMAL and GSHP (Table 5). Specifically, sprint dogs with poor heat tolerance had similar allele frequencies to AMAL. Elite heat tolerance sprint dogs had a decreased allele frequency at these same two SNPs, with GSHP having the lowest allele frequencies. Previous research associating muscle temperature elevation and power output, combined with our GWAS and fine-mapping results, highlight the *MYH9* gene as an intriguing candidate, potentially affecting the heat tolerance attribute in sprint sled dogs.

Our current study corroborated our previous finding that Alaskan sled dogs are two distinct populations, largely attributed to selective breed for their divergent racing styles (Huson et al., 2010). A number of candidate genes potentially affecting performance were highlighted by GWAS and selective sweep analyses within the sled dogs. In addition, we implemented methods from admixture mapping to pinpoint genomic regions that have an excess of a particular reference breed. We found *MYH9* to be associated with heat tolerance performance in sprint dogs, demonstrating the success of researching performance mechanisms within a group of recently admixed dogs. This study provides a foundation for the study of sled dog performance genetics, as well as breed origins. As ever-denser GWAS studies are performed and data sets are increased in size, the power to fine map and eventually identify truly causative variants will increase (Ostrander et al. 2009). Finally, our preliminary evidence suggesting a role for the *MYH9* gene in heat tolerance among sprint sled dogs highlights the types of genes and gene families that will likely become the basis of functional studies regarding performance enhancing genes in the years to come.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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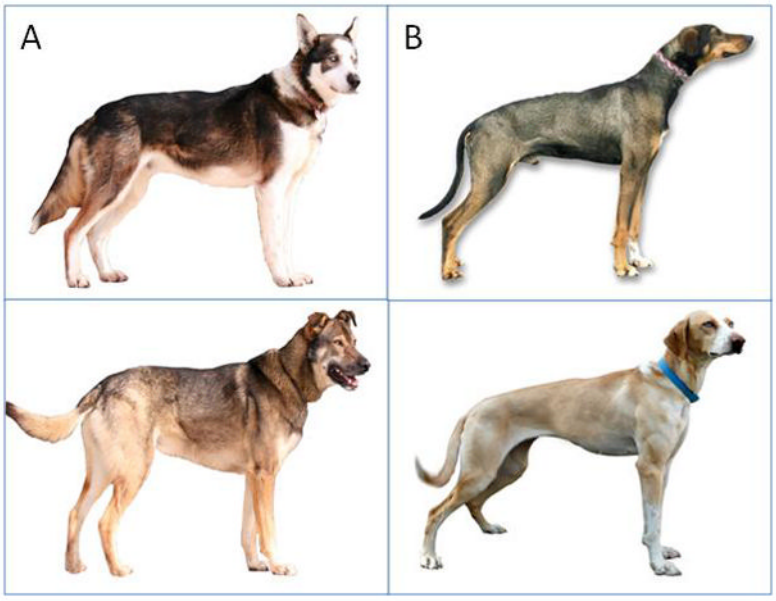

Figure 1.
Alaskan sled dogs are a mixed breed dog, bred strictly for performance attributes. **A**) Left column: distance racing dogs. **B**) Right column: sprint racing dogs.

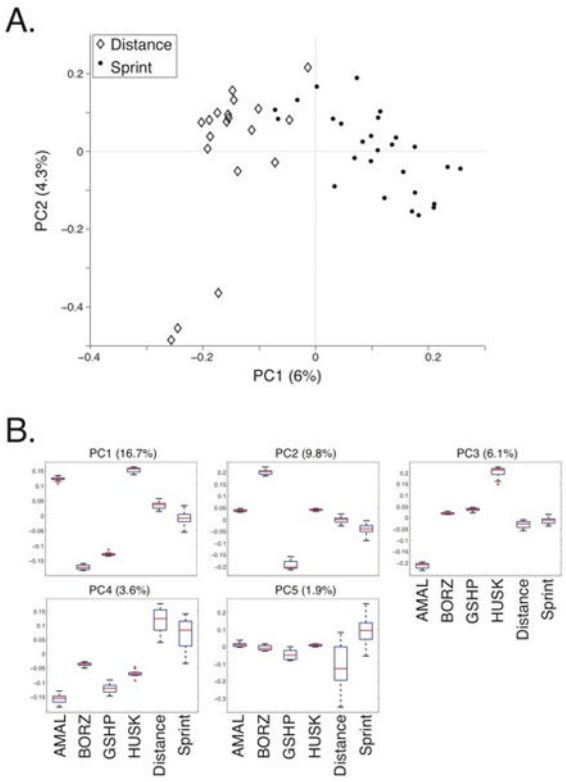

Figure 2.

Principle component analysis plots of Alaskan sled dogs (**A** and **B**) and four ancestry reference breeds (**B**) using a panel of 7K highly (F_{ST} >0.35) informative SNPs. **A**) Alaskan sled dogs from either distance (DIST-blue) or sprint (SPRT-red) racing kennels. **B**) Four ancestry reference breeds including AMAL, BORZ, GSHP, and HUSK as well as Alaskan sled dogs divided into their two populations of distance and sprint.

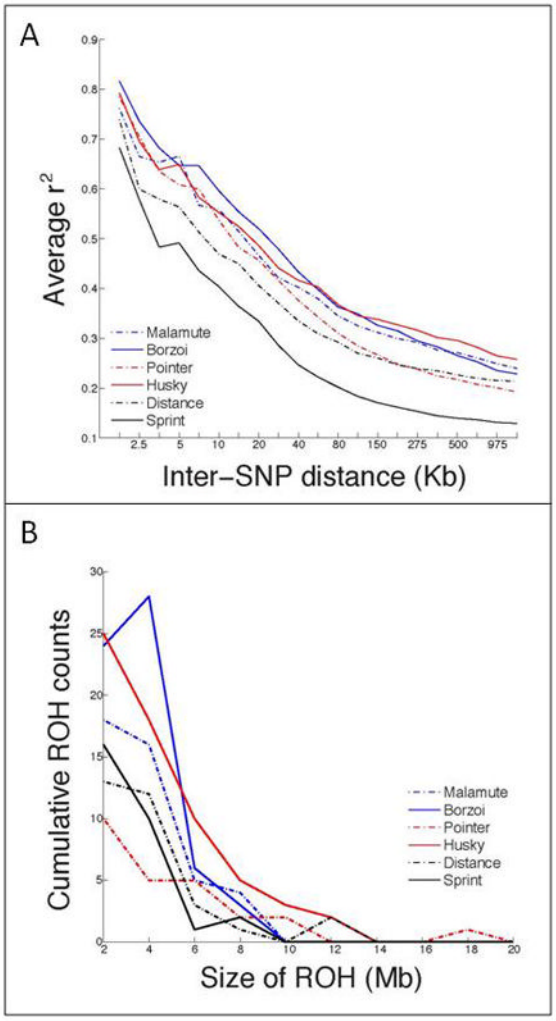

Figure 3.

The estimated decay of linkage disequilibrium and degree of autozygosity among Alaskan sled dogs and their four ancestral component breeds. Alaskan sled dogs are divided into distance and sprint racing styles, and compared with their four ancestral reference populations. **A**) The decay of linkage disequilibrium (LD) is estimated from the distance at which the genotypic association, r^2, reaches a threshold of 0.5. **B**) The degree of autozygosity is determined through the cumulative number of runs of homozygosity (ROH) of various length (Mb).

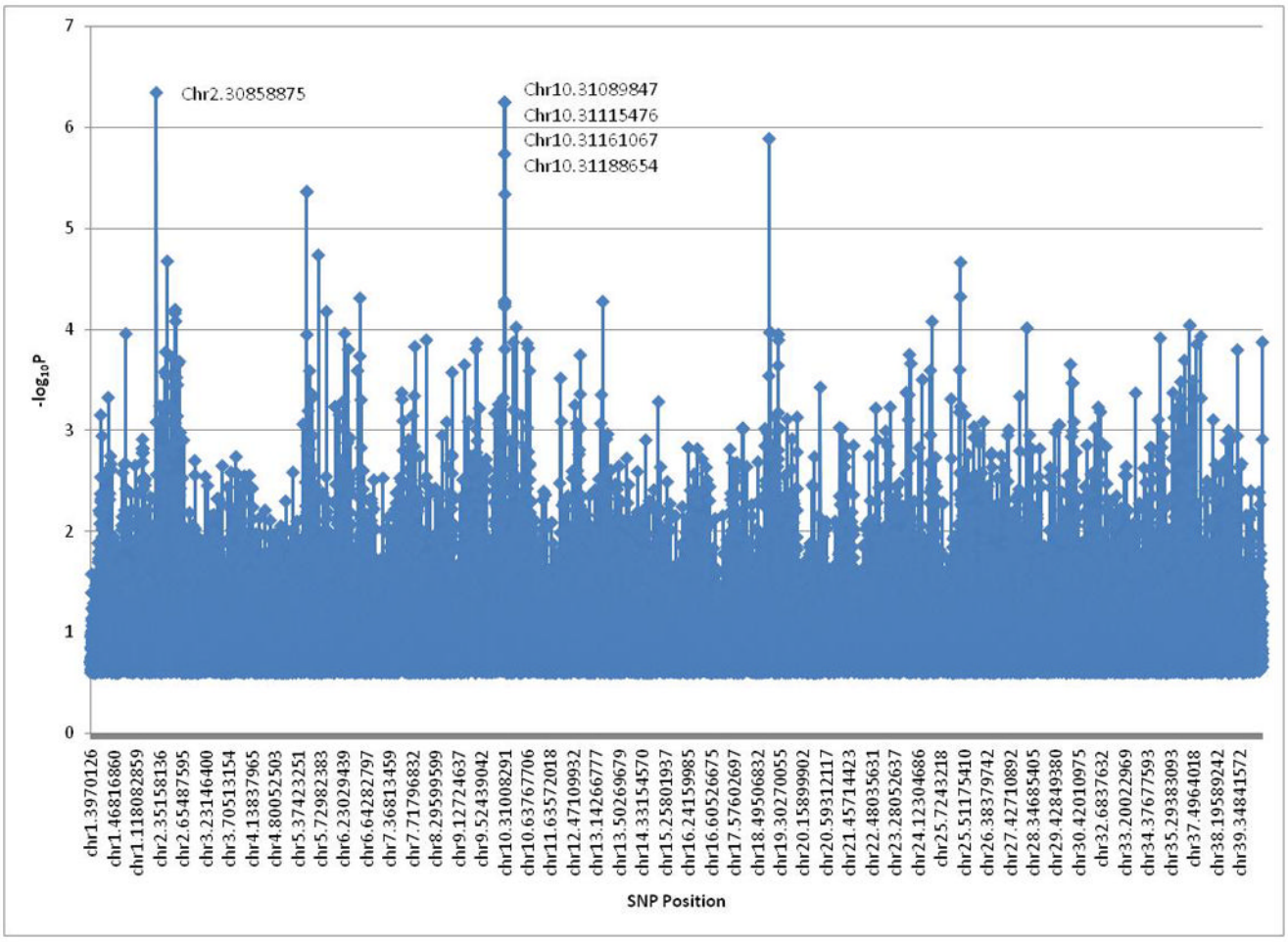

Figure 4.

Genome-wide association results of elite versus poorly performing sprint dogs for the heat tolerance attribute. Two genomic loci located on CFA2 and 10 were identified in a comparison of 21 elite and 17 poor performing sprint dogs with regard to the heat tolerance attribute. A panel of 115,425 SNPs, spanning all autosomes and the X chromosome was tested. The x-axis denotes SNP positions in increasing genomic order from CFA 1 through 38 and the X chromosome. The y-axis indicates the $-\log_{10}$ p-value as determined in an association analysis using the program EMMAX.

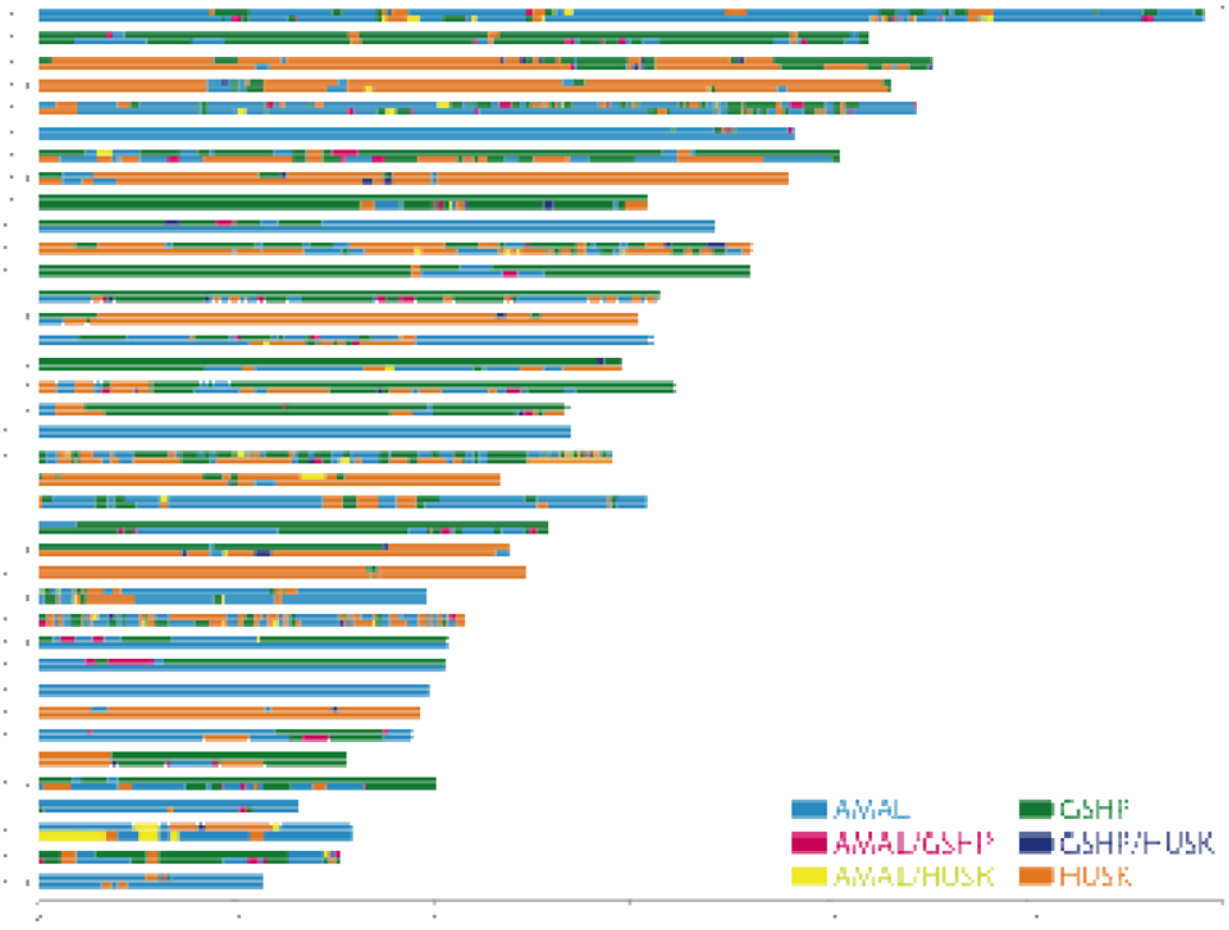

Figure 5.
A comparison of the most prevalent diploid state ancestry blocks across the genome of sprint and distance sled dogs. Individual chromosomes are indicated on the x-axis denoting genomic position (Mb). The most common diploid ancestry blocks across the genome are visualized using the following color scheme with the diploid states (homozygous or heterozygous) defined in the figure legend.

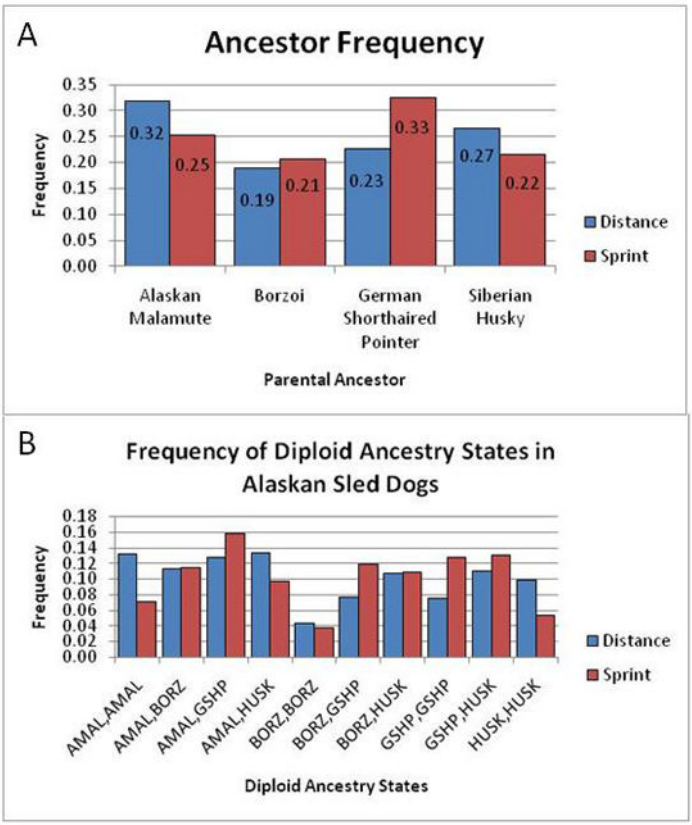

Figure 6.

A comparison of the genome-wide frequency of four ancestral reference breeds within the distance and sprint sled dog populations. **A**) The genome-wide proportion of the individual ancestral reference breeds of AMAL, BORZ, GSHP, and HUSK within the distance and sprint populations. **B**) The genome-wide proportion of diploid ancestry states within the distance and sprint populations.

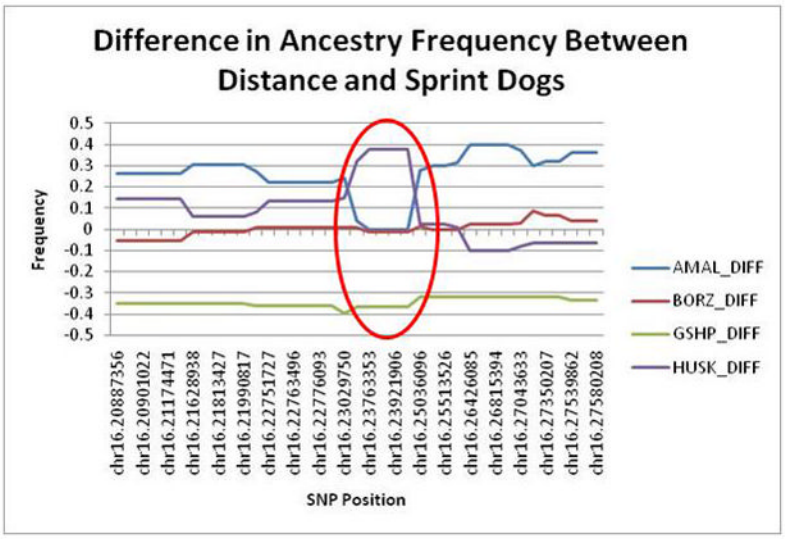

Figure 7.

Chromosome 16 SNP frequency differences for the four ancestral breeds when comparing distance and sprint populations. The difference in frequency scores (y-axis) between distance and sprint dogs for each ancestral breed was plotted in relation to chromosome 16 SNPs (x-axis). A more positive frequency difference corresponds to a higher selection of the ancestral breed within the distance population while the more negative frequency difference corresponds to a greater selection of the ancestral breed within the sprint population. The region within the red circle denotes an area highlighted as being in the top 5% of genomic regions demonstrating the greatest degree of ancestry selection between sprint and distance dogs, as well as corresponding to a region of selective sweep within distance dogs.

Table 1

The genome-wide frequency (*f*) of individual ancestral populations and their respective diploid ancestry states within the distance and sprint sled dog populations. Breed abbreviations are as in the Methods.

	Distance Sled Dogs[a]			
Breed[b]	**AMAL**	**BORZ**	**GSHP**	**HUSK**
AMAL	0.1328	0.1136	0.1279	0.1337
BORZ		0.043	0.0768	0.1074
GSHP			0.0754	0.1096
HUSK				0.0992
Total *f*(Distance)	0.3181	0.1884	0.2271	0.2664
	Sprint Sled Dogs[a]			
Breed	AMAL	BORZ	GSHP	HUSK
AMAL	0.071	0.1153	0.1582	0.0966
BORZ		0.0373	0.1194	0.1093
GSHP			0.1275	0.1313
HUSK				0.0535
Total *f*(Sprint)	0.2533	0.2059	0.3251	0.2158

[a] A total of 19 distance dogs and 27 sprint dogs, all unrelated at the grandparent generation, were used to generate population frequencies;

[b] A matrix of the diploid ancestry states with their respective genome-wide frequencies (*f*)

Table 2

The overall number, median length, and genome-wide frequency (*f*) of diploid ancestry blocks found exclusive to either the distance (**A**) or sprint (**B**) sled dog populations. Breed abbreviations are as in the Methods.

A.

	AMAL	**BORZ**	**GSHP**	**HUSK**
Number of ancestry blocks (total n=447)				
AMAL	45	35	80	72
BORZ		12	35	44
GSHP			40	52
HUSK				32
Median length (Kb) of ancestry block				
AMAL	2354	1660	1464	1428
BORZ		1046	1062	1151
GSHP			1740	1083
HUSK				1581
f (ancestry block)				
AMAL	0.101	0.078	0.179	0.161
BORZ		0.027	0.078	0.098
GSHP			0.09	0.116
HUSK				0.071

B.

	AMAL	BORZ	GSHP	HUSK
Number of ancestry blocks (total n=392)				
AMAL	17	37	54	58
BORZ		9	65	46
GSHP			39	44
HUSK				23
Median length (Kb) of ancestry block				
AMAL	1671	1054	939	967
BORZ		1112	926	1112
GSHP			996	1333
HUSK				1891
f (ancestry block)				
AMAL	0.043	0.094	0.138	0.148
BORZ		0.023	0.166	0.117
GSHP			0.01	0.112
HUSK				0.059

Table 3

Description of the genetic loci demonstrating the highest degree of interest for population differentiation or performance association within Alaskan sled dogs. SNP positions are based on the CanFam2 assembly.

Method of Identification[a]	Chr	Start (bp)	End (bp)	Block length (bp)	Sled Dog Population[b]	Ancestry Population[c]	GWAS Association[d]	Performance Candidate Genes	Number of Genes within Region[e]
Selective Sweep, SABER	3	71896408	71898732	2,324	Distance	HUSK		*SLC2A9*	11
Selective Sweep, SABER	3	72727082	72784438	57,356	Distance	HUSK		*SLC2A9*	14
GWAS	3	82650187					Population	*ARL2BP*	2
Selective Sweep	3	83775932	83798854	22,922	Distance			*ARL2BP*	2
Selective Sweep, SABER	10	11081762	11121003	39,241	Distance	GSHP		*MSRB3*	15
GWAS, SABER	10	31089847	31188654	98,807		GSHP	Heat Tolerance	*MYH9*	34
SABER	11	18482294	23584745	5,102,451	Distance	HUSK		*FBN1, FBN2, ACSL6, SLC27A6, HINT1*	51
GWAS, SABER	11	22331950	23117401	785,451		GSHP/HUSK	Population	*HINT1*	25
Selective Sweep, SABER	16	23391731	23391985	254	Distance	GSHP		*PTPRN2*	13
Selective Sweep, SABER	28	29046328	29143901	97,573	Distance	GSHP		*ATRNL1*	12
GWAS, SABER	32	8774288				German Shorthaired GSHP	Population	*HBZ*	11

[a] Genomic regions of interest were determined by demonstrating an excess of breed ancestry (SABER), selective sweep, or genome-wide association;

[b] The sled dog population in which the selective sweep was significant;

[c] The reference breed population of excess ancestry;

[d] The sled dog population in which the genome-wide association was significant;

[e] Total number of human genes annotated within the genomic region of interest as well as 1MB upstream and 1MB downstream of said region.

Table 4

SNPs within and surrounding the *MYH9* gene on canine chromosome 10 associated with heat tolerance performance in sprint racing Alaskan sled dogs. (heat tolerance, HT; minor allele frequency, MAF)

CanFam2 Position	Alleles[a]	Poor HT[b] MAF	Elite HT[c] MAF	Poor HT Assoc Allele	p-value	Permutation p-value
31089847	A:C	0.240	0.700	A	1.28E-05	0.0008
31105851	A:G	0.222	0.643	A	7.83E-06	0.0004
31115476	G:A	0.160	0.643	G	2.02E-06	0.0001
31121778	A:G	0.338	0.700	A	2.00E-04	0.0082
31123184	C:T	0.553	0.262	T	0.0024	0.0645
31128725	G:A	0.320	0.643	G	0.002	0.0612
31134023	C:A	0.320	0.643	C	0.002	0.0612
31145292	G:A	0.320	0.650	G	0.0018	0.054
31156535	C:A	0.132	0.350	C	0.0058	0.2197
31161067	C:T	0.263	0.643	C	5.48E-05	0.0024
31172587	T:C	0.385	0.690	T	0.0014	0.0425
31176097	C:T	0.270	0.619	C	2.00E-04	0.0086
31188654	G:A	0.365	0.619	G	0.0083	0.3093
31234860	G:A	0.840	1.000	A	0.0067	0.2402

[a] Major:minor allele;

[b] Frequency of the minor allele in 32 poorly performing heat tolerance sprint dogs (cases);

[c] Frequency of the minor allele in 21 elite performing heat tolerance sprint dogs (controls).

Table 5

MYH9 gene SNPs on canine chromosome 10 associated to either the Alaskan Malamute or German Shorthaired Pointer breeds. (heat tolerance, HT; minor allele frequency, MAF)

CanFam2 Position	Alleles[a]	AMAL[b] MAF	GSHP[c] MAF	AMAL Associated Allele	p-value	Permutation p-value
31115476	A:G	0.700	0.091	G	4.92E-05	0.0001
31123184	C:T	0.700	0.062	T	6.00E-04	0.0047
31156486	G:A	0.700	0.071	A	0.0013	0.0093

[a] Major:minor allele;

[b] Frequency of the minor allele in 6 Alaskan Malamutes (cases);

[c] Frequency of the minor allele in 8 German Shorthaired Pointers (controls).