



BACKGROUND

- Siberian Huskies were originally bred 3,000 years ago by the Chukchi people of northeastern Asia. Changing conditions forced natives to expand hunting grounds, forcing them to develop a unique sled dog breed. They created an endurance sled dog, capable of traveling long distances at moderate speed, carrying a light load in low temperatures. (AKC, 2017)
- These dogs were brought to Alaska in the late 1800s to aid in the Alaska Gold Rush. In 1909, a team of Siberians was imported to Nome by a Russian fur trader. This team one first place in the All Alaska Sweepstakes that year. (SHCA, 2009)
- ✤ In 1925, a huge diphtheria epidemic occurred. Dog driver, Leonard Seppala, completed the last leg of a volunteer sled dog relay into Nome with 20 Siberian Huskies covering 600 miles.



Left: Leonard Seppala, 1925

Right: Tsuga Racing Siberians Kennel. 2008. Yukon Quest.

- Siberian Husky (SH) popularity gained them recognition by the American Kennel Club in 1930.
- ✤ Modern Siberian Huskies remain proficient in sledding but are also bred as show and companion animals.
- ✤ Racing SH are selected for endurance and hardiness, while show dogs undergo more rigid selection for their appearance and stature. Companion dogs are often selected for behavior and may not meet sledding or show requirements.

OBJECTIVES

- To explore the performance and conformation variation within Siberian Huskies particularly with regards to those bred as sledding, show, or companion dogs.
- To identify the genetic variants responsible for the selection criteria prioritized within each subgroup

STUDY DESIGN & METHODS

- Health and usage of the animal were owner reported. Pedigrees were collected when available. ANOVA and Principle Component Analysis (PCA) were used to evaluate phenotypic variation.
- PCA, marker based F_{ST} , ROH, and GWAS were used to explore genetic variation in the breed

Phenotypic analysis

Genetic analysis



RESULTS

Conformational Variation in Siberian Huskies

- ✤ 43 sled, 55 show-sled, 29 show, and 31 pets were used in this analysis.
- ✤ PC1, accounting for 28.35% variation, reflected overall body size.
- ✤ PC2, reflecting 14.22% variation, separated sled dogs from the remaining groups; these dogs were taller in height with larger chests, but had shorter legs in proportion to their bodies.
- PC3 represented dogs with wider head dimensions and larger bone circumferences being shorter in length and height. This indicated that dogs with a stockier frame are being distinguished from taller, finer boned dogs

THE IMPACT OF SELECTION ON GENETICS WITHIN SIBERIAN HUSKY BREED

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Innisfree Kennel. Siberian Specialty Show.

Figure 1: Principal Component Analysis of Body Measurements of 158 Siberians







F _{st} analysis	Gen
Pet vs Show	Cellu
	stres
	gluco
Pet vs Sled	Mitra
	iron (
	proce
Show vs Total	Heat
	neur
Sled vs Show	Chole
	oxyge
Sled vs Total	Plate
	meta
	nervo





Genetic Variation in Siberian Huskies continued

* Runs of Homozygosity (ROH) is a method to determine signatures of selection. If a mutation gives a population a positive advantage, then the frequency of this mutation will increase over time.

Gene functions

Lipid catabolism, cAMP pathway in glucose and lipid metabolism, cardiac muscle/circulation, world class endurance athletes

Retinal development, development of cranial bones, disorders associated with facial/skeletal malformations, neurological disorder associated with respiratory failure

Enhancement in contextual fear, spatial memory, food motivation, age-induced motor coordination decline

Nervous system evolution, leg weakness related traits, coat color, ADHD, stress response, muscle damage response

DISCUSSION

Phenotypic analysis: Based on all 158 dogs. Conformational differences

Three principle components were generated. Although the first PC represented overall body growth and did not vary between groups, PC2 showed differences in comparing sled dogs to the remaining population.

Using PCA, it was evident that animals tended to cluster together based on usage identification suggesting phenotypic selection criteria led to the selection of genes differentiating animals by subgroup

Genes identified in Fst comparisons seem to reflect some biological advantage that would be useful for sled dogs, such as protein and lipid catabolism and oxygen transport. ROH identified clusters that were more prevalent in a given

- Genes within the ROH for sled dogs again related to catabolism for energy. One gene was associated with human world class endurance athletes!
- Gene functions for show dogs related to conformation and skeletal formation.
- Show-sled dogs had genes relating to memory and food motivation, which might be necessary to preform in both sledding and show.
- Pets might not have the mental or physical stress tolerance to be a part of the other groups.

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