Introduction

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The publication of a “canines only” issue of Mammalian Genome represents a landmark for the field. Previously, it was unclear that the field was big enough, and the stories sufficiently provocative, that such an issue would make compelling reading for the larger fields of mammalian genetics and genomics. However the amazing progress of the field in the last 10 years, as demonstrated by the following papers, easily allays that worry.

Dogs have fascinated geneticists since at least the time of Darwin. Locked within their genome is an astounding amount of morphologic and behavioral variation that manifests in the 300 plus dog breeds that exist worldwide. Although not all, most dog breeds have been around for a comparatively short time, perhaps just a couple hundred years as reviewed in the paper by Wayne and vonHoldt. The population structure of many breeds, as reviewed by Parker, features popular sires whose gene pool is over-represented in the breed, as well as bottlenecks that decreased the number and then expanded the frequency of particular alleles. The structure of each breed has been further shaped by the common practice of breeding closely related individuals in an effort to propagate particular morphologic and behavioral features within each breed. This makes dogs unique in the field of genetics. While a few dozen isolated human populations exist and have proven useful for mapping disease genes, literally hundreds of dog breeds exist, offering a much broader opportunity to map genes associated with morphology, behavior, and disease susceptibility.

It is often said that modern domestic dog breeds display a greater level of morphologic variation than is seen in any other land mammals. Examples of extreme differences in size (from 2 to nearly 200 lbs) are often cited as examples, along with differences in pelage, leg length, width, and skull shape. The strong selection for particular morphologic traits has resulted in an excess of some diseases among particular breeds, as deleterious alleles have presumably “piggybacked” along with desired traits. This offers a unique opportunity for comparative geneticists to study disorders that have proven intractable through studies of human populations or families. Unlike mice, most canine diseases present in a way that is reminiscent of the comparative human disorder with similarities in presentation, pathology, disease progression, treatment and outcome. Several of the reviews, therefore, deal with various classes of canine diseases such as copper metabolism, epilepsy, and retinopathies. Renowned experts in their respective fields present new data for retinal degeneration, pancreatic acinar atrophy, dwarfism and disorders of the vascular system. The applicability of findings from canine genetic studies to humans is also reviewed in, for example, the article by Kornegay, who describes the use of canine models of Duchenne Muscular Dystrophy to assess putative therapies for humans. Not surprisingly many of these types of studies have resulted in the development of genetic tests, and the current status of genetic testing in domestic dogs is reviewed by Mellersh.

All of these studies have been made possible by the availability of a 7.8× whole genome assembly of the dog and the associated availability of single nucleotide polymorphism chips. The current status of canine sequence annotation, including a discussion on finding missing genes, is reviewed by Dierren and colleagues. Studies of gene families, in particular the olfactory gene family is

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discussed by Quignon et al. and our current understanding of copy number variation in the dog, particularly as it relates to phenotypic changes, is summarized by Alvarez and Akey.

No discussion of canine genetics would be complete without some commentary on behavior. This issue contains two such papers. The first is a review of a long term project aimed at finding genes for domestication in the silver fox through generational breeding of animals showing ever less aggressive behavioral traits. The study is expansive with aims of finding genes that account for present day changes in both morphology and behavior, as reviewed by Kukekova and colleagues. The second paper is an original article that addresses the genetics of performance in

Alaskan sled dogs who excel at long versus short distance races by Huson et al. Finally, we are fortunate to have a proposal in this issue by Wilson and Wade, who suggest the existence of an international central repository for breed-based genetic analysis and information. Modeled on a similar repository in existence for dairy cattle, the repository would facilitate the work of everyone in the dog genetics community by providing up-to-date and ready access to critical information.

In summary, canine genetics is a field that has blossomed enormously in the last 10 years. This issue represents some of the best that the field currently has to offer. We hope you enjoy reading and look forward to assembling similar issues in the future.