

# Tracking genes and finding mutations: finding genes for complex traits in the domestic dog (*Canis familiaris*)

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## Introduction

The wide variety of physical variation exhibited among the 155 recognized dog breeds in the United States, coupled with the low genetic diversity within each breed, and a completed draft genome sequence make the dog an excellent genetic system for mapping complex traits of interest. Here, we present results for simultaneous whole-genome association mapping of morphological trait differences among various dog breeds.

## Methods and materials

We genotyped a total of 900 domestic dogs, representing 85 breeds and 100 wild canids. Genotyping data were collected using the Affymetrix Canine Array v.2.0, which provides usable data on ~ 60 000 single nucleotide polymorphisms (SNPs) per sample. Population genetic analysis of the SNP chip data revealed clear genetic clustering of pure-bred dogs into breeds with well-defined boundaries, with shallow clustering of some breeds into higher order groups and substructures within popular breeds (e.g. Beagles and Labradors).

## Results

Using a mapping strategy that accounts for expected high genetic relatedness within a breed, we identified regions of the dog genome associated with over 50 unique traits. Specifically we replicated previously identified gene-trait

associations, including the link between the *IGF-1* gene and body size. Subsequent analyses identified additional loci for body size, and loci for leg length and width, proportional dwarfism, and hair-specific phenotypes including growth pattern, length and curl and skull shape. For several traits, overlying 'peaks' of association with signatures of selection enabled us to refine our signals to a just a few or even one candidate gene.

## Conclusions

Genes and loci identified in this study are likely to be important in multiple other contexts with regard to mammalian development and disease. Thus, these data have implications for understanding the genetic structure of the dogs, and understanding the vocabulary of genes that contribute to seemingly complex phenotypes.

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