Identification of obesity risk variants in the dog genome using whole-genome sequencing

Popular summary

The dog is an important companion species and animal model in biomedical studies. Obesity is an important disease in dogs. Because obesity decreases life span and is related to several other diseases, we need to understand the causes of obesity for prevention and treatment. Obesity is caused by many genetic variants but most of them remain unknown. In animal DNA there are many regions with duplications of missing fragments (CNVs). The primary goal of this study is to search for CNVs associated with obesity in dogs. Our second goal is to improve annotation of dog DNA. We will sequence whole DNA from obese and control dogs in order to detect CNVs that occur in obese dogs but not in control dogs. Moreover, we will describe all CNVs in dog genome and compare them to CNVs in human genome.

Our research will contribute to understanding of the mechanism of fat tissue accumulation, including obesity in humans, which has become an epidemic disease. Common environmental factors shared between humans and dogs give a chance that investigation of mechanism under gene-environment interaction in dogs will elucidate the way in which environmental factors influence obesity in humans. Moreover, the unique structure of dog genome variability brings a chance for identification of casual variants with smaller effect that were missed in studies on humans or variants that are rare in human populations but frequent in dogs.