Public Abstract

First Name:Holly

Middle Name:R

Last Name:Ramey

Adviser's First Name:Jeremy

Adviser's Last Name:Taylor

Co-Adviser's First Name:

Co-Adviser's Last Name:

Graduation Term:SP 2015

Department:Genetics Area Program

Degree:PhD

Title:Mapping natural and artificial selection events in animal genomes

Selection events, of both artificial (human-imposed) and natural origin, have left their mark on animal genomes. These signatures are detectable through a variety of analyses and utilizing these types of studies in large animal datasets and are advantageous for the discovery and identification of causal mutations that significantly affect the way an animal or even human look or behave. Elucidating the mutations or variants responsible for these types of variation is important to understand what makes individuals or groups of animals unique. Which mutations create the change in nucleotide sequence that is responsible for black coat colour in Angus cattle, the flattened facial appearance in Pugs, or the quality of meat an animal produces? These types of questions can be investigated by genetic mapping. The research herein pertains to mapping within the genes of an individual or a breed group. Runs of homozygosity, regions of the DNA where every individual or a large proportion of individuals within a population share the same genetic sequence, are indicative of selection events. Furthermore the interaction of multiple genes, epistasis, is helpful in determining where not only one mutation but multiple mutations interact and have an effect on a trait that is larger than any single mutation. This dissertation provides a look at homozygosity mapping and detection of epistasis to determine genes and regions of the genetic sequence that are under selection for various reasons. The work presented will help to provide deeper insight into the unique genetic variation that makes individuals.