Public Abstract

First Name:Jared

Middle Name:Egan

Last Name:Decker

Adviser's First Name:Jeremy

Adviser's Last Name:Taylor

Co-Adviser's First Name:

Co-Adviser's Last Name:

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As the world's population grows, the need to grow food in a sustainable and efficient manner will become increasingly important. To achieve this goal for beef production, traits for which it has traditionally been difficult to produce estimates of genetic merit will need to be altered using artificial selection. Accomplishing this will require the use of genomic tools to identify superior animals. In this population genomics research, the worldwide genetic diversity of cattle is described. This information is important for the design of future studies, such as the discovery of genetic variants underlying phenotypic variation or for across-breed genome-wide association studies. Furthermore, this research clarifies the history of cattle domestication, transportation, breed formation, and selection, and provides a glimpse into the recent history of our own species. This research also identifies regions of the genome which have been the targets of natural and artificial selection. These regions are important as they must contain mutations which affect the variation in important fitness and production traits. The analysis methods developed in this dissertation can be applied to other species including human.