

# EVOLUTIONARY RELATIONSHIPS AND SIGNATURES OF SELECTION IN CATTLE ESTABLISHED USING GENOME-WIDE SINGLE NUCLEOTIDE POLYMORPHISMS

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## ABSTRACT

Although high-throughput single nucleotide polymorphism (SNP) microarray assays were primarily developed for association studies, they are a powerful tool in the study of evolution and population genetics. The applications of SNP genotypes to phylogenomics and population genetics were extended in this dissertation. Using SNP probes designed in a single species, a well-resolved phylogeny of 61 species was produced. Ancestral relationships between cattle breeds were analyzed using parsimony analysis of homozygous genotypes, parsimony analysis of all genotypes, network analysis using  $F_{ST}$  estimates, principal component analysis, and admixture analysis. A novel method to identify molecular signatures of selection was deployed. In this method, birth date was analyzed as the dependent variable in a mixed model framework to identify SNP loci which predict birth date. It was shown that predictive loci changed in allele frequency much more than theoretically expected due to genetic drift alone; thus, these loci are in linkage disequilibrium with selected casual variants. In addition to identifying loci under artificial selection, loci putatively responding to natural selection were also identified.