Mapping Recent and Ongoing Polygenic Selection in Beef Cattle Populations.

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Abstract: Understanding the underlying effects of ongoing selection is of interest to livestock breeding programs. Commercial livestock genotyping has generated datasets well-suited to explore how strong artificial selection has impacted the genome over very short time periods. We have developed a method for mapping ongoing polygenic selection in populations with temporally stratified genomic data called Generation Proxy Selection Mapping (GPSM). GPSM utilizes a genome-wide linear mixed model to identify allelic associations with an animal's generation number or some proxy (i.e., birth date). We applied GPSM to two large contemporary beef cattle datasets from Red Angus (n = 46,454) and Simmental (n = 90,580) breeds, with 11,759,568 high-quality imputed variants per animal. This analysis identified 294 distinct loci actively under selection. Due to the high power of these datasets, we found that GPSM could detect very small and recent (< 10 years) allele frequency changes consistent with polygenic selection. These analyses identified 294 distinct loci actively under selection. Due to the high power of these datasets, we found that GPSM could detect very small and recent (< 10 years) allele frequency changes consistent with polygenic selection. These analyses identified variants within genomic regions associated with known breed characteristics, like fertility and maternal ability in Red Angus and carcass merit and coat color in Simmental. Over 60% of GPSM loci resided in or near (< 50kb) annotated genes. We leveraged the resolution of our imputed sequence variants to overlay known epigenetic marks and possibly functional regions. 36% of GPSM loci overlapped these putatively functional regions genomic intervals. In addition to GPSM, we used two other more traditional selective sweep methods, the number of segregating loci (nSL) and Raised Accuracy in Sweep Detecting (RAiSD), to detect selection in this data. We observed minimal overlap (< 10% of loci) between traditional selective sweep mapping and GPSM. This suggests that selection mapping with GPSM can complement traditional sweep mapping methods when temporal genomic data exists. In addition to better understanding the biological processes and features that underlie artificial selection, GPSM signatures might serve as important genomic annotations.

Keywords: beef, selection, GWAS

Origins, Timing and Introgression of Domestic Geese Revealed by Whole Genome Data.

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Abstract: Geese are one of the most important poultry around the world. For the origin of goose, the current generally accepted hypothesis is that the European domestic goose were originated from the greylag goose (Anser anser), and the Chinese domestic goose have two origins, most breeds of which originated from the swan goose (Anser cygnoides), and the Yili goose originated from the greylag goose. In order to explain the origin and demographic history of goose, we selected 14 goose breeds from Europe and China and wild populations of swan goose and greylag goose, whole genome resequencing data were obtained for 74 samples. Population structure analysis and phylogenetic trees showed that the wild ancestor of the Chinese domestic goose except for Yili was the swan goose, and the wild ancestor of the Chinese Yili goose and European domestic goose was the greylag goose. Analysis of the demographic history suggests that the domestication of the Chinese goose occurred about 3499 years ago and that of the European goose happened about 7552 years ago. Furthermore, there is gene flow found between the domestic goose and their wild ancestors. Analysis of introgression showed that Yili geese had been introgressed by the Chinese domestic goose, and the body size of Yili goose could be influenced by the introgression events of some growth-related genes including IGF-1. Our study provides evidence for the origin of goose at the genome-wide level, and advances the understanding of the history of goose domestication and the traits affected by introgression events.

Keywords: goose; domestication; phylogeny; introgression