

Abstract by Anthony Doran - Genome-Wide Associations for Carcass Traits in Irish Holstein-Friesian Cattle

Genome-wide methods have been identified as the foremost approach to fully investigate polygenic traits such as disease susceptibility, health and growth. The aim of this study was to unravel the genetic architecture influencing growth and carcass characteristics using phenotypes of four carcass traits; carcass weight (CWT), carcass fat (CFAT), carcass conformation (CONF) of progeny as well as cow carcass weight (CULL). Two genome-wide association approaches were performed on data from 1,061 Holstein-Friesian artificial insemination bulls with progeny in Ireland. The first approach included SNPs individually in a linear mixed model. Following adjustment for a false discovery rate of <5%, the number of SNPs associated with each trait were 2, 25, 496 and 48 for CWT, CFAT, CONF and CULL respectively. The second statistical approach used a Bayesian mixture model. This method allowed the incorporation of prior knowledge about the distribution of SNP variances and effects. SNP posterior probabilities (PP) for each trait were calculated using alternative prior distributions of the proportion of SNPs that were associated with each trait. Investigation of PP and the occurrence rate of SNPs across priors found 4, 5, 6, and 5 SNPs for CWT, CFAT, CONF and CULL respectively. Results from this study have identified candidate regions of the genome that warrant further investigation to identify key genes and gene pathways involved in growth and carcass related traits.