

Impact of genomic selection for growth on feet and leg structure in Angus cattle

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We aimed to examine genetic parameter changes in feet and leg structure, and growth traits over time in Angus cattle. Additionally, new predictivity-based formulas were tested for estimating heritability and genetic correlations. The analysis was conducted using the blupf90+ family of programs. To estimate variance components (VCE), sampled data (2011-2022) from the American Angus population included 311K growth traits (GT) records [birth (BW), weaning weight (WW), and post-weaning gain (PWG)], ~70K feet traits (FT) records [claw set (CS) and feet angle (FA)], and 142K genotypes. The dataset was split into five-year intervals. Since FT ranged from 5-9, and 5 is ideal, a negative correlation is desired between FT and GT. The correlation FA-PWG, changed in an undesirable way over time, as it was -0.15 in the first interval, and it was 0.02 in the last interval. The correlation FA-WW is becoming more favourable over time, shifting from 0.05 in the first interval to -0.18 in the last interval. The GT selection process shifted the correlations between CS and GT in the desired direction, changing from positive (~0.1) to almost zero in the more recent two intervals. To test the predictivity-based formulas, Genomic Estimated Breeding Values (GEBV) were estimated using GT data from 6.3M animals born from 2000 to 2022. The data was divided into four slices, each with a 2-year validation period. Over time, heritabilities remained constant: ~0.3 for BW and WW and ~0.2 for PWG. Correlations between GT also remained constant over time, approximately at 0.45 for BW-WW, 0.3 for BW-PWG, and 0.75 for WW-PWG. Although the formulas show promising results for heritabilities, interpreting the outcomes of genetic correlation estimation remains unclear, needing further tests. While certain correlations between FT and GT suggest a positive impact of genomic selection over time, there are also some undesirable outcomes. This emphasizes the need for a multi-trait genomic selection approach to mitigate genetic antagonism. The adoption of predictivity-based formulas not only reduces the time required for genetic parameter estimation but also enables the utilization of complete data information instead of sampled data, as is currently done