Genomic testing does not correlate with performance trait phenotype in crossbred calves

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Interest in genetic improvement of performance traits in beef cattle using genomic testing is increasing. Genomic testing is especially appealing for young animals who have no progeny of their own on which to judge their genetic merit. In crossbred production systems, medium density genomic panels measuring 50,000 single nucleotide polymorphisms are compared to values from purebred individuals. However, research in crossbred cattle validating accuracy of genomic testing results when compared to actual traits expressed by individual animals (phenotype) is lacking. The objective was to compare actual performance traits in weaned calves to results provided by 2 independent genomic testing companies (Neogen, Lansing, MI and Zoetis, Parsippany, NJ). It was hypothesized that genomic testing results for performance traits are highly correlated with phenotype. Crossbred (predominately Angus) calves (n = 94) pastured at Oregon State University's Soap Creek Ranch were included in this study. Birth and weaning weights were recorded for each calf. On the first day after weaning, calves were restrained in a squeeze chute and 10 ml of blood was collected from the tail vein into Vacutainer® tubes with EDTA. As calves were released from the chute, docility was scored using a 1 - 6 scale.[1] In accordance with instructions provided by each genomics testing provider, 1 or 2 drops of blood from each calf were deposited onto each manufacturers' blood cards and they were shipped overnight to each manufacturer for testing. On the second day after weaning, calves were restrained in a squeeze chute for ultrasonographic evaluation of two carcass traits using a 5 MHz, linear array transducer. Briefly, hair was shaved over the area of interest and 75% ethanol, followed by ultrasound coupling gel, was applied to the skin. Ribeye area (in^2) and backfat thickness (in) were measured by the same technician at a point three fourths the distance from the medial end of the longissimus dorsi muscle (12th - 13th rib interface).[2] Averages of 3 ultrasound measurements for both carcass traits from each calf were used for comparison with genomic results. Docility scoring was repeated as calves were released from the chute and average docility score for each calf was compared to genomic testing. Comparisons between actual phenotype traits and genomic results were made using simple linear regression. Correlations between Zoetis's genomic results and actual phenotype were very weak (birth weight ($r^2 = 0.0493$), weaning weight ($r^2 = 0.0020$), docility ($r^2 = 0.0006$), back fat ($r^2 = 0.0040$), and rib eye area ($r^2 = 0.0039$) and not significant ($p > 0.05$). Correlations between Neogen's genomic results and actual phenotype were also very weak (birth weight ($r^2 = 0.1165$), weaning weight ($r^2 = 0.00159$), docility ($r^2 = 0.0188$), back fat ($r^2 = 0.0039$) and rib eye area ($r^2 = 0.0007$) and not significant ($p > 0.05$). We concluded that there was little cost benefit to producers of crossbred cattle to use genomic testing for prediction of performance traits.

Keywords: Backfat thickness, birth weight, docility score, ribeye area, weaning weight

References

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