PSVI-21 Including Gene-Edited Individuals in Genetic Evaluations can Bias the Estimated Breeding Values of Their Progeny. 
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Abstract: Gene-editing offers the potential to increase genetic gain for complex traits, but practical issues for routine genetic evaluations need to be addressed to ensure kinship-based predictions are not biased. The objective of this study was to quantify differences in estimated breeding values (EBV) using a 8-generation simulated beef cattle population with progeny of gene-edited (GE) sires. After generating haplotypes, 99 quantitative trait nucleotides (QTN) and 6,000 single nucleotide polymorphisms (SNP) were distributed across 3 chromosomes. A single trait (h2 =0.4) was simulated. After 8 generations, GE sires (n=1, 25, or 50) were introduced. The number of QTN edited (% additive variation) was 1 (2%), 3 (5%), or 13 (20%). All scenarios were replicated 15 times. Genetic evaluations were performed using pedigree (A), genomic (G), or combined (H) kinship matrices. Relationships were also weighted (w) based on the proportion of genetic variance explained by the edited QTN. To create Aw, weights were based on the expected difference between G and Gw. Hw was formed using Aw and Gw. Scenarios were compared using accuracy (correlation of true BV (TBV) and EBV), average absolute bias, and the slope (b) of the regression of TBV on EBV. Accuracy of EBV between GE vs. non-GE sired progeny did not differ. EBV of GE sired progeny were under-dispersed (b from 0.61 to 0.92) and associated with greater average absolute bias (0.8 to 3.8), and these issues increased in severity with the number of edited QTN. Weighting kinship reduced the average absolute bias (from 2.7 to 0.9 with 13 edited QTN) and the dispersion of EBV (from 0.7 to 0.9 with 13 edited QTN). The same pattern was observed across all kinship matrices. Results indicate that including GE individuals in genetic evaluations could lead to biased EBV, but weighting kinship could partially mitigate this concern.

Keywords: breeding value, gene-editing, simulation

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Abstract: The objective was to determine if delivery method of organic trace minerals and Saccharomyces cerevisiae yeast culture product influence growth performance, feed efficiency, and hepatic trace mineral measures in newly-weaned steers. Crossbred steers (n = 192; 256 ± 14 kg) were used in a 49-d receiving experiment. Within 36h of weaning, steers were weighed, allotted to 24 pens (n = 8 steers/pen; 8 pens/treatment) and randomly assigned to treatments: traditional receiving diet (Con); traditional receiving diet plus the “stress-pack” directly in the diet (Force); traditional receiving diet plus a low-moisture, cooked molasses block fortified with the “stress-pack” (Tub). “Stress-pack” was offered the first 28 d of the 49-d. Biopsy samples were collected from a subsample of steers (n = 14 steers) on the day of weaning and subsequent samples were collected from the same steer (n = 1 steer/pen) on d 14, 28 and 49 for hepatic trace mineral concentration determination. A treatment × day interaction (P≤0.01) for hepatic Cu concentration was noted. Force had greater hepatic Cu (P≤0.05) compared to Tub and Con for the entire period. Tub had greater hepatic Cu compared to Con on d 14 and 28 (P < 0.05), but was similar to Con on d 49 (P>0.10). Force tended (P=0.08) to have greater DMI compared to Tub from d 1 to 14. From d 15 to 28, steers offered “stress-pack” had greater DMI (P=0.01) and tended (P=0.07) to have greater ADG compared to Con by 12.5%. From d 29 to 49, “stress-pack” steers had greater DMI (P=0.01) and Force consumed 6.9% more DM compared to Tub (P=0.01). Cumulative DMI (P=0.01) and ADG (P=0.05) was greater for Force compared to Tub by 5.4% and 9.4%, respectively. Application of “stress-pack” in diets offered to newly-weaned cattle enhanced production responses, but delivery method influences DMI and daily gain.

Keywords: minerals, stress-pack, newly-weaned.