Further, when heteroskedasticity was high, the absolute magnitude of the estimated signal for the most prominent QTL expressed as a posterior *z*-score was enhanced by 20% and 34% for heteroskedastic RR-BLUP and BayesA, respectively. The inferential advantages of heteroskedastic models over homoscedastic ones were particularly apparent under a BayesA specification. A data application involving three quantitative carcass and meat quality traits from a swine resource population representing high, mild and low levels of heteroskedasticity yielded proportionally enhanced differential detection signal for the heteroskedastic models relative to the homoscedastic ones, consistent with results from the simulation study. In conclusion, accounting for residual heteroskedasticity can be expected to enhance power in the identification of important genomic regions for traits of interest.

Key Words: genome-wide association, residual heteroskedasticity, genomic prediction model

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0306 Exploring the feasibility of using copy number variants as genetic markers through large-scale whole genome sequencing experiments.

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Copy number variants (CNV) are large scale duplications or deletions of genomic sequence that are caused by a diverse set of molecular phenomena that are distinct from single nucleotide polymorphism (SNP) formation. Due to their different mechanisms of formation, CNVs are often difficult to track using SNP-based linkage disequilibrium inference. This can result in decreased reliabilities of prediction for CNV causal mutations tracked by SNP genotyping arrays. To test if CNVs can serve as suitable genetic markers, we sequenced 75 individual bulls from eight different breeds and two subspecies of cattle (*Bos taurus taurus*: Angus, Holstein, Jersey, Limousin, Romagnola; *Bos taurus indicus*: Brahman, Gir, Nellore) to 11X coverage. We identified 1853 non-redundant CNV regions (CNVR) that comprise ~3.1% (87.5 Megabases) of the cattle genome, which represents an increase over previous cattle genome variability estimates (~2%). With the discrete genome copy number values identified in our analysis, we selected the top 1% (n = 80) of CNV sites found to be variable among the sequenced breeds by a modified F statistical measure to perform population structure analyses. We were able to distinctly separate breeds of cattle based on genomic copy number, suggesting that CNVs may have utility as genetic markers. Further analysis revealed that 77.5% (62/80) of our selected CNV windows could reliably be assessed for variability and that 54 of these loci were, in turn, located near tandem duplications. CNV genotyping remains a difficult endeavor and suffers from several obstacles related to their detection and mechanisms of formation; however, these initial results suggest that our current methods can be refined and may provide suitable utility for genomic evaluation in the future.

Key Words: sequence data, genetic markers, genotyping

0307 Use of marker × environment interaction whole genome regression model to incorporate genetic heterogeneity for residual feed intake, dry matter intake, net energy in milk, and metabolic body weight in dairy cattle.

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Feed efficiency in dairy cattle has gained much attention recently. Due to the cost prohibitive measurement of individual feed intakes, combining data from multiple countries is usually necessary to ensure a large enough reference population. It may then be essential to model genetic heterogeneity when making inferences about feed efficiency or selecting efficient cattle using genomic information. In this study, we constructed a marker × environment interaction model that decomposed marker effects into main effects and interaction components that were specific to each environment. We compared environment-specific variance component estimates and prediction accuracies of the interaction model analysis, an across-environment analysis ignoring population stratification, and a within-environment analysis on the feed efficiency data set. Phenotype traits included residual feed intake (RFI), dry matter intake (DMI), net energy in milk (MilkE), and metabolic body weight (MBW) from 3656 cows measured