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GENOME WIDE CNV ANALYSIS REVEALS VARIANTS ASSOCIATED WITH GROWTH TRAITS IN BOS INDICUS

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Apart from single nucleotide polymorphism (SNP), copy number variation (CNV) is another important type of genetic variation, which may affect growth traits and play key roles for the production of beef cattle. To date, no genome-wide association study (GWAS) for CNV and body traits in beef cattle has been reported. The Nellore breed comprises the vast majority of beef cattle in Brazil, which also represents one of the most important cattle subspecies (Bos indicus). In this study, we used intensity data from over 700,000 SNP probes scattered across all bovine chromosomes to detect common CNVs in a sample of 2,230 Nellore animals, and performed GWAS between the detected CNVs and 9 growth traits. Phenotypes for weaning gain, conformation at weaning, muscling at weaning, precocity at weaning, conformation at yearling, muscling at yearling, and precocity at yearling were found to be moderately correlated. After filtering for frequency and length, a total of 228 CNVs ranging from 894 bp to 4,855,088 bp were tested as predictors for each growth trait using a linear regression analysis with principal components correction. There were 45 significant associations identified among 16 CNVs and 7 body traits after false discovery rate (FDR) correction. Among the 16 CNVs, 3 CNVs were or tended to be significantly associated with all the traits. We compared the locations of each associated CNVs with quantitative trait locus (QTL) and RefGene databases, and found 9 CNVs and 8 CNVs overlapping with known QTLs and genes, respectively. The gene overlapping with CNV98, *KCNJ12*, is a functional candidate for muscle development and plays critical roles in muscling traits. This study presents the first CNV-based GWAS of growth traits using high density SNP microarray data in cattle. We detected 16 CNVs significantly associated with 7 growth traits and CNV98 may be involved in growth traits through *KCNJ12*.