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Genome-wide association studies using copy number variants in Brown Swiss Dairy cattle.

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Abstract

Detecting Copy Number Variation (CNV) in cattle provides the opportunity to study their association with quantitative traits (Winchester et al., 2009; Zhang et al., 2009; Hou et al., 2011; Clop et al., 2012; de Almeida et al., 2016;). The aim of this study was to map CNVs in 1,410 Brown Swiss males and females using Illumina BovineHD Genotyping BeadChip data and to perform a genome-wide association analysis for production functional and health traits. After quality control, CNVs were called with the GoldenHelix SVS 8.3.1 and PennCNV software and were summarized to CNV regions (CNVRs) at a population level, using BEDTools. Additionally, common CNVRs between the two software were set as consensus. CNV-association studies were executed with the CNVRuler software using a linear regression model. Genes within significant associated CNVRs for each trait were annotated with a GO analysis using the DAVID Bioinformatics Resources 6.7.

The quality control filtered out 294 samples. The GoldenHelix SVS 8.3.1 software identified 25,030 CNVs summarized to 398 CNVRs while PennCNV identified 62,341 CNVs summarized to 5,578 CNVRs. A total of 127 CNVRs were identified to be significantly associated with one or more of the evaluated traits. The result of this study is a comprehensive genomic analysis of the Brown Swiss breed, which enriches the bovine CNV map in its genome. Finally, the results of the association studies deliver new information for quantitative traits considered in selection programs of the Brown Swiss breed.

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