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## A high-resolution CNV map across Brown Swiss cattle populations.

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### ABSTRACT

Genomic studies and their use in selection programs are having a strong impact in dairy cattle selection (E. Liu et al., 2010). The first aim was to create a high resolution map of CNV regions (CNVRs) in Brown Swiss cattle and the characterization of identified CNVs as markers for quantitative and population genetic studies. CNVs were called in a set of 164 sires with PennCNV and genoCN. PennCNV identified 2,377 CNVRs comprising 1,162 and 1,131 gain and loss events, respectively, and 84 regions of complex nature. GenoCN detected 41,519 CNVRs comprising 3,475 and 34,485 gain and loss events, respectively, and 3,559 regions of complex ones. Consensus calls between algorithms were summarized to CNVRs at the population level. GenoCN was also used to identify total allelic content in consensus CNVRs. Moreover, population haplotype frequencies were calculated. Linkage disequilibrium (LD) was established between CNVs and SNPs in and around CNVRs. In this study the potential contribution of CNVs as genetic markers for genome wide association studies (GWAS) has been assessed thanks to PIC and LD values. The next aim is to investigate genomic structural variation in cattle using dense SNP information in more than 1000 samples of the Italian and Swiss Brown Swiss breed genotyped on HD Bovine BeadChips. Today there is still no CNV map available across Brown Swiss populations belonging to different countries. This study therefore expands the catalogue of CNVRs in the bovine genome, delivers an international based high-resolution map of CNVRs specific to Brown Swiss dairy cattle and will lastly provide information for GEBV estimation with CNVs.

Liu GE, Hou Y, Zhu B, Cardone MF, Jiang L, Cellamare A, Mitra A, Alexander LJ, Coutinho LL, Dell'Aquila ME, Gasbarre LC, Lacalandra G, Li RW, Matukumalli LK, Nonneman D, Regitano LC, Smith TP, Song J, Sonstegard TS, Van Tassell CP, Ventura M, Eichler EE, McDanel TG, Keele JW: Analysis of copy number variations among diverse cattle breeds. *Genome Res* 2010, 20:693-703.