

Abstracts

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genotypes obtained using the Bovine HD BeadChip array and the same variants identified by sequencing was about 99.05%. The annotation of variants identified numerous nonsynonymous SNVs and frameshift InDels, which could affect phenotypic variation. Functional enrichment analysis was performed by the David (v. 6.8) tool and revealed that variants in the olfactory transduction pathway were overrepresented in all three cattle breeds, while the ECM-receptor interaction pathway was overrepresented only in the Girolando breed, the ABC transporters pathway was overrepresented only in the Holstein breed, and the metabolic pathways were overrepresented only in the Gyr breed. Therefore, the genetic variants discovered in this study provide a rich resource to help identify potential genomic markers and their associated molecular mechanisms that impact economically important traits for Gyr, Girolando, and Holstein breeding programs.

Key Words: composite breed, deletion, insertion
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165 Genetic variants with potential loss of function in Gyr, Girolando, and Guzerat cattle breeds by resequencing. N. B. Stafuzza*¹, A. Zerlotini², F. P. Lobo², M. E. B. Yamagishi², M. E. Buzanskas³, T. C. S. Chud¹, A. R. Caetano⁴, D. P. Munari¹, D. J. Garrick⁵, M. A. Machado⁶, M. F. Martins⁶, M. R. Carvalho⁷, J. B. Cole⁸, and M. V. G. B. da Silva⁶, ¹*Departamento de Ciências Exatas, Universidade Estadual Paulista, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil*, ²*Embrapa Informática Agropecuária, Campinas, Brazil*, ³*Departamento de Zootecnia, Universidade Federal da Paraíba, Areia, Brazil*, ⁴*Embrapa Recursos Genéticos e Biotecnologia, Brasília, Brazil*, ⁵*Department of Animal Science, Iowa State University, Ames*, ⁶*Embrapa Gado de Leite, Juiz de Fora, Brazil*, ⁷*Departamento de Biologia Geral, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil*, ⁸*Animal Genomics and Improvement Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD*.

The aim of this study was to detect, by whole-genome resequencing, SNVs (single nucleotide variants) and indels (insertion/deletions) and annotate them into functional categories in order to identify functionally relevant variants in three important cattle breeds in Brazil: Gyr and Girolando (dairy production) and Guzerat (dual-purpose). A total of approximately 2.7 billion reads from an Illumina HiSeq 2000 sequencer generated for each animal 10.9- to 16.4-fold genome coverage. Sequencing reads were mapped to the UMD 3.1 bovine genome assembly using the Burrows-Wheeler Aligner tool (v.0.7.10-r789). Picard tools (v.1.54) were used to eliminate PCR duplicates, and the variant calling was conducted with

FreeBayes. The resulting variant lists were filtered by vcfFilter in order to remove SNVs and indels with quality scores lower than 30 or coverage lower than 7. A total of 25,020,024 SNVs (16,743,392 from Guzerat, 15,941,804 from Gyr, and 13,286,669 from Girolando) and 3,249,148 indels (1,975,563 from Guzerat, 1,833,387 from Gyr, and 1,413,047 from Girolando) were detected in the DNA samples. A total of 13,253, 13,817, and 12,480 genes showed genetic variation in Guzerat, Gyr, and Girolando, respectively, of which 64.84% of genes with SNVs and 31.29% of genes with indels were shared among all breeds. The functional enrichment analysis by the DAVID (v.6.8) tool revealed 24, 27, and 28 enriched KEGG pathways (FDR < 10%) in Guzerat, Gyr, and Girolando, respectively, of which 14 pathways were common to all breeds, three pathways were significantly overrepresented only in Guzerat (arachidonic acid metabolism, Fc gamma R-mediated phagocytosis, and aldosterone-regulated sodium reabsorption), six pathways only in Gyr (alanine, aspartate and glutamate metabolism, inflammatory mediator regulation of TRP channels, thyroid hormone synthesis, pancreatic secretion, central carbon metabolism in cancer, and choline metabolism in cancer), and eight pathways only in Girolando (amino sugar and nucleotide sugar metabolism, inositol phosphate metabolism, vascular smooth muscle contraction, tight junction, regulation of actin cytoskeleton, amoebiasis, small cell lung cancer, and dilated cardiomyopathy). Although the genetic variants identified were distributed throughout the genomes, a large number of novel variants were clustered in specific genes. A total of 61 genes were identified with novel variants common in all breeds, while 349, 404, and 206 genes were identified as enriched with novel variants exclusively in the Guzerat, Gyr, and Girolando breeds, respectively. These genes are related to many biological processes, providing valuable information about genomic variants that may be responsible for variation in economically important traits among these breeds.

Key Words: indels, pathways, single nucleotide variants
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166 Effects of genetic and non-genetic factors on bovine milk cholesterol content. D. N. Do^{1,2}, F. S. Schenkel³, F. Miglior^{3,4}, X. Zhao², and E. M. Ibeagha-Awemu*¹, ¹*Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, QC, Canada*, ²*McGill University, Department of Animal Science, Ste-Anne-de-Bellevue, QC, Canada*, ³*Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada*, ⁴*Canadian Dairy Network, Guelph, ON, Canada*.

Dairy products are rich in cholesterol (CHL); therefore, monitoring CHL levels in cow milk may become an important factor. This study aimed to (a) determine the factors that influence milk CHL content, (b) estimate (co) variances and heritability