

increase selection responses for MY and FP in the Thai multi-breed dairy cattle population.

**Key Words:** dairy cattle, genomic evaluation, random regression  
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**163 Population structure and genetic diversity of Russian native cattle breeds.** A. V. Dotsev<sup>1</sup>, A. A. Sermyagin<sup>1</sup>, E. A. Gladyr<sup>1</sup>, T. Deniskova<sup>\*1</sup>, K. Wimmers<sup>2</sup>, H. Reyer<sup>2</sup>, G. Brem<sup>1,3</sup>, and N. A. Zinovieva<sup>1</sup>, <sup>1</sup>L.K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation, <sup>2</sup>Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, <sup>3</sup>Institute of Animal Breeding and Genetics, VMU, Vienna, Austria.

Conservation of native cattle populations' biodiversity is a crucial element in breeding selection programs. Reduction of local and improved livestock gene pool leads to the loss of valuable alleles for adaptation to specific environments. In our work, we investigated the genetic structure of the most essential native cattle breeds in Russia. Using Illumina Bovine 50K BeadChip, we genotyped nine breeds: Bestuzhev (BEST, n = 26), Black and White (BLWT, n = 21), Kalmyk (KALM, n = 14), Kholmogor (KHLM, n = 25), Kostroma (KSTR, n = 20), Red Gorbato (RGBT, n = 23), Suksun (SKSN, n = 20), Yakut (YAKT, n = 25), and Yaroslavl (YRSL, n = 21). Statistical analysis was performed with PLINK 1.07, Admixture 1.3 software, and R packages "diveRsity" and "adegenet." Multi-dimensional scaling (MDS) analysis showed that all of the breeds formed their own clusters. The YAKT cluster was completely separated on the first component (C1) and was most distant from all other populations. KALM also separated on C1 but was much closer to the other clusters. Both of these breeds are of Asian origin. The other seven breeds, which are of European origin, separated from one another mostly on the second component (C2). Admixture analysis showed that the most probable number of populations (K) was 8. At K = 2, YAKT was separated from the other populations. Considerable admixture of YAKT was only found in the KALM cluster (from K = 2 to K = 8). At K = 8, all of the breeds but KALM formed their own clusters. KALM was combined from the seven other breed fragments (all but SKSN). Pairwise genetic distances ( $F_{ST}$ ) values were higher for YAKT (from 0.126 with KALM to 0.187 with RGBT).  $F_{ST}$  values between the other breeds ranged from 0.036 (BLWT and SKSN) to 0.103 (KSTR and RGBT). The lowest rarefied allelic richness value was observed for YAKT ( $1.781 \pm 0.002$ ). For all of the other breeds, it ranged from  $1.919 \pm 0.001$  for KSTR to  $1.958 \pm 0.001$  for KALM. Expected heterozygosity was the lowest in YAKT ( $0.273 \pm 0.001$ ) while in all of the other breeds it ranged from  $0.329 \pm 0.001$  in KSTR and RGBT to  $0.352 \pm 0.001$  in BEST. Inbreeding coefficient ( $F_{IS}$ ) values in all of the breeds were close to zero (from -0.05 to 0.01). Our study revealed that

all of the evaluated Russian breeds were structured, and only KALM had a more complex admixture. The most diverged, indigenous YAKT breed had a lower genetic diversity than all of the other breeds. The study was supported by the Russian Science Foundation within Project no.14-36-00039.

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**164 Single nucleotide variants and indels identified from whole-genome resequencing of Gyr, Girolando, and Holstein cattle breeds.** N. B. Stafuzza<sup>\*1</sup>, A. Zerlotini<sup>2</sup>, F. P. Lobo<sup>3</sup>, M. E. B. Yamagishi<sup>2</sup>, T. C. S. Chud<sup>1</sup>, A. R. Caetano<sup>3</sup>, D. P. Munari<sup>1</sup>, D. J. Garrick<sup>4</sup>, J. B. Cole<sup>5</sup>, M. A. Machado<sup>6</sup>, M. F. Martins<sup>6</sup>, M. R. Carvalho<sup>7</sup>, and M. V. G. B. da Silva<sup>6</sup>, <sup>1</sup>Departamento de Ciências Exatas, Universidade Estadual Paulista, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, <sup>2</sup>Embrapa Informática Agropecuária, Campinas, Brazil, <sup>3</sup>Embrapa Recursos Genéticos e Biotecnologia, Brasília, Brazil, <sup>4</sup>Department of Animal Science, Iowa State University, Ames, <sup>5</sup>Animal Genomics and Improvement Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD, <sup>6</sup>Embrapa Gado de Leite, Juiz de Fora, Brazil, <sup>7</sup>Departamento de Biologia Geral, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.

Whole-genome resequencing, alignment, and annotation analyses were undertaken for ten sires representing Gyr, Girolando, and Holstein cattle breeds to detect and make publicly available genome-wide single nucleotide variations (SNVs) and insertions/deletions (InDels). A total of approximately 3.5 billion reads from an Illumina HiSeq 2000 sequencer generated for each animal 10.7 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) with default parameters. Picard tools (v. 1.54) were used to eliminate PCR duplicates, and the variant calling was conducted with FreeBayes. The resulting variant lists obtained for each animal were filtered by vcfFilter in order to remove variants with quality scores lower than 30 or coverage lower than 7. A total of 23,743,970 SNVs and 3,171,711 InDels were detected in the samples, of which approximately 2,224,013 SNVs and 798,8910 [Editor: Please check number.] InDels were novel. The high number of genetic variants identified for each animal within the same breed shows the importance of resequencing to identify novel variants for monitoring genetic diversity in the cattle breeds and for developing strategies to prevent some eventual loss of genetic variability. The submission of these genetic variants to the dbSNP database significantly increased the number of known variants, particularly for the indicine genome. The concordance rate between

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.

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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.

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#### 166 Effects of genetic and non-genetic factors on bovine milk cholesterol content.

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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