surprisingly comparable. The horse MSY gene catalog establishes a basis to study the contribution of Y genes to stallion reproductive biology and provides new insight into Y chromosome evolution and function in mammals.

**Key Words:** Y chromosome, genes, horse, comparative

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**P8005 Genes responding to recent selection in Berkshire and Duroc pigs.** K. D. D. Song (The Animal Molecular Genetics and Breeding Center, Chonbuk National University, Jeonju, South Korea), D. Shin* and H. K. Lee (Department of Animal Biotechnology, Chonbuk National University, Jeonju, South Korea)

Berkshire and Duroc pigs have been developed for unique pork quality during the last one or two centuries. To reveal the region under selection, selection signatures were identified by comparisons between Duroc and Berkshire pigs ($N$ = 720) based on the analysis of extended haplotype homozygosity (EHH) using 60 k single nucleotide polymorphisms (SNPs). Moreover, the selected regions were examined further using the genomic sequences of 46 pigs. Although animals in the two pig breeds selected for common objectives, each breed showed unique signatures of selection. Using 60 K SNPs, the analyses of EHH identified 10 to 15 substantial selection signatures within a breed, or comparisons between two breeds, which may reveal the regions under recent selection. The haplotype pattern decided by SNPs were in agreement with the analyses of variations extracted from the genomic sequences. In particular, genomic regions on chromosomes 4 and 17 in Berkshires were likely to be affected by recent selection, and considerable EHH was identified on chromosomes 6 and 14 in Durocs. To refine the regions supported by the relatively long range of haplotype homozygosity (>1 Mb), the mean Fst of SNPs for each gene was calculated. In summary, more than 50 genes that are involved in fat or protein metabolism were located in the recently selected regions. Identifying the regions involved in differential selection will be useful to find causal mutations affecting unique traits that explain the meat quality in Berkshire and Duroc pigs.

**Key Words:** Berkshire, Duroc, pork quality, selection signatures, haplotype

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**P8006 Identification and characterization of copy number variations in cattle.** R. Letaief*[1], D. Esquerré[2], J. Barbieri[2], C. Grohs[1], S. Fritz[1,3], C. Klopp[4], R. Philippe[5], V. Blanquet[5], D. Boichard[6], D. Rocha[1], and M. Boussaha[1] ([1]GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, [2]Get-PlaGe, INRA, Castanet-Tolosan, France, [3]ALLICE, Paris, France, [4]SIGENAE, INRA, Castanet Tolosan, France, [5]GMA, INRA, Université de Limoges, Limoges, France, [6]GABI, INRA, AgroParisTech, Universite Paris Saclay, Jouy-en-Josas, France)

Copy number variations (CNVs) are an important source of genetic changes. They are defined as a gain or loss of genomic region ranging from 50 bp to several megabases. CNVs have been shown to be associated with many diseases and some phenotypic traits in several species, including cattle. We used Pindel, Delly, BreakDancer, and CNVnator to identify CNVs using whole-genome sequencing data of 200 animals from eight French dairy and beef cattle breeds. We selected only deletions and duplications predicted by at least two tools and present in at least two animals. We identified a total of 29,132 autosomal deletions and duplications which cover between 31 to 34% (784 to 865 Mb) of the autosomal genome, with an average of 6,000 events per animal. Among these deletions and duplications, 27,690 were present in at least two animals. Out of theses, 26,417 events were deletions, 674 were duplications and 599 regions were both (deletion and duplication within the same region). We defined a CNV as deletion and duplication in the same region, and we termed this region as CNV-Region (CNVR). The size of CNVRs ranged from 100 bp to 9.3 Mb with a median of 1.3 kb and a mean of 45 kb. From the identified deletions and duplications, 8,283 overlapped with 9,733 annotated genes including 290 CNVRs overlapping with 974 annotated genes, including some genes known to be implicated in some traits of economic importance. Our study provides an extensive view of the CNVRs in French dairy and beef breeds. CNVRs with an effect on some commercially interesting phenotypes could be used to improve genetic selection of these eight French breeds.

**Key Words:** copy number variations, whole-genome sequencing, dairy and beef breeds, genome plasticity, bioinformatics

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**P8007 RefSeq and Gene—NCBI resources to support comparative genomics.** K. D. Pruitt*, T. D. Murphy, F. Thibaud-Nissen, and P. A. Kitts (National Institutes of Health, NCBI, Bethesda, MD)

The National Center for Biotechnology Information (NCBI) Reference Sequence (RefSeq) project provides several resources to support the animal genetics research community. These include whole genome annotation, evidence-based transcript and protein sequence records, BLAST databases, FTP data, and entries in NCBI's Gene database resource. Gene, transcript, and protein data are provided using