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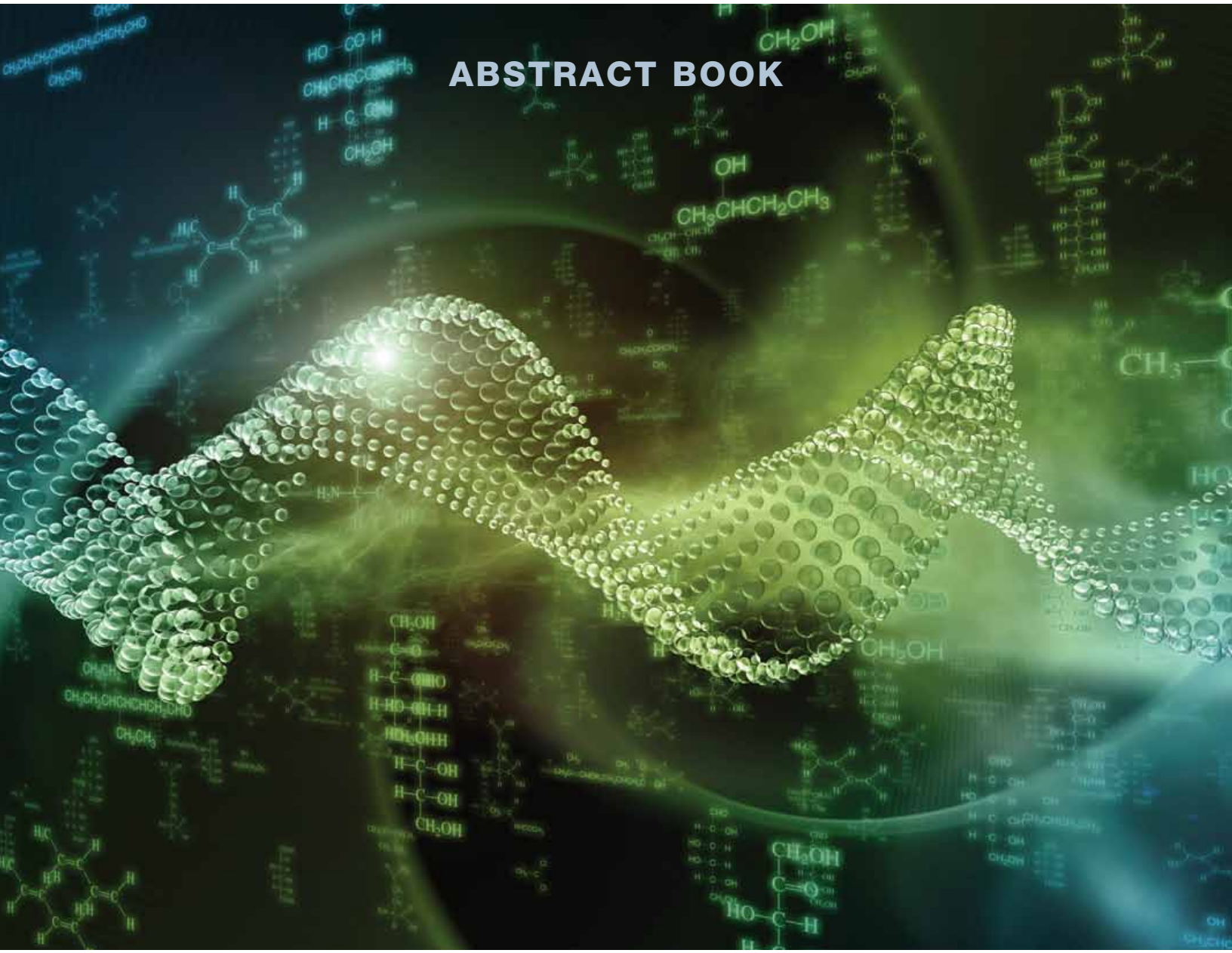

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P4027 Systematic profiling of short tandem repeats in the cattle genome. L. Xu (Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD), R. Haasl (University of Wisconsin–Platteville, Platteville, WI), J. Sun (South China Agricultural University, Guangzhou, China), Y. Zhou (Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD), D. Bickhart (Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD), J. Li (Institute of Animal Science of Chinese Academy of Agricultural Sciences, Beijing, China, Beijing, China), J. Song (University of Maryland, Animal Science and Avian, College Park, MD), T. Sonstegard (Recombinetics Inc., St Paul, MN), C. P. VanTassell (Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD), H. Lewin (University of California, Davis, Department of Evolution and Ecology, David, CA), G. E. Liu* (Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD)

Short tandem repeats (STRs), or microsatellites (MS), are genetic variants with repetitive 2–6 base pair motifs in many genomes. Using high-throughput sequencing and experimental validations, we systematically profiled STRs in five Holsteins. We identified a total of 60,106 microsatellites and generated the first high-resolution STR map, representing a substantial pool of polymorphism in cattle. We observed significant STR overlaps with RefSeq genes and quantitative trait loci (QTL). We performed evolutionary and population genetic analyses using over 20,000 common dinucleotide STRs. Besides corroborating the well-established positive correlation between allele size and variance in allele size, these analyses also identified dozens of outlier STRs based on two anomalous relationships that counter expected characteristics of neutral evolution. And one STR locus overlaps with a significant region of a summary statistic designed to detect STR-related selection. Additionally, we showed that only 57.1% of STRs are located within SNP-based linkage disequilibrium (LD) blocks, while the other 42.9% are not. Therefore, a substantial number of STRs are not tagged by SNPs in the cattle genome, likely due to STR's distinct mutation mechanism and elevated polymorphism. This study provides the foundation for future STR-based studies of cattle genome evolution and selection.

Key Words: cattle genome, short tandem repeat (STR), whole genome sequencing (WGS)

P4028 Hematopoietic chimerism in Italian horses. C. Grasso* (UNIRELAB, Settimo Milanese, Italy), M. Bonuglia (UNIRELAB, Settimo Milanese, Italy), M. Dobosz (University of Perugia, Perugia, Italy), V. Chiofalo (UNIRELAB s.r.l., Settimo Milanese, Italy)

A chimera is an organism whose cells derive from two or more zygotes. This phenomenon has been detected in a wide variety of organisms, including mammalians. Chimeras can be phenotypically normal, so most of them have been discovered only by chance and the frequency of spontaneous chimerism might have been greatly underestimated. Cells with the "extra" genotype might be found in any part of the body, according to the mechanism of its development. We found several cases of chimeric horses during routine genotyping: They show more than two alleles for each locus, leading to a false incompatibility between the foal and its parents. Each of these subjects was derived from twins pregnancy, and we hypothesize that they could be hematopoietic chimeras, where an exchange of blood cells between the fetuses occurred in utero and these additional alleles derived from cells contributed by his twin sibling because of the establishment of vascular anastomoses between the developing placentas. This exchange occurs in utero, when the twins are immunologically tolerant and this condition of "mixed" blood" could take place. The number of extraneous cells in every twin can change and decrease over time. In some cases, depending on the moment in which anastomoses takes place, this number could exceed the number of cells of the original genotype. The presence of blood chimerism can lead to a false interpretation of trace analysis in criminal cases or in the investigation of kinship. In suspected cases, it is advisable to determine which profile represents the real one, typing biological samples derived from other body districts.

Key Words: horse, chimerism, STR

P4029 Launching SheepGenomesDB: 100 million variants from nearly 500 sheep genomes. J. Kijas* (CSIRO Agriculture, Brisbane, Australia), R. Brauning (AgResearch, Mosgiel, New Zealand), S. M. Clarke (AgResearch, Mosgiel, New Zealand), A. McCulloch (AgResearch Limited, Mosgiel, New Zealand), N. E. Cockett (Utah State University, Logan, UT), G. Saunders (EMBL-EBI, Hinxton, United Kingdom), M. Naval Sanchez (CSIRO Agriculture, Brisbane, Australia), S. McWilliam (CSIRO Agriculture, Brisbane, Australia),