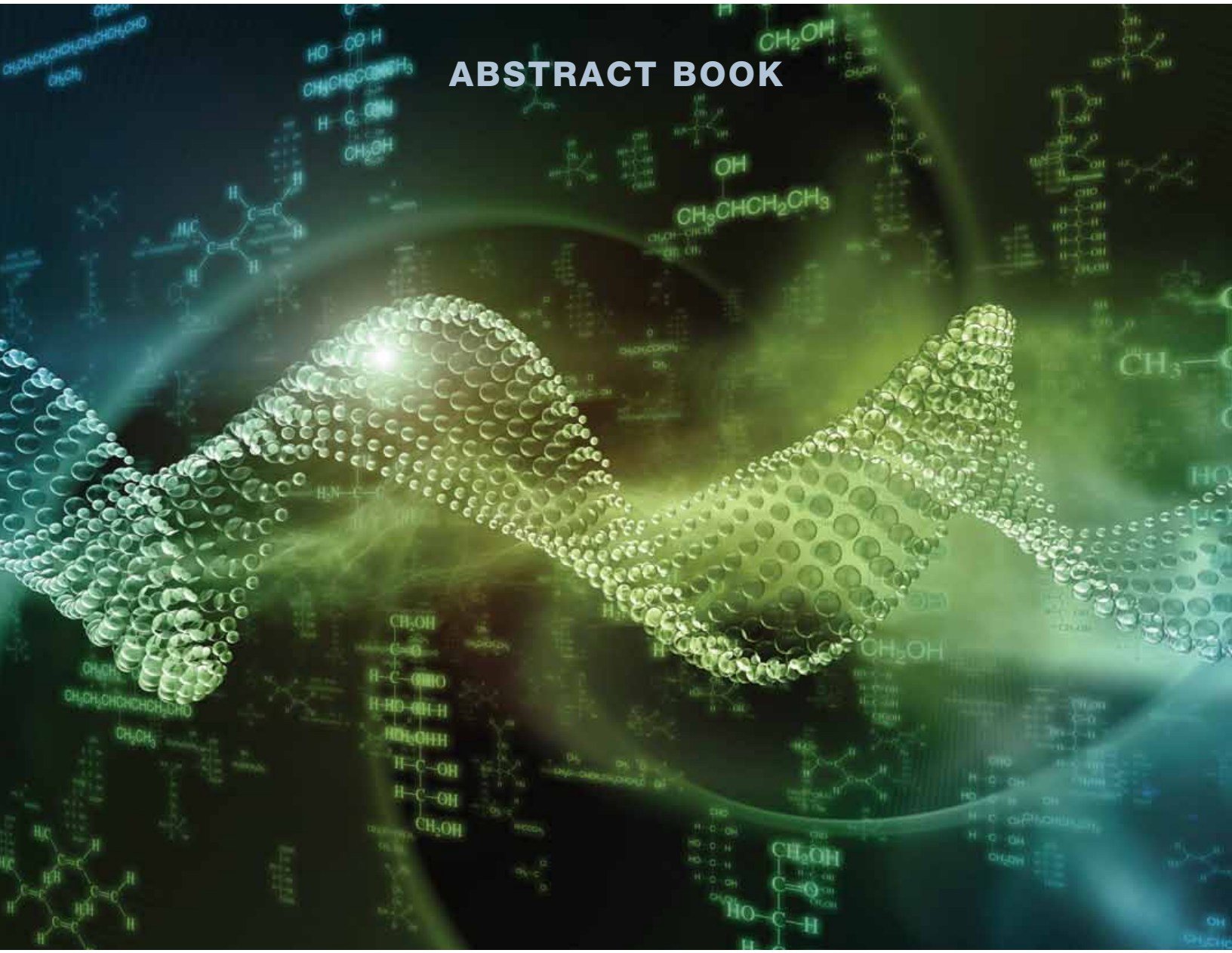
35th INTERNATIONAL SOCIETY FOR ANIMAL GENETICS CONFERENCE

7.23.16 – 7.27.2016 • Salt Lake City, Utah



https://www.asas.org/meetings/isag2016

appears to encode a canonical class I-like protein with 8 exons while two other variants encode proteins either lacking exon 3 (α 2 domain) or exons 3 and 4 (α 2 and 3 domains). These data suggest that SLA-11 could be an expressed class Ib-like gene within the class Ia gene cluster. The committee will consider reclassifying SLA-11 as a putative functional gene as additional evidence accumulates. A systematic nomenclature for the genes, alleles and haplotypes of the swine MHC is critical to the research in swine genetic diversity, immunology, health, vaccinology, and organ or cell transplantation. Continuous efforts on characterizing SLA alleles and haplotypes and studying of their diversity in various pig populations will further our understanding of the architecture and polymorphism of the SLA system and their role in disease, vaccine and allo- or xeno-graft responses.

Key Words: alleles, haplotypes, swine leukocyte antigen nomenclature

---

P4053 Prospects for whole genome sequencing of ancient Finnish cattle. M. B. Weldenegodguad (Department of Environmental and Biological Sciences, University of Eastern Finland, Kuopio, Finland; Natural Resources Institute Finland (Luke), Jokioinen, Finland), C. Der Sarkissian (Centre for GeoGenetics, University of Copenhagen, Copenhagen, Denmark), A. Bläuer (Natural Resources Institute Finland (Luke), Jokioinen, Finland; Department of Archeology, University of Turku, Turku, Finland), K. Pokharel (Department of Environmental and Biological Sciences, University of Eastern Finland, Kuopio, Finland; Natural Resources Institute Finland (Luke), Jokioinen, Finland), J. P. Taavitsainen (Department of Archeology, University of Turku, Turku, Finland), L. Orlando (Centre for GeoGenetics, University of Copenhagen, Copenhagen, Denmark), and J. Kantanen (Department of Environmental and Biological Sciences, University of Eastern Finland, Kuopio, Finland; Natural Resources Institute Finland (Luke), Jokioinen, Finland)

Genetic diversity and population structure of prehistorical and historical cattle populations have been typically investigated by analyzing partial D-loop of mitochondrial DNA and Y-chromosomal DNA-markers. However, autosomal nuclear markers would offer more detailed information on ancient animals than uniparentally inherited markers. By comparing ancient animals with modern animals one could also investigate temporal changes in genetic diversity occurred through different time periods. We have applied the next generation sequencing (NGS) technology to decipher for the first time genome sequences of ancient cattle specimens in Finland. Four ancient cattle bones from three different excavation sites were selected for the sequencing study. We successfully extracted the DNA and built indexed Illumina libraries from ancient DNA extracts from 2 specimens: a sample of Late Iron Age Western Finland (coded as 'Mulli-2'; approximately 1200 y old) and that of Medieval Eastern Finland ('Viipuri-4'; approximately 500 y old). Shallow sequencing revealed minimal proportions of reads aligning uniquely against the cattle reference genome, providing $\leq$ 0.1X genome coverage. Read alignments showed typical DNA damage signatures, consisting of an excess of "C→T and G→A transitions" toward read termini. This pleads in favor of the sequence authenticity. Further sequencing aimed at recovering the whole genome sequence is ongoing, but the data already available, especially at sites overlapping the OMIA database, revealed for example the presence of disease-related allele in ancient Finnish cattle. As this is absent in contemporary breeds, this suggests possible recent genetic changes in the Finnish livestock.

Key Words: ancient DNA, Finnish cattle, genetic diversity

P4054 Resolving misassembled cattle immune gene clusters with hierarchical, long read sequencing. D. Bickhart (Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD), J. A. Hammond (The Pirbright Institute, Guildford, United Kingdom), J. C. Schwartz (The Pirbright Institute, Woking, United Kingdom), D. Harrison (The Pirbright Insitute, Woking, United Kingdom), and T. P. L. Smith (USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE)

Animal health is a critical component of productivity; however, current genomic selection genotyping tools have a paucity of genetic markers within key immune gene clusters (IGC) involved in the cattle innate and adaptive immune systems. With diseases such as Bovine Tuberculosis and Johne's disease costing the UK and US industries an annual £50 million and $200 million, respectively, identifying genetic markers associated with disease resistance will greatly assist producers. The high genetic diversity and highly repetitive nature of IGCs also means that the cattle reference genome assembly contains many mistakes or greatly underrepresents the true diversity of alleles in these clusters. To properly identify and annotate the breadth of IGC alleles, we use a hierarchical assembly approach that sequences bacterial artificial chromosome (BAC) library clones that span target sites with long read sequencing. The sequencing of

46 such BACs has already identified an alternative allele for the natural killer cell (NKC) cluster that is currently not represented on the cattle reference genome. In total, replacement NKC sequence fills 10 existing sequence gaps on the genome and removes an improperly assigned contig containing olfactory receptor genes. Further assembly polishing using this approach will finally enable the interrogation of functional variants within IGC regions, thereby enabling future genomic selection of animal health traits.

Key Words: cattle genome, assembly, immune genes

P4055 Assessing the genomic status of South African mutton, pelt and dual purpose sheep breeds using genome-wide single nucleotide genotypes. E. F. Dzomba (University of KwaZulu-Natal, Pietermaritzburg, South Africa), M. A. Snyman (Grootfontein Agriculture Development Institute, Middelburg, South Africa), M. Chimonyo (University of KwaZulu-Natal, Pietermaritzburg, South Africa), and F. C. Muchadeyi (Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa)

South Africa has a vibrant sheep industry which contributes significantly to livestock gross domestic product through meat, wool and pelt production. Several industrial breeds are reared mainly on commercial farms with extensively raised breeds found mainly in the smallholder areas. Most breeds have been developed for adaptive and functional traits leading to a diverse array of phenotypically-distinct breeds. To gain an insight into the genome diversity of the various sheep breeds, we undertook a study to assess their breed history and population genetic structure. The study used the Illumina OvineSNP50 BeadChip to Genotype 376 animals belonging to 10 breeds representing mutton (23 Dorper, 8 Blackhead Persian, 48 Meatmaster, 30 Nguni, 10 South African Mutton Merino and 4 Namaqua Afrikaner animals), pelt (96 Swakara animals) and mutton and wool dual purpose (56 South African Merino, 50 Dohne Merino and 51 Afrino animals) breeds. Nguni sheep samples obtained from Makhathini Research Station (KwaZulu-Natal, South Africa) were included as a representative of indigenous breeds that are reared in smallholder farming areas while the Swakara, sampled from private farms in Namibia and were partitioned into four groups based on their coat color and the sub-vital genetic disorder phenotypes. The rest of the sheep samples were obtained from the biorepository at Grootfontein Agricultural Development Institute (GADI) in Middelburg, South Africa where tissue samples of the major sheep breeds are kept for biodiversity research and conservation. Across breeds, genetic diversity ranged from $H_E = 0.621$ (Dohne Merino) to $H_E = 0.742$ (Namaqua Afrikaner) with an overall mean of 0.633. Namaqua Afrikaner ($F = 0.330$) and Nguni and Blackhead Persian ($F = 0.274$) were the most inbred breeds with Dohne Merino ($F = 0.0162$), SA Merino ($F = 0.0570$) and Afrino ($F = 0.0667$) the least. The first principal component grouped the Merinos, Swakara, and the other breeds into separate clusters. The second principal component explained approximately 80.55% of the total variation and clustered the breeds according to their function and historical origin, splitting the different Merino specialized breeds and distinguishing the Nguni, Namaqua Afrikaner, Blackhead Persian, Afrino and Dorper breeds. The optimal cluster $K = 9$ for ADMIXTURE revealed various sources of within and among breeds genomic variation associated with purpose, adaptation and history of the breeds. These results are useful in understanding the current status of the sheep genetic resources of South Africa.

Key Words: sheep breeds, SNP genotypes, diversity, population structure, South Africa

---

P4056 Evaluation of single nucleotide polymorphism (SNP) markers for canine parentage analysis. J. Qiu (GeneSeek, a Neogen Company, Lincoln, NE), B. Simpson (GeneSeek, a Neogen Company, Lincoln, NE), L. Kock (GeneSeek, a Neogen Company, Lincoln, NE), J. Donner (Genoscoper Laboratories, Helsinki, Finland), C. Cole (Mars Veterinary, Portland, OR), S. Davison (Mars Veterinary, Portland, OR), M. Dunn (American Kennel Club, Raleigh, NC), D. Bannasch (School of Veterinary Medicine, Univ. California Davis, Davis, CA), and A. Boyko (Cornell University, Ithaca, NY)

Microsatellite markers (a.k.a. short tandem repeats, STRs) have traditionally been used to determine pedigree or parentage in canines. However, some parentage issues involving closely related sires can be difficult to resolve using current STRs due to limited allelic variations. The use of SNP markers has been shown to be very effective in resolving parentage issues in other species such as cattle and has been officially adopted by the ISAG/ICAR. Recently, a number of genome mapping studies have identified hundreds of informative SNPs that could be potentially used for canine parentage analysis. The objectives of this study were 1) to evaluate minor allele frequencies (MAF) of a few hundred selected canine SNPs for major dog breeds, 2) to design multiplex SNP panel(s) using a subset of these SNPs for evaluating their effectiveness