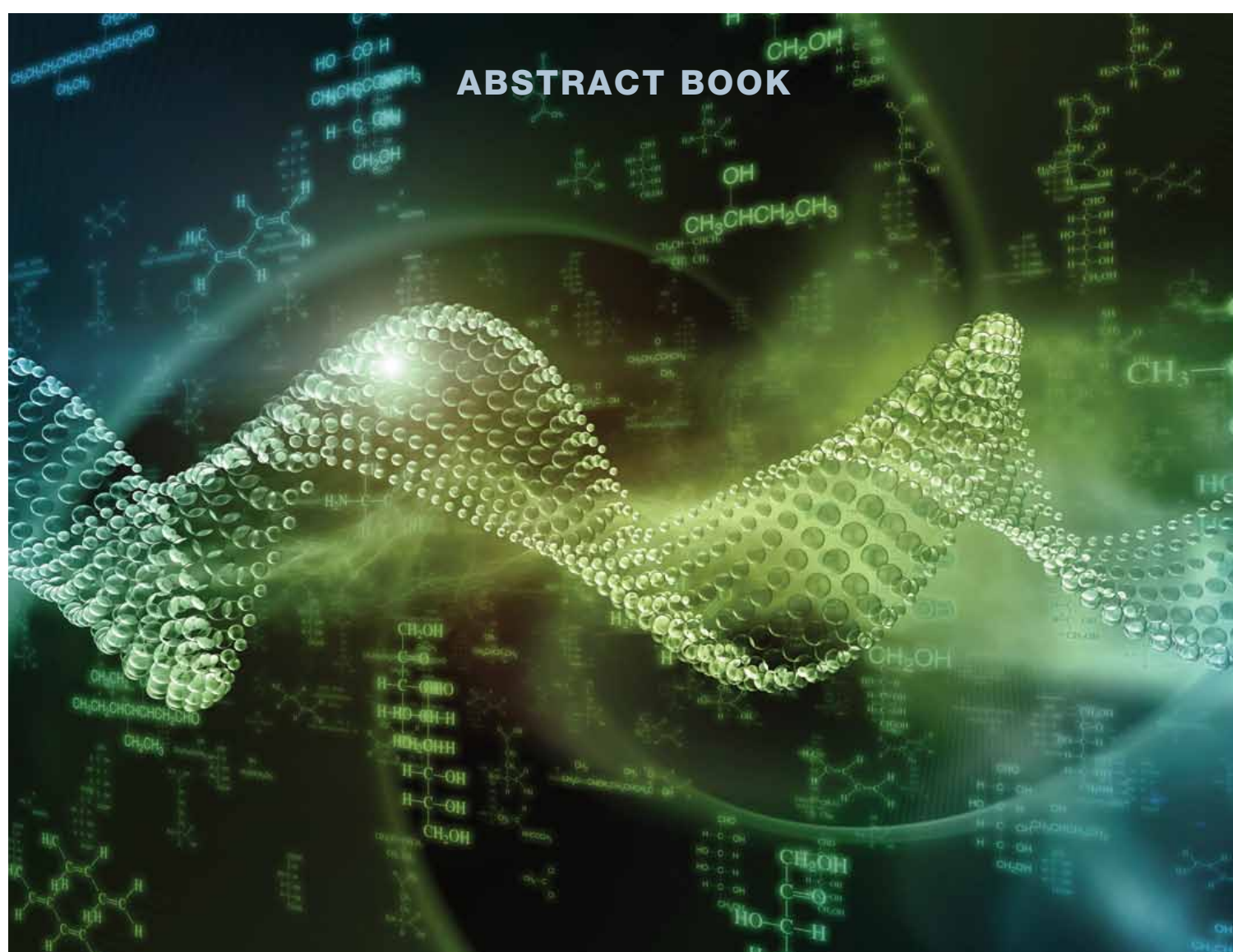




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Illumina reads, 16X coverage of long-read single molecule sequences (PacBio), and 69X coverage from a chromatin, cross-linking library (Dovetail Genomics). Many sequencing errors, mis-assemblies, and missing segments in EquCab2 have been resolved with concurrent substantial increases to the contig N50 and scaffold lengths. To date, functional annotation improvements have centered on greater accuracy in the nucleotide coordinates that define gene loci and individual exons, but efforts are now extending in association with the FAANG initiative to include transcriptional regulatory binding sites and epigenomic parameters. Advancing the structural and functional annotation of the equine reference genome will further enhance genome to phenome studies in the horse.

Key Words: horse, FAANG, gene

INVITED SPEAKERS: ISAG-FAO GENETIC DIVERSITY

S0123 The adaptation of farm animals to northern and arctic environments. J. Kantanen* (Natural Resources Institute Finland (Luke), Jokioinen, Finland)

Natural and human-made selection enables animals to adapt, survive, be productive and reproduce in challenging environments. In the Arctic, traditional animal husbandry is based almost exclusively on reindeer (*Rangifer tarandus*), but in Fennoscandian Lapland, northern Russia and Siberia, other locally adapted animals, namely cattle (*Bos taurus*) and horse (*Equus caballus*) also are used for food production and other societal and cultural needs (for example, Northern Finncattle, Yakutian cattle, Mezen horse and Yakutian horse). These animal breeds represent a valuable genetic resource for northern agriculture and pastoralism.

From the animal science point of view, the Arctic environment guided toward selection of animals with specific metabolic, morphological and reproductive adjustments. From the animal genomics point of view, adaptations to extreme environments or diets are typically associated with structural and functional genomic variations. “Adaptation traits” are complex and often polygenic by nature, but positive selection footprints can be studied through next-generation sequencing (NGS) applications, such as whole genome and mRNA sequencing, analysis of regulatory (miRNAs) elements and DNA methylation profiles. Reindeer, cattle and horse may have different biological capacities to adapt to extremes in temperature, daylight and feed availability. It is suggested that reindeer descended from

a large Eurasian glacial reindeer population have the longest adaptation history (but the shortest domestication history) among the three species and can be considered as native to the Arctic. Cattle and horses, on the other hand, have longer domestication histories but have shorter adaptation histories and are regarded as having been “imported” into the Arctic. The recent study on complete genomes of modern Yakutian horses and ancient horses that lived in Sakha (Yakutia) around 5200 yr ago provided evidence that the native Yakutian horse descends from domestic livestock and not from extinct wild horse populations that once existed in Sakha. Genomics of Arctic and northern domestic animals — cattle, horse and reindeer — are studied and compared with Mediterranean cattle and horse breeds native to Portugal in a multidisciplinary study, “Arctic Ark. Human–Animal Adaptations to the Arctic Environment: Natural and Folk Selection Practices (Arc-Ark).” The project is a consortium work between colleagues from genetics and animal science at the Finnish Natural Resources Institute (Luke), Yakutian Research Institute of Agriculture (FGBNU Yakutskij NIISH) and University of Porto and the anthropology team of the Arctic Centre of University of Lapland. The project belongs to the Arctic Research Program “Arktiko” of the Academy of Finland.

Key Words: Arctic, genomics, livestock

INVITED SPEAKERS: LIVESTOCK GENOMICS FOR DEVELOPING COUNTRIES

S0124 Indigenous stocks as treasure troves for sustainable livestock production in the 21st century: Insights from small ruminant genomics.

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The versatility of indigenous sheep and goats to adapt to diverse environmental conditions and production systems positions them as significant animal genetic resources for sustaining livelihoods of

agro-pastoralists, pastoralists and small holder farmers in many developing countries. In most of these countries, recording phenotypic and pedigree information has remained a challenge, cohorts of contemporaries are often of inadequate size, breeding infrastructures are non-existent and where they exist are rudimentary, and advanced reproductive technologies are difficult to implement. These drawbacks can however, be circumvented through community-based breeding programmes (CBBP) which can provide a framework to design and implement basic recording and mating schemes. Variants of the CBBP have been implemented successfully in some countries in Africa and Latin America. The integration of case-control protocols for use in genome-wide association analyses with CBBP offer great opportunities to identify genomic regions with major gene effects that can be used for genomic selection and/or introgression. Furthermore, the availability of genomic data can facilitate the determination of breed composition and admixture in the absence of pedigree records, assessment of genetic diversity and structure to harness biodiversity, and the identification of genome-wide footprints of positive selection. Such data can provide a platform to design mating schemes that optimize productivity and adaptability in a diverse gene pool of indigenous sheep and goats and the development of suitable breeds. In the context of the CBBP, the propagation of alleles, underlying production and adaptation traits, via gene/genome/haplotype block editing could be combined with genomic selection in the process of developing synthetic breeds that optimize productivity and adaptability across diverse production and agro-ecological systems. In this regard, genomic data generated recently using various indigenous African sheep and goats and revealing levels of admixture and genome-level multiple breed combinations, genome-wide signatures of positive selection for adaptation to marginal environments and fecundity traits and their potential applications will be discussed.

Key Words: developing countries, genome-wide, goats, selection signatures, sheep

INVITED SPEAKERS: RUMINANT GENETICS AND GENOMICS

S0125 Changing patterns of genomic variability

following domestication of sheep. M. Naval

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Patterns of genome variation are highly informative for understanding the diversity and evolutionary history of domestic animal species. We analyzed sheep genomes from a broad collection of domestic breeds, along with their wild ancestor (*O. orientalis*) and other wild sheep species (*O. canadensis* and *O. dalli*). Following variant calling to identify ~30 million high confidence SNP, we calculated nucleotide diversity to assess genome-wide differences in variability and applied homozygosity-based metrics to search for specific genomic regions that have undergone selection sweeps. As might be expected for a wild species, mouflon genomes had generally higher nucleotide diversity compared with domestic sheep. Furthermore, bighorn and thin-horn genomes showed depressed diversity, likely reflecting a strong founder effect and the impact of low effective population size. To approach a deeper understanding of changing patterns of diversity following domestication, we used available gene models and comparative information from human enhancer databases (ENCODE, Epigenetic Roadmap) to partition genomic sequence into a collection of features. These included exons, introns, UTRs, intergenic regions, and the components of gene regulatory machinery, such as promoters. For each genome feature, we compared the distribution in nucleotide diversity between wild and domestic sheep. We found clear evidence that exons have undergone a marked decrease in nucleotide diversity, when comparing wild to domestic sheep, in contrast to other genome features tested. We will also report on the collection of chromosomal regions that have undergone sweeps to build a deeper understanding of the impact of domestication in this important farmyard species.

Key Words: sheep, domestication, polymorphisms, genetic diversity