

from a systematic assessment of the gene content of associated genomic regions. This revealed genes involved with energy metabolism, neuroendocrinology and steroid biosynthesis.

**Key Words:** salmon, GWAS

**WT86 Reconstructing the complex structure of the sex determination locus in Atlantic herring using SMRT sequencing.** N. Rafati\*<sup>1</sup>, C.-J. Rubin<sup>1</sup>, C. Feng<sup>1</sup>, M. Petterson<sup>1</sup>, A. Bario Martinez<sup>2</sup>, S. Lamichhaney<sup>1</sup>, I. Bunikis<sup>3</sup>, and L. Andersson<sup>1,5</sup>, <sup>1</sup>Science for Life Laboratory, Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden; <sup>2</sup>Science for Life Laboratory, Department of Cell and Molecular Biology, Uppsala University, Uppsala, Sweden; <sup>3</sup>Science for Life Laboratory, National Genomics Infrastructure, Uppsala University, Uppsala, Sweden; <sup>4</sup>Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden; <sup>5</sup>Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX, USA.

The mechanism for sex determination considerably varies among species. Fish (similar to some of reptiles) have established two distinct sex determination systems: environmental sex determination (ESD) and genetic sex determination (GSD), and sometimes both systems work in concert. GSD can be under control of sex chromosomes or master genes on autosomal chromosomes, yet in most fish species genes with predominant roles in sex determination

have not been reported. An exception is the *dmrt1* paralogous copy (*dmy*) on medaka's (*Oryzias latipes*) Y-chromosome governing sex determination. It is now clear that a GSD system has evolved independently in several lineages of teleosts. However in the majority of them, including Atlantic herring (*Clupea harengus*), the sex determination system is still unknown. Herring is among the most abundant species with vast economical and ecological importance in Northern Atlantic. Atlantic herring reproduces throughout the Baltic Sea and Atlantic Ocean in different salinities (2–35‰) and seasons. We generated a high-quality draft genome assembly by short read sequencing technology to unravel the genetic basis of ecological adaptation to both salinity and seasonal reproduction. We identified a large region (~100 Kb) for which males and females showed significant differentiation (male specific region). Our study on unmapped reads revealed male unique sequences belonging to a member of the *cation channel sperm-associated protein (CATSPER)* gene. But our efforts in linking these two segments by PCR failed. To gain further insight into the herring genome, we generated a new assembly by single-molecule real-time (SMRT) sequencing technology. In this new assembly, we revealed the organisation of the previously identified signals indicative of early stages of sex chromosome evolution. This is the first report on identifying a sex determination locus and proto-Y chromosome in Atlantic herring. This study enhances our understanding of the evolution of sex chromosome in this species and other teleosts.

**Key Words:** sex determination, evolution, sex chromosome, reproduction, SMRT sequencing

## Livestock Genomics for Developing Countries

**WT87 Genomic diversity and population structure analysis reveal few genetic differences among Ethiopian indigenous sheep populations.** A. Ahbara\*<sup>1,2</sup>, J. Mwacharo<sup>3</sup>, H. Bahbahani<sup>4</sup>, S. Mastrangelo<sup>5</sup>, F. Pilla<sup>6</sup>, E. Ciani<sup>7</sup>, and O. Hanotte<sup>1</sup>, <sup>1</sup>School of Life Sciences, University of Nottingham, Nottingham, Nottinghamshire, UK; <sup>2</sup>Department of Zoology, Faculty of Sciences, Misurata University, Misurata, Libya; <sup>3</sup>Small Ruminant Genetics and Genomics Group, International Center for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia; <sup>4</sup>Department of Biological Sciences, Faculty of Science, Kuwait University, Safat, Kuwait; <sup>5</sup>Dipartimento di Scienze Agrarie e Forestali, University of Palermo, Palermo, Italy; <sup>6</sup>Dipartimento Agricoltura, Ambiente e Alimenti, Università degli Studi del Molise, Campobasso, Italy; <sup>7</sup>Dipartimento di Bioscienze, Biotechnologie e Biofarmaceutica, Università degli Studi di Bari 'Aldo Moro', Bari, Italy.

African sheep, like other domestic sheep, are domesticated from the Asiatic mouflon (*Ovis orientalis*). They entered the continent through the North and the Horn of Africa regions following maritime and terrestrial trading routes. Ethiopia is one of the main entry points of various plant and animal domesticates into Africa. It is characterised by diverse agro-ecologies, ancient human ethnic diversity and the presence of indigenous sheep breeds/populations of unprecedented morphological diversity (e.g. tail types). Here, we investigate the genome diversity and population structure of 146 unrelated animals from 11 Ethiopian indigenous sheep populations. DNA was extracted from ear tissue punches and genotyped with the Illumina Ovine 50K SNP BeadChip assay. Sheep populations from The Caribbean, Europe, Middle East and China as well as from western, northern and southern Africa were included to clarify the genetic history of origin, introduction and dispersal of the species into Ethiopia. Principal component analysis (PCA), clearly separated all Ethiopian sheep from the other populations. Population structure and phylogenetic (neighbour-joining tree) analysis subdivided the Ethiopian indigenous sheep into three genetic clusters corresponding to their tail morphology (rump fat-tailed, short fat-tailed and long fat/thin-tailed population). It supports a common genetic

ancestry for populations of each tail type in the country. Genetic distances among the Ethiopian populations were positively correlated with geographic distances (Mantel test,  $P < 0.001$ ,  $r = 0.465$ ) and the highest genetic diversity was recorded in the fat-tailed (short, rump and/or long fat-tailed) close to the Bab-el-Mandeb strait. However, despite their distinct morphology and separate geographic distribution, little genetic differentiation between Ethiopian populations are observed. This is most likely a consequence of their ancient and modern intermixing following their introduction into the country.

**Key Words:** sheep, genome-wide association, population structure, breed diversity, population

**WT88 Genetic admixture in indigenous Ugandan goat breeds using genome-wide SNP data.** R. B. Onzima\*<sup>1,3</sup>, M. R. Upadhyay<sup>1</sup>, R. Mukibi<sup>2</sup>, E. Kanis<sup>1</sup>, and R. Crooijmans<sup>1</sup>, <sup>1</sup>Wageningen University and Research Animal Breeding and Genomics, Wageningen, the Netherlands; <sup>2</sup>Department of Agriculture, Food and Nutritional Sciences (AFNS), Faculty of Agriculture, Life and Environmental Sciences University of Alberta, Alberta, Canada; <sup>3</sup>National Agricultural Research Organization (NARO), Entebbe, Uganda.

Well-adapted indigenous goats are an important genetic resource for future sustainable production in marginal areas. The introduction of exotic Boer goats for meat production in Uganda has had an effect on the diversity of the goat genetic resources in the country. Little is known about the effect of exotic Boer goats on the genetic diversity and population structure of the goat breeds in Uganda. The objective of this study was therefore to assess genetic admixture and population structure in goat population in Uganda. Five indigenous Ugandan goats of Mubende ( $n = 29$ ), Kigezi ( $n = 29$ ), Small East African ( $n = 29$ ), Sebei ( $n = 29$ ) and Karamojong ( $n = 15$ ) and exotic Boer ( $n = 13$ ) were assessed using caprine SNP50 bead chip. The polymorphism (MAF  $> 0.05$ ) across the breeds was 93.4% with the highest polymorphism observed in Sebei (92.8%) and lowest in Kigezi (88.5%). The average heterozygosity across