mation of HF and JER. Our findings highlight the potential functional impact of CNVs, and their role in recent selection.

Key Words: copy number variations, population divergence, dairy cattle

OP179 Chromatin accessibility conservation across four livestock species. S. Djebali*[1], S. Foissac[1], N. Vialaneix[2], K. Munyard[3], A. Rau[4], T. Faraut[1], S. Lagarrigue[5], H. Acloque[4], E. Giuffra[4], and FR-AgENCODE Consortium[1,4], *[1]GenPhySE, University of Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France, [2]MIAT, INRA, Castanet Tolosan, France, [3]Curtin University, School of Biomedical Sciences, CHIRI Biosciences, Perth, Australia, [4]GABI, AgroParisTech, INRA, Université Paris Saclay, Jouy-en-Josas, France, [5]UMR PEGASE, INRA, Rennes, France and UMR PEGASE, Agrocampus Ouest, Rennes, France.*

Within the FAANG consortium, the FR-AgENCODE pilot project has generated transcriptome (RNA-seq) and chromatin accessibility (ATAC-seq) data in the liver and immune cells of 2 males and 2 females of 4 vertebrate species (cattle, goat, chicken and pig), in addition to Hi-C data (see abstract #79896 by S. Foissac et al.). The first single-assay and integrative analyses performed on these data were mostly done on each species separately. Although these analyses provided several interesting insights (https://www.biorxiv.org/content/10.1101/316091v1), they did not take full advantage of our data richness, namely the availability of the same kind of functional data on species belonging to different parts of the phylogenetic tree. Here we have investigated the relationship between chromatin accessibility conservation across vertebrates and functionality. We first defined orthologous accessible regions by projecting accessible regions from our 4 species to the human genome. Two accessible regions are called orthologous if their projection on the human genome overlap. In doing so we identified 19,982, 7,877 and 1,083 regions shared between 2, 3 and 4 species, respectively. Our main results are as follows: The level of accessibility of a region, measured by ATAC-seq, increases with the number of shared accessibility-orthologs. Regions with more shared accessibility-orthologs are more likely to be close to gene promoters. The functional conservation of an accessible region, measured by the number of species exhibiting a tissue-differential accessibility, is correlated with sequence conservation, measured by phastCons. This confirms and reinforces previous findings in human and mouse. A hierarchical clustering of ATAC-seq samples based on the correlation between the accessibility of the 1083 orthologous regions shared between 4 species shows that clustering occurs first by species and then by tissue. This is different from what we found for RNA-seq (i.e., all liver samples clustering together). Based on these findings, we are currently working to define more precisely the functional regulatory relationships in liver and immune cells in light of their conservation during evolution. We anticipate that the comparison of these relationships to known QTLs should provide interesting results.

Key Words: ATAC-seq, comparative genomics, bioinformatics, vertebrate livestock species, FAANG

OP180 Meta-analysis of differentially co-expressed gene modules for high- and sub-fertile beef cows. P. A. de Souza Fonseca*, A. Suárez-Vega, S. Lam, F. S. Schenkel, S. Id-Lahoucine, and A. Canovas, *University of Guelph, Guelph, ON, Canada.*

Improved reproductive efficiency may lead to economic benefits for livestock. However, several factors limit our understanding of fertility traits, including genetic differences between populations and statistical limitations. This study identified differentially co-expressed (DcoEx) gene modules between 10 high- (HF) and 10 sub-fertile (SF) beef cows (predominantly Angus heifers). The fertility status was based on the pregnancy outcome ratio after successive high-quality embryo transfers protocol of estrus synchronization (PG-6d-CIDR and GnRH) where heifers that did not exhibit standing estrus received GnRH injection on d 0. RNA-sequencing (RNA-Seq) data from endometrium of HF and SF cows were retrieved from Gene Expression Omnibus (ID: GSE81449, GSE107891). RNA-Seq data was aligned using STAR software, read counts were obtained using RSEM software and DESeq2 package was used to normalize and calculate the Fragments Per Kilobase of transcript per Million mapped reads (FPKM) values. The identification of DcoEx modules was performed by the R package WGCNA using shared genes between HF and SF with an FPKM >0.2 in each group (16,439 genes). The R package km2gcn was used to reallocate the genes within modules using a k-means clustering approach. Three and 9 DcoExp modules were identified with a unique co-expression pattern in HF and SF cows, respectively. The genes within these modules are associated with fertility-related processes, including fertilization, decidualization, and steroid biosynthesis. In addition, SNPs and INDELs exclusive to HF or SF groups were called and annotated (20,076 and 18,764, respectively). The top 10 hub-genes of each module were scrutinized for variants identified exclusively in one of the groups and the co-localization with previously reported fertility-related female QTLs. Four and 21 top-hub genes in the HF and SF DcoExp modules emerged as functional candidate genes, respectively. The identification of hub-genes in DcoExp modules for contrasting the fertility based groups analyzed here may help to identify functional candidate genes and biological processes associated with implantation and retention of the embryos in beef cattle.

Key Words: fertility, bioinformatics, WGCNA, RNA-seq, systems biology

OP181 Broadening the miRNA catalogue in livestock species: A contribution to the functional annotation of animal genomes. A. J. Amaral*[1], C. Anthon[2], G. Corsi[2], A. Vasconcelos[1], S. Marthey[3], A. Hoffman[4], J. Lagnel[5], F. Haack[6], K. Pokharel[7], O. Palasca[2], S. Seemann[2], L. T. Gama[1], M. A. M. Groenen[8], J. Kantanen[7], R. P. M. A. Crooijmans[8], M. Rijnkels[9], T. Kalbfleisch[10], E. Giuffra[3], P. F. Stadler[4], O. Madsen[8], and J. Gorodkin[2], *[1]Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal, [2]Center for noncoding RNA in Technology and Health, Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg C, Denmark, [3]GABI, AgroParisTech, INRA, Université Paris Saclay, Jouy-en-Josas, France, [4]Bioinformatics Group, Department of Computer Science University of Leipzig, Leipzig, Germany, [5]INRA PACA, Montfavet Cedex, France, [6]Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany, [7]Natural Resources Institute Finland, Jokioinen, Finland, [8]Wageningen University, Wageningen, Netherlands, [9]Veterinary Integrative Biosciences,College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA, [10]Department of Biochemistry and Molecular Genetics, School of Medicine, University of Louisville, Louisville, KY, USA.*

MicroRNAs play a crucial role in the regulation of gene expression. Their action is crucial in many biological processes and functions, such as cell development and differentiation, and in response to disease. Moreover, it has been shown that polymorphisms in miRNAs can be linked to diseases and complex traits. An improved annotation of miRNAs in domestic animals is therefore required to acquire a comprehensive understanding of their impact on livestock traits. There are a large number of published studies with public data sets across most of livestock species and covering a wide range of tissues. However there have been few resources to capitalize on these data to better understand these features, distribution and biogenesis in these genomes. Therefore, a working group was established for the development of analysis pipelines and methods of data analysis of small-RNA-seq data in the framework of COST-Action FAANG-Europe. A total of 846 quality approved small-RNA-seq data sets available from public repositories for 6 livestock species (*Gallus gallus, Sus scrofa, Equus caballus, Ovis aries, Capra hircus and Bos taurus*) were used to quantify miRNA expression in different tissues as well as to identify putative novel miRNA candidates. Our analyses has identified across the 6 species a total of 1,404 novel pre-miRNAs, with a larger impact for *Bos taurus and Sus scrofa,* in which these represent an increase of 50% for these species in comparison with miRBase v22. We will use these to perform large-scale