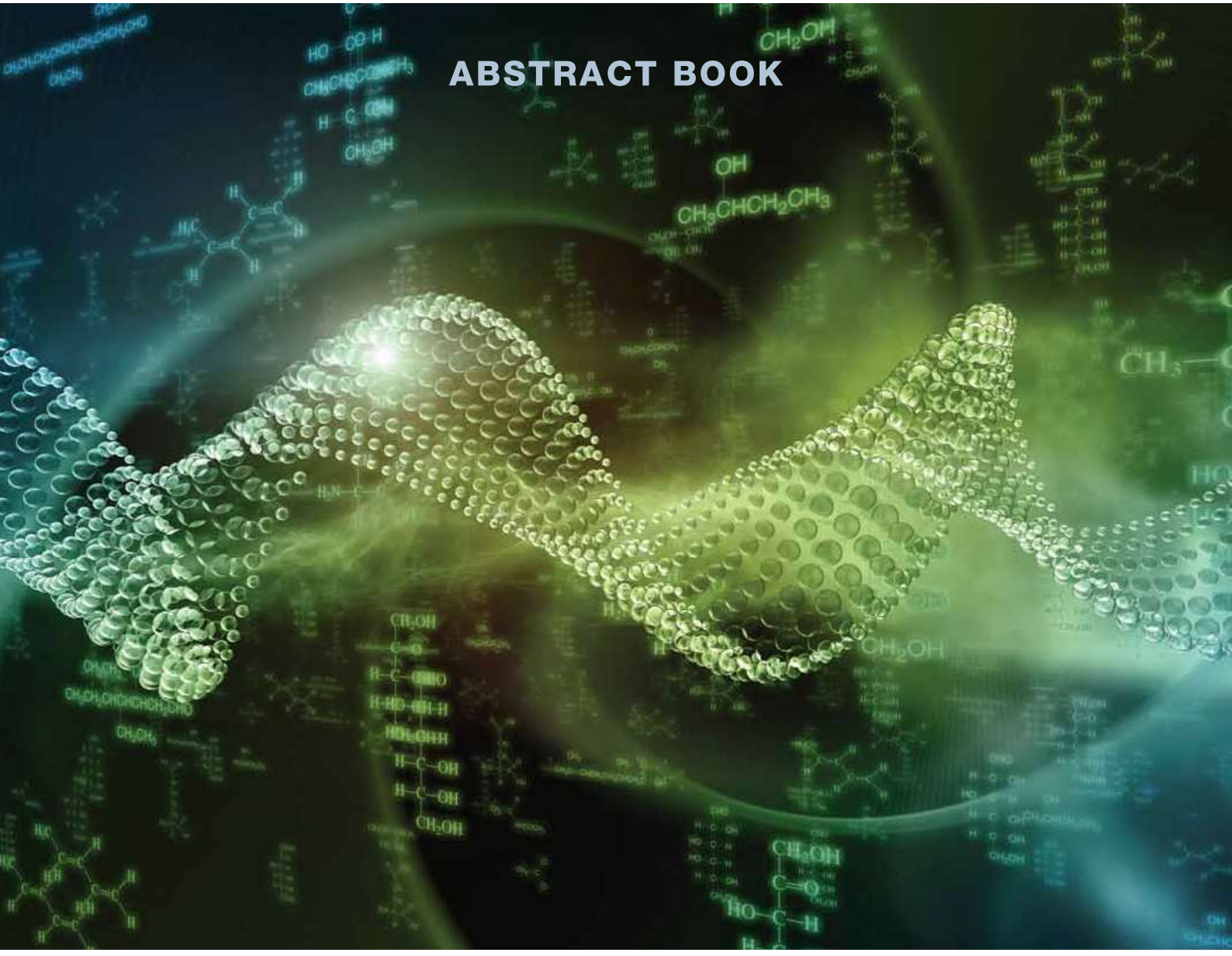
35th INTERNATIONAL SOCIETY FOR ANIMAL GENETICS CONFERENCE

7.23.16 – 7.27.2016 • Salt Lake City, Utah



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were called using MACS2. The ATAC-seq and DNase-seq data were compared for signal-to-noise ratio, intersection of peaks and correlation of peak intensities. The fragment length distribution of ATAC-seq reads recapitulated the expected nucleosome spacing pattern, and ATAC-seq peaks generally coincided with DNase-seq peaks. These results suggest that ATAC-seq, preceded by appropriate nuclei preparation, may be used as an alternative to DNase-seq for profiling regions of open chromatin in tissues.

Key Words: ATAC-seq, chicken, open chromatin

P2025 Identification of tissue-specific promoters in chickens. C. Kern* (University of California, Davis, CA), P. Saelao (University of California, Davis, CA), Y. Wang (University of California, Davis, CA), M. Halstead (University of California, Davis, CA), J. Chitwood (University of California, Davis, CA), T. Kim (University of California, Davis, CA), P. J. Ross (University of California, Davis, CA), I. Korf (University of California, Davis, CA), M. E. Delany (University of California, Davis, CA), H. Cheng (USDA-ARS Avian Disease and Oncology Laboratory, East Lansing, MI), H. Zhou (University of California, Davis, CA)

The importance of epigenetics in understanding the link between an organism's genome and resultant phenotypes has become clear in recent years. This is especially significant in the food production industry, where such knowledge can be used to improve production efficiency, animal welfare and food safety. We present our progress toward compiling a catalog of functional genomic elements for the chicken, a species utilized in one of the largest global meat production industries. We have generated genome-wide profiles of DNase I hypersensitivity (DHS) sites as well as H3K4me3 and H3K27me3 histone modifications from cerebellum, cortex, liver, lung and spleen tissues. Two biological replicates were used to permit consistent identification of DHS sites and histone modification peaks, with only those features present in both replicates being used for further analysis. DHS sites and H3K4me3 peaks are associated with enhanced gene expression when found in promoter regions, while H3K27me3 is associated with repressed expression. A total of 25,503 promoter regions (2kb upstream of transcription start site) belonging to annotated transcripts contained a DHS site co-localizing with an H3K4me3 peak that was seen in each of the five tissues. The number of tissue-specific active promoters varied considerably among tissues, with 175 identified in liver, 180 in cerebellum, 458 in cortex, 800 in lung and 2615 in spleen. Combining such data with RNA expression measurements further verified the regulatory role of these features and supports the existence of expressed, but unannotated, transcripts, such as novel isoforms and long noncoding RNA.

Key Words: epigenetics, tissue-specific, promoters

P2026 Polar overdominance and maternal genome effects in placenta drive heterosis in utero. C. A. S. Estrella (Robinson Research Institute, The University of Adelaide, Adelaide, Australia; JS Davies Epigenetics and Genetics Group, School of Animal and Veterinary Sciences, Roseworthy Campus, Adelaide, Australia), K. L. Kind (Robinson Research Institute, The University of Adelaide, Adelaide, Australia; School of Animal and Veterinary Sciences, Roseworthy Campus, Adelaide, Australia), M. Ghanipoor-Samami (Robinson Research Institute, The University of Adelaide, Adelaide, Australia; JS Davies Epigenetics and Genetics Group, School of Animal and Veterinary Sciences, Roseworthy Campus, Adelaide, Australia), A. Javadmanesh (Robinson Research Institute, The University of Adelaide, Adelaide, Australia; JS Davies Epigenetics and Genetics Group, School of Animal and Veterinary Sciences, Roseworthy Campus, Adelaide, Australia), C. T. Roberts (Robinson Research Institute, The University of Adelaide, Adelaide, Australia; Discipline of Obstetrics and Gynecology, School of Medicine, The University of Adelaide, Adelaide, Australia), S. Hiendleder* (Robinson Research Institute, The University of Adelaide, Adelaide, Australia; JS Davies Epigenetics and Genetics Group, School of Animal and Veterinary Sciences, Roseworthy Campus, Adelaide, Australia)

Heterosis, defined as the superior performance of F_1 hybrids over their parents, has been used for centuries to increase yield in plants and animals. However, the biological basis of heterosis is poorly understood, as it does not follow standard genetic models. Based on theoretical prediction that genomic imprinting may mimic overdominance and heterosis, we investigated whether imprinting effects could explain heterosis. We used purebred and reciprocal cross *Bos taurus taurus* (Angus, A) and *Bos taurus indicus* (Brahman, B) cattle that display one of the strongest known heterotic phenotypes in mammals. We intercepted concepti at mid-gestation, when the fetus enters accelerated growth but does not yet display heterosis in weight, to map drivers of heterosis in placenta as the major organ regulating prenatal growth that predicts postnatal performance. Our analyses at the gross morphological, histomorphological and molecular level revealed nine

maternal, three paternal and nine polar over/underdominance patterns consistent with genomic imprinting effects but only two with additive genetic effects. Strikingly, placental polar overdominance patterns at midgestation mirrored polar overdominance in birth weight. We found that increased nutrient supply via maternal A genome effects on placental phenotype, combined with increased nutrient transfer capacity via polar overdominance effects of paternal B genome on umbilical cord phenotype, provide the basis for heterosis in birth weight of B×A hybrids. Polar overdominance in expression of imprinted *IGF2R* in *Placenta fetalis* of B×A hybrids, and correlation of transcript abundance with number of feto-maternal syncytia in placenta, are consistent with an active signaling role of IGF2R in placenta and a further indicator of superior placental performance as the driver of heterosis. In conclusion, we have shown that phenotypic expression patterns consistent with imprinting effects on placental and umbilical cord parameters and in agreement with the conflict of interest theory of genomic imprinting drive mammalian heterosis in utero.

Key Words: heterosis, polar overdominance, maternal and paternal genome effects, placenta, IGF, bovine

POSTERS: FUNCTIONAL GENOMICS

P3000 Variation of goat interferon regulatory factor 3 gene and its implication in goat evolution.

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Members of the interferon regulatory factor (*IRF*) gene family are major regulators of host defense in vertebrates, controlling many different aspects of the innate and adaptive immune responses. Among these, *IRF3* plays important roles in many biological processes. Considering that immune systems are crucially fundamental for the survival and evolution of all species, patterns of selection and polymorphisms in innate immune loci are of significant interest in molecular evolution research. We assembled and evaluated 1353 bases on the encoding regions of the *IRF3* gene in domesticated goats from Nigeria (West Africa), Ethiopia (East Africa), Iran (West Asia) and China (East Asia) and in wild goat (*Capra aegagrus*). The sequence diversity in domesticated goats was quite low but significantly different from that of wild goats. The Fu and Li's tests were significant and positive, while the Tajima's D test was significant but negative, suggesting a deviation from neutrality. Two of the six observed haplotypes across all the sequences were common in Asian goats. Two haplotypes were shared with wild goat, by West African Dwarf (WAD) and African Borena goats. In assessing the mode of evolutionary activity affecting the evolution of the gene, we found that the codon models d_N/d_S ratio for all goats was greater than a unit (1.667; $P = 0.025$). Likelihood ratio test (LRT) to compare the models used was significant (24.56; $P < 0.001$). Positive diversifying selection inferred with recent evolutionary changes in domesticated goat *IRF3* led us to conclude that the gene evolution has been influenced by domestication process in goats.

Key Words: evolution, goat, gene