es for depth studies on their demographic trajectory, dating and wide geographic spread, as well as the genetic mechanisms underlying their breeding and response to natural/artificial selection for rapid adaptation to diversified environmental, climatic and management conditions. The development of genomic technology, multi-function database, and bio-informatic tools will be expected to facilitate data sharing and mining. We have been therefore trying to establish a world-wide collaborative network of scientists from multidisciplinary fields, to work together and contribute to this important initiative.

**Key Words:** chicken, genome, diversity, adaptation, history

**OP60** A new 55K SNP genotyping array for the chicken. R. Liu1,2, S. Xing2,3, R. P. M. A. Crooijmans2, G. Zhao1,3, and J. Wen4, 1Chinese Academy of Agricultural Sciences Institute of Animal Science, Beijing, China, 2Animal Breeding and Genomics, Wageningen University & Research, Wageningen, the Netherlands.

Background: China has the richest local chicken breeding resources in the world, and is the world’s second largest producer of meat-type chickens. Development of a moderate-density SNP array for genetic analysis of indigenous chickens and breeding of meat-type chickens is urgently needed for conventional farms, the breeding industry and research areas. Results: Eight representative local breeds and 2 commercial broiler lines with 3 pools of 48 individuals within each line were sequenced and supplied the major resource of SNPs. There were 7.09 million - 9.41 million SNPs detected in each breed/line. After filtering using multiple criteria such as preferred incorporation of trait-related SNPs and uniformity of distribution across the genome, 52.18 K SNPs were involved in the final array. It consists of: (i) 19.22 K SNPs from the genomes of white-feathered, yellow-feathered, and cyan-shank partridge chickens; (ii) 5.98 K SNPs related to economic traits from the Illumina 60 K SNP Bead Chip, which were found as significant associated SNPs with 15 traits in an F resource population, Beijing-Yu crossed Cobb, by genome-wide association study (GWAS) analysis; (iii) 7.63 K SNPs from 861 candidate genes of economic traits; (iv) the 0.94 K SNPs related to residual feed intake; and (v) 18.41 K from chicken SNPs. The economic traits mentioned in the categories (ii) and (iii) included growth, feed efficiency, meat quality, immune traits, etc. The polymorphisms of 9 extra local breeds and 3 commercial lines were examined with this array, and 40 - 47 K SNPs were polymorphic (with minor allele frequency >0.05) in those breeds. The multidimensional scaling result showed that those breeds can be clearly distinguished by this newly developed genotyping array. Conclusions: We successfully developed a 55 K genotyping array designed using SNPs segregated in typical local breeds and commercial broiler lines, and 14.55 K SNPs associated with economic traits were incorporated. The array has a wide range of application potentials such as breeding with genomic selection, genome-wide association studies of traits of interest, and investigation of diversity of different chicken breeds.

**Key Words:** genotyping array, SNP, indigenous chicken, genome-wide

**OP61** An open chromatin region on GGA1 has an important effect on regulating chicken growth. X. Cao1,2, Y. Wang1,2, and X. Hu1,2, 1College of Biological Sciences, China Agricultural University, Beijing, China, 2State Key Laboratory of Agro-biotechnology, China Agricultural University, Beijing, China.

Body weight is one of the most important economic traits of chickens. Exploring the genetic mechanism of body weight has vital significance for chicken meat industry. In our previous study, a 1.2 Mb QTL and a 12 Kb haplotype in the QTL interval associated with body weight were detected on the chicken (Gallus gallus) chromosome (GGA) 1 using an advanced intercross population constructed by Huiyong Beard Chicken (a slow-growing domestic breed) and High Quality chicken Line A (a fast-growing broiler). In current study, we explored the 12 Kb haplotype block and its effect on regulating gene expression and chicken growth in duodenum at 7 weeks, as the digestion and absorption of food play an important role in gaining weight. The favorable allele for high body weight was defined as H haplotype utilizing 6 tag SNPs, in contrast to L haplotype for low body weight. Progeny test demonstrated that HH genotype chickens had a significantly higher body weight comparing to LL genotype chickens. In the 1.2 Mb QTL region, 3 genes presented different expression in duodenum between HH and LL individuals, which have been proved involving in gastrointestinal motility or energy metabolism. Through ATAC-Seq, we detected an open chromatin region containing 2 tag SNPs in the haplotype block and it suggested that 1) the open chromatin region might affect the expression of genes in the QTL region, and 2) the SNPs in the open chromatin region lead to the change of gene expression. Considering the effect of energy metabolism on growth, we measured protein levels of AMP-activated protein kinase (AMPK), the key regulator in energy regulation, through Western Blot. The increasing expression of both AMPK and phosphorylated AMPK in LL chickens comparing to HH chickens, suggested that the open chromatin region in the 12 Kb haplotype block might affect the body weight of chicken in a way of regulating energy metabolism.

**Key Words:** chicken, animal breeding, duodenum, genotyping, ATAC-Seq

**OP64** Transcriptome sequencing reveals key potential long non-coding RNAs related to duration of fertility trait in the uterovaginal junction of egg-laying hens. A. Adetula1, L. Gu1, C. Nwafor2, X. Du1, S. Zhao1, and S. Li1, 1Key Laboratory of Agricultural Animal Genetics, Breeding, and Reproduction, Ministry of Education, Key Laboratory of Poultry Genetics and Breeding of the Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, Hubei Province, China, 2Faculty of Agriculture, Benson Idahosa University, Benin, Edo State, Nigeria.

Duration of fertility (DF) is an important functional trait in poultry production and IncRNAs have emerged as important regulators of various process including fertility. In this study we applied a genome-guided strategy to reconstruct the uterovaginal junction (UJV) transcriptome of 14 egg-laying birds with long- and short-DF (n = 7); and sought to uncover key IncRNAs related to duration of fertility traits by RNA-sequencing technology. Examination of RNA-seq data revealed a total of 9,977 IncRNAs including 2,576 novel IncRNAs. Differential expression (DE) analysis of IncRNA identified 223 IncRNAs differentially expressed between the long- and short-DF groups, with 81 upregulated and 142 downregulated. DE-IncRNA target genes prediction uncovered over 200 IncRNA target genes and functional enrichment tests predict a potential function of DE-IncRNAs. Gene ontology classification and pathway analysis revealed 8 DE-IncRNAs, with the majority of their target genes enriched in biological functions such as cellular response to cytokine, response to protein homodimerization, reproductive structure development, developmental process involved in reproduction, regulation of protein modification, osteoblast differentiation and ossification, in uterus embryonic development, response to cytokine, carbohydrate binding, chromatin organization, response to growth factors, and immune pathways. Differential expression of IncRNAs and target genes were confirmed by qPCR. The discovery of these 2,576 novel IncRNAs in this study significantly expands the utility of the UJV transcriptome and our analysis identification of key IncRNAs and their target genes regulating DF will form the baseline for understanding the molecular functions of IncRNAs regulating DF and extend the knowledge of the molecular mechanisms underlying fertility.

**Key Words:** duration of fertility, long non-coding RNAs, egg-laying hens, uterovaginal junction, RNA-seq

**OP65** Sauropsida ribosomal repeat: Deciphering of the intergenic spacer in chicken and terrapin. A. Dyomin1,2, S. Galkina1, V. Fillon1, S. Cauet1, C. Lopez-Roques1, N. Rodde1, C. Klopp1, A. Vignal1, A. Sokolovskaya1, A. Safidinova1, and E. Gaginskaya1, 1Institute of Biological Sciences, Russian Academy of Sciences (IBS), Moscow, Russia, 2Federal Research Center for Physiological Ecology, Russian Academy of Sciences, St. Petersburg, Russia.

Sauropsida ribosomal repeat was found in the intergenic spacer region of the ribosomal RNA gene cluster of chicken and terrapin. The repeat is composed of two units of 631 and 725 bp. The repeat was shown to be present in the genomic DNA of several other reptiles and birds, as well as in the same region of the ribosomal RNA gene cluster of human, mouse and chicken. The repeat is highly conserved in all these species, and its presence is thought to be a characteristic feature of the Sauropsida. The repeat has been shown to play a role in the regulation of the expression of the ribosomal RNA genes. The repeat is transcribed into a large non-coding RNA transcript, which is thought to be involved in the regulation of the expression of the ribosomal RNA genes. The repeat is also transcribed into a small non-coding RNA transcript, which is thought to be involved in the regulation of the expression of the ribosomal RNA genes. The repeat is thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional regulator. The repeat is also thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional repressor. The repeat is also thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional activator. The repeat is also thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional enhancer. The repeat is also thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional silencer. The repeat is also thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional promoter. The repeat is also thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional terminator. The repeat is also thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional regulator. The repeat is also thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional repressor. The repeat is also thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional activator. The repeat is also thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional enhancer. The repeat is also thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional silencer. The repeat is also thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional promoter. The repeat is also thought to be involved in the regulation of the expression of the ribosomal RNA genes by acting as a transcriptional terminator.
Each ribosomal repeat (rDNA unit) consists of a pre-rRNA gene cluster (5′ETS, 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA, 3′ETS) transcribing in a single molecule and intergenic spacer (IGS) containing regulatory elements. In chicken, *Gallus gallus* rDNA units are situated in the only Nucleolar organizer region (NOR) on chromosome 16. As in many other eukaryotes, chicken rDNA repetitive units are missing in the current version of assembled genome (GRCg6a). Our previous attempt to assemble a full rDNA unit using Illumina data was not successful due to the complex structure of repeats in IGS, only transcribed rRNA gene cluster has been deciphered (NCBI Nucleotide: KT445934). Here, we describe a chicken IGS structure basing on PacBio single-molecule sequencing of a BAC clone WAG137G04 containing chicken NOR fragment with 3 complete IGSs from one White Leghorn individual. Also, Red jungle fowl contig NT_45123.1 was included into analysis. We identified several novel tandem repeats, which form regular highly organized structures. Most of repeats are highly GC-rich (65–81%) contributing to the total IGS high GC composition (68% vs. 52% in human). IGS is heterogeneous in length due to a copy number variation of some repeats. The alignment of transcriptome reads from different chicken tissues against the most complete rDNA sequence from WAG137G4_utg0 contig has revealed a weak transcriptional activity at certain central sites of IGS. We have compared the IGS organization between chicken and terrapin (*Malaclemys terrapin*), the complete ribosomal repeat sequence of terrapin was assembled using the raw data of sequencing. In both species, the IGS contains very long conservative GC rich tandem repeats and lack of the inverted sequence copies capable to form hairpins. It turned out that on contrast to IGS of mammals, amphibians and fish, the IGS in chicken and terrapin are GC-enriched and contain many putative CpG islands. These common features in the IGS structure appear to be significant when considering the genome evolution in the Sauropsida group. Financial and technical support: RFBR (#18-04-01276), “Chromas” and “Molecular and Cell Technologies” Resource Centres of Saint Petersburg State University, SPBU project 1.40.1625.2017.

**Key Words:** *Gallus gallus*, *Malaclemys terrapin*, nucleolus organizer region (NOR), rRNA genes, tandem DNA repeats


Body size is a phenotypic trait studied in many species. One of the extreme forms of this phenotype is dwarfism, which occurs in many forms and many species. In chicken, dwarfism is known in different forms, including autosomal dwarfism, sex-linked dwarfism and, bantam. Of these, the bantam phenotype is the most common form. In the last decades, fancy breeders in the Netherlands have utilized traditional bantams to “bantamize” the Dutch large fowls to produce dwarf versions of the original native breeds. Hence, for every large form of the traditional breed there is now also a bantam form with the same appearance as the large fowl. The resources of the historical Dutch large fowls and their small-sized counterparts offer a powerful opportunity to study the complexity of bantam phenotype and human-mediated selection. Using whole-genome sequence data we conducted Genome-Wide Association Study (GWAS) on 136 chickens from 38 breeds, including traditional bantams, like Dutch bantam. Based on the bantamization breeding history, the chickens were grouped into 3 groups according to the bantams used for the bantamization procedure. Here, each GWAS were performed on the group of chickens from the traditional large breeds, their bantam counterparts, and the true bantam breeds used as the bantam origin. Results of GWAS did not show any commonly shared genomic region between these 3 groups potentially associated with dwarfism, which suggests that the bantam trait within Dutch population is not a simple trait caused by a single underlying gene. Despite that, 2 of the studies revealed a shared significant locus, potentially regulates body size. Further validation of the associated locus is ongoing. Our findings reveal the novel genetic nature underlying the bantam phenotype in traditional Dutch breeds, providing significance in the breeding of dwarf chickens.

**Key Words:** chicken, body size, bantam, GWAS

**OP67**  Running and stunting syndrome in sex-linked dwarf chicken is associated with mitochondrial DNA depletion. H. Li*, Q. Nie, Q. Luo, W. Luo, and X. Zhang, Department of Animal Genetics, Breeding and Reproduction, College of Animal Science, South China Agricultural University, Guangzhou, Guangdong, China.

Running and stunting syndrome (RSS), which is characterized by low body weight, generally occurs early in life and leads to considerable economic losses in the commercial broiler industry. Our previous study has reported that RSS is a kind of mitochondrial disease with mtDNA depletion in poultry. However, the molecular mechanism of RSS remains unknown. In this study, we identified a homogeneous mutation c.409G > A (p. Ala137Thr) of *TWNK* gene in RSS chickens from strain N301. Bioinformatics investigations supported the pathogenicity of the *TWNK* mutation, which is located on the linker region of Twinkle primase domain and might further lead to mtDNA depletion in chicken. In addition, we also found that overexpression of the *TWNK* wild-type can increase mtDNA content in LMH and DF-1 cells, whereas overexpression of the *TWNK* A137T can cause mtDNA depletion in LMH and DF-1 cells. In conclusion, we demonstrated for the first time that the homogeneous *TWNK* c. 409G > A (p. Ala137Thr) mutation is associated with Running and Stunting Syndrome and mtDNA depletion in chicken.

**Key Words:** mitochondrial DNA, mitochondrial DNA depletion syndrome, running and stunting syndrome, SLD chicken, TKNK mutation

**OP68**  Discovering lethal alleles across the turkey genome using transmission ratio distortion approach. E. A. Abdalla*, S. Id-Lahoucine1, B. J. Wood1, A. Cánovas1, J. Casellas2, and F. C. Baes1, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, 1Hybrid Turkeys, Kitchener, ON, Canada.

Reproductive efficiency is one of the most important challenges in livestock production and with the availability of large genomic data sets there are research opportunities available to discover lethal alleles that have an impact on reproduction. For instance, it is possible to trace the inheritance of both alleles and allelic combinations inherited from parent to offspring using genotype trios. A trio is the information of sire, dam and offspring genotypes together. Tracing lethal alleles can be achieved using transmission ratio distortion (TRD) methodologies which are observable difference in the expected inheritance pattern. The objective of this study was to assess TRD in a turkey population to identify lethal alleles which are observable difference in the expected inheritance pattern. The results of this study revealed novel candidate lethal haplotypes and

**Key Words:** chicken, dwarf, transmission ratio distortion

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