
The microbiota is a complex and balanced community of hundreds of microbial species that play critical roles in diverse processes of the host, including digestion of food, disease and immune function. The gut microbiota in avian species is thought to be influenced by both environmental and genetic factors. However, little research has been conducted to examine the effects of host genetics on the structure and diversity of the bacterial communities found in the chicken gut. The purpose of this study was to understand the influence of genetics on the gut microbiota for the first 4 wk post-hatch by comparing 3 different strains of chickens reared intermingled in a common environment. A wild-type bird originating from Southeast Asia in the 1950s and now maintained at the University of Arkansas (giant jungle fowl), a randomly mated commercial bird representing the broiler of the 1990s, and a modern day commercial bird were raised on clean pine shavings with feed and water provided ad libitum. Complete ceca were collected at hatch, 2, 7, and 28 d post-hatch. Genomic DNA was isolated from cecal contents and used as templates for PCR amplification targeting hypervariable region V6 in the 16S rRNA gene. About 1.5 million sequences per sample will be obtained by high-throughput Illumina sequencing and analyzed to understand the structure and diversity of the bacterial communities as influenced by ages and lines. This study could provide valuable insights on the genetic factors influencing bacterial colonies in gut and the role of the gut bacterial colonies in growth characteristics of the birds. Data will be presented regarding statistical relationships between bacterial colonies, age and strain of bird.

Key Words: chicken, 16S rRNA, bacterial communities, gut health, genetics

125 Identification of high-utility genetic marker genes for chronic stress in chickens using high-throughput genome sequencing of genetically selected stress lines of Japanese quail.

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The objective of this study was to explore genetic markers for chronic stress in male broilers by performing genome sequencing of a genetically selected low stress line (LS) and high stress line (HS) of Japanese quail (Coturnix coturnix japonica). The 2 lines of Japanese quail were established by Dan Satterlee (Poult. Sci. 1988 67:25-32) based upon their corticosterone response to immobilization stress. Previous studies evaluated the potential usefulness of these quail lines for modeling the effects of the stress response on susceptibility to disease and pathogen colonization. In this study, whole genomes of Japanese quail LS and HS were sequenced using the Illumina HiSeq 2500 (rapid run flow cell, a paired end read of 2 \times 150 bp). Data were assembled and analyzed using software DNAstar Lasergene and Ingenuity Pathway Analysis. Over 3 million single nucleotide polymorphisms (SNP) were identified in each line and over 97% of SNP were found in the intergenic regions. In the coding DNA sequences, SNP that generated synonymous, non-synonymous, non-sense, no start, and no stop mutations were 69.4, 30.1, 0.3, 0.07, and 0.03%, respectively. Genes containing SNP were compared with stress-responsive genes which were previously identified by chicken microarray studies using male broilers that were subjected to repeated immobilization. Fifty-seven of the most reliable genetic marker genes were chosen by the following parameters: over 75% SNP rate, over 16 depth (read counts of contig), and differential changes of mRNA in the brain and anterior pituitary gland of chronically stressed chickens. Hence, most reliable SNP identified in this study may be utilized as genetic biomarkers to detect chronic psychogeneic-stress resistance or susceptibility. This study was supported in part by the National Animal Genome Research Program-Poultry (NRSP-8) and NSF grant #IOS-0842937.

Key Words: stress, genome sequencing, SNP, genetic marker, Japanese quail

126 The genetic relationship between feed efficiency and reproduction traits in the turkey (Meleagris gallopavo). B. J. Wood, T. Boersma, and O. W. Willems, Hybrid Turkeys, Kitchener, ON, Canada.

The objective was to calculate the heritability and genetic relationship between the feed efficiency traits (feed conversion ratio (FCR) and residual feed intake (RFI)) and the reproductive traits of egg production (EP), fertility (FERT) and hatch of fertile (HOF) in the turkey. Data was collected from a sire line of Large White turkeys with records between 2005 and 2012 with a full pedigree available for all individuals. Data was available for the reproductive traits in females, EP (n = 9,446), FERT (n = 11,757), and HOF (n = 11,481). Feed intake and body weight gain were also available in related males (n = 8,278). Egg production was measured as a percentage of days where an egg was produced, FERT was measured as a proportion of eggs that were candled fertile and HOF was measured as a percentage of fertile eggs producing a live poult. ASReml 3.0 was used to calculate the genetic variances using the model: Trait = hatchweek + hatchweekdam + animal + e, where trait represents the reproductive or feed efficiency trait, hatchweek is a fixed contemporary group effect, hatchweekdam is a fixed effect for dam age, included to take year into account, animal is the random additive genetic effect, and e represents the random residual effect. Genetic correlations were calculated using a bivariate analysis. The heritabilities and standard errors in parentheses of EP, FERT, HOF, RFI and FCR were 0.26 (0.04), 0.07 (0.02), 0.19 (0.04), 0.29 (0.05) and 0.13 (0.04), respectively. Genetic correlations and standard errors between FCR and FERT, HOF, EP were −0.38 (0.23), −0.22 (0.19) and −0.39 (0.16), respectively and similarly with RFI they were −0.29 (0.18), −0.44 (0.14) and −0.34 (0.13). As has been found in other species, competitive resource allocation between commercial and reproductive traits results in significantly negative correlations between the 2 sets of traits. If not accounted for in an appropriately weighted selection index, this may lead to unexpected selection consequences and potentially decrease in consistent egg production.

Key Words: reproduction, feed efficiency, resource allocation, turkey

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