



BIOINFORMATICS 2017 Spring SEMINAR SERIES

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<http://bioinformatics.udel.edu/Seminars/Current>

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3:30pm

DBI Room 102

Comparison of Allele Specific Expression in Various Tissues of Chickens

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ABSTRACT:

Allele specific expression (ASE) is the process where one allele in a heterozygous individual is expressed at a higher level in comparison to the other when equal expression is expected. ASE is of great interest to the agricultural field because it is associated with a measurable phenotypic trait. This means ASE could give breeders valuable genetic information that is of scientific or financial interest. In a recent study investigating Marek's disease in chickens, it was found that ASE SNPs were effective markers for elucidating the complex trait of disease resistance and showed progenies overall disease resistance could be increased by selecting for these specific ASE SNPs. However, no studies have been performed looking at ASE in an unchallenged chicken model, therefore no information is currently available about ASE in healthy birds that could help breeders in selecting for beneficial non-disease related traits. In our study we performed RNA-sequencing on 100 samples collected from various populations of chickens. We then followed GATK's "Best Practices for Variant Calling on RNAseq" using recommended settings. We aligned the sequence reads to the chicken reference genome sequence (*Gallus_gallus*-5.0) from Ensemble. Based on the first round of alignment of STAR, the average number of reads was 36,196,012.79 with an average mapping rate of 85.35%. We identified a total 3,147,284 variants (SNPs and Indels) and then used these variants to mask the reference genome for initial alignment. The final variants were filtered using various parameters and then examined for ASE using the binominal test. The total number of SNPs showing ASE were 14,276 SNPs in liver, 14,733 SNPs in abdominal fat and 23,970 SNPs in breast muscle. Interestingly, the overlap between tissues was found to be only several thousand SNPs with only 1,627 SNPs found in common between all tissues. These findings suggest that ASE is clearly a tissue dependent mechanism in chickens.