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P0503: Single Nucleotide Polymorphism Associated with Breast Trait in Chickens

In previous studies conducted in our research group, two QTLs were mapped for breast weight (BRW) and yield (BR%) in a paternal broiler male line (TT). Within these QTLs, analysis of resequencing data from 14 parental animals resulted in the identification of 12 non-tolerated Single Nucleotide Polymorphisms (SNPs), determined by SIFT score, in nine candidate genes. For each SNP, a region of 75 bp up and down stream was amplified and sequenced in 237 animals with Illumina Custom Amplicon Sequencing technology. The raw sequencing data was aligned against the chicken reference genome (Galgal_5.0) and the SNP calling was performed with SAMtools software followed by functional annotation using VEP tool. Association analysis for BRW and BR% with the non-tolerant SNPs were performed one SNP at time, with the Linear Mixed Model in SAS software. Body weight at 42 days of age was used as a covariate for BRW; sex, hatch and SNP were considered as fixed effects, family and residual as random effects. Only one SNP located within the *WDR77* gene (GGA26, rs736010549) was associated ($p < 0.1$) with BRW. This gene is related to the activation or increase in the rate or extent of cell proliferation and differentiation and has an important role in protein-protein complexes formations. Our results are not conclusive. We can not differentiate if rs736010549 is the causal mutation or if it is in linkage disequilibrium (LD) with the causal mutation. Further functional studies are necessary to elucidate these findings.

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