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## P0502: Inherited CNVs in Regions Related to Breast Muscle Development in a Broiler Population

Copy number variation (CNV) is an important genome polymorphism that contributes to phenotypic variation in a wide range of species, including chicken. We studied inherited CNVs in a Brazilian broiler population that overlap with breast muscle weight QTLs. A total of 826 chickens developed by Embrapa were genotyped using an Affymetrix 600K SNP array. The allele frequencies and intensities were analyzed by PennCNV (joint option) which detected 21,077 inherited CNVs. The CNVs were concatenated into 3,240 CNV regions (CNVRs) which cover 128.46 Mb (10.44%) of the autosomal chicken chromosomes (Galgal5). The length of the CNVRs ranges from 1 to 2,887 kb (average of 39.65 kb) and includes 492 losses, 2,461 gains and 287 harboring both losses and gains. Of these CNVRs, 41 overlap with breast muscle weight QTLs. In these regions, the CNVRs overlap with 79 genes. A CNVR gain of 20,771 bp was observed in *FGFR2*, a gene related with growth of fibroblasts. Two other CNVRs (a gain of 1,212 bp and a loss/gain of 50,942 bp) overlap with *WNT9A* and *SOCS3* respectively, two genes involved in cell differentiation. A gain CNVR of 6,414 bp overlaps with the *SLIT2* gene while another gain CNVR of 2,458 bp overlaps with *HTRA1*, both genes that are related with cell growth. In future studies, genome-wide association analysis with CNVs for breast muscle traits will complement the current results, helping to understand the genetic architecture of breast muscle development in chickens.

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