

**P0646****Identification of CNVs on the Genome of Brazilian Chicken Lines**

**Thais Fernanda Godoy** , University of São Paulo/ESALQ, Piracicaba, SP, Brazil  
Gabriel C M Moreira , University of São Paulo/ESALQ, Piracicaba, Brazil  
Vinicius H. Silva , University of São Paulo/ESALQ, Piracicaba, Brazil  
Clarissa Boschiero , University of São Paulo/ESALQ, Piracicaba, Brazil  
Monica Correa Ledur , Embrapa Swine and Poultry, Concordia, Brazil  
Ana Silvia Alves M. T. Moura , São Paulo State University/FMVZ, Botucatu, Brazil  
Luiz L. Coutinho , University of São Paulo/ESALQ, Piracicaba, Brazil

The aim of this study was to identify and characterize the distribution of CNVs in the genome of a Brazilian population of chickens developed by Embrapa. A total of 1,896 chickens were genotyped by Affymetrix 600 K SNP array. Samples with Dish quality control (DQC) <0.82 and call rates <95% were excluded by *Axiom™ Analysis Suite*, which resulted in 1,759 analyzed animals. The *Log R Ratio (LRR)* of each sample was corrected for genomic wave (GC content estimated in genomic windows of 100 kb around each marker). CNVs calls were inferred by PennCNV algorithm with the cutoffs: standard deviation of LRR at 0.35, BAF drift at 0.01 and waviness factor at 0.05. CNVs longer than 5 kb and samples with less than 1,000 CNV calls were retained. A total of 1,059 CNVs calls were retained and CNV region (CNVR) concatenation by CNVRuler, identified 392 estimated CNVRs covering 4.15 Mb (4.37%) of the autosomal chicken chromosomes (Gallgal4). The length of CNVRs ranged from 6.11 to 959 Kb (average of 101.87 kb), including 274 which were losses, 105 gains and 13 with loss and gain. The CNVRs were annotated by VEP tool (Ensembl), resulting in 14% of the CNVRs in coding regions, 16% in intron regions, and 7% in transcription and in 3'/5' regions. These CNVRs overlapped with 602 genes from which six are related to muscle development (ACTG2, CACNB4, COL11A1, FOXF1, GPHN and KCNMA1). In future studies these CNVRs will be validated and associated with weight and yield of breast muscle.

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