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INFORMATIVENESS OF SNPS ON THE GENOME OF THE BRAZILIAN CHICKEN BROILER AND LAYER LINES USING 60K ILLUMINA BEADCHIP

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Association studies may be carried out in different populations, including those that have already been developed for QTL mapping. Embrapa Swine and Poultry and ESALQ/USP developed the Embrapa F_2 Chicken Resource Population by crossing of 7 males from a broiler (TT) and 7 females from a layer line (CC) to map QTL using microsatellite markers. However, the development of the 60k Illumina SNP BeadChip, with 57,636 SNPs, from Cobb-Vantress, USDA and Hendrix Genetics Consortium, has enabled a high saturation of genomic regions where QTL were previously mapped. Therefore, our aim was to assess the informativeness of SNPs on the genome of the TCTC population founders using the 60k SNP chip. Genomic DNA was extracted from blood and genotyping followed the protocol *Infinium® II Assay Super* (Illumina®). Genotypes were analyzed based on the GenomeStudio (Illumina®) and Excel (Microsoft®) softwares, considering the parameters: missing genotypes proportion, average distance between SNPs, and minor allele frequency (MAF). A total of 806,904 genotypes were obtained (14 chickens x 57,636 SNPs with average distance of 3.56 ranging from 0.001 up to 89.91 k) with call rate >0.99, of which 2.4% (19,418) were missed due to the ScoreGenCall <0.15. Out of these, 9,779 were in TT and 9,639 in CC line. Consequently, we obtained 787.486 genotypes with success (97.6%). In the TT line 11,169 SNPs showed MAF = 0 (~20%) while in CC were 23,578 (~42%). Among SNPs with MAF = 0 (34,747), 8,214 were the same in both lines. SNPs with MAF = 0 correspond to those with fixed alleles (monomorphic SNPs) which present lower genotypic variability than those with MAF > 0. The fact that CC had more SNPs with MAF=0 than TT may be explained by the selection period in which these lines were subjected. CC and TT were selected for eight and six generations for egg and performance traits, respectively. Therefore, favorable alleles for traits of interest in each line tend to fixation. Also, it is important to note that both lines have different genetic backgrounds, where CC was originated from only one breed, White Leghorn, while TT had three distinct breeds (White Plymouth Rock, New Hampshire and White Cornish). Finally, it was possible to verify the informativeness of SNPs which are segregating in each line using the 60k Illumina SNP BeadChip. The next step will be to select the most informative SNPs in QTL regions for chip customization and genotyping of the F_2 chickens to implement association studies. Financial Support: CNPq, FAPESP and Embrapa/PRODETAB.