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Linkage disequilibrium and effective population size in a paternal broiler line.

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The patterns of linkage disequilibrium (LD) in the genome of livestock play a major role in genome-wide association studies (GWAS) and genomic selection. For quantitative trait loci (QTL) mapping, strong LD between markers and QTL are needed. By definition, LD is the non-random relationship of alleles between two loci within a population. The LD information can be used to infer population demography based on the changes in the historical effective population size (*Ne*), which is a measure of genetic variability and genetic contribution of ancestors. This study aimed to characterize the LD and determined *Ne* of a paternal broiler line (called TT) developed by Embrapa Swine and Poultry. A total of 1,430 chickens (652 males and 778 females) were genotyped with the 600K Affymetrix® Axiom® HD panel. For genotype quality control, SNPs with call rate <98%, MAF <0.03 and that deviated from HWE ($p < 10^{-6}$) were removed, remaining 353,589 SNPs for LD analyses using Plink v.1.9 software. The LD was calculated by the correlation between two consecutive SNPs (r^2) considering different distances according to the autosomal chromosomes: macrochromosomes (GGA1 to GGA5), intermediate chromosomes (GGA 6 to GGA10) and microchromosomes (GGA11 to GGA28). The *Ne* was calculated from the LD data for up to 200 generations ago using SNP1101 v.1.0 software. The LD decreased as the physical distance between the markers in all classes of chromosomes increased. The average r^2 which was equal to or higher than 0.30 extended for up to 500-550 Kb in macro, 350-400 Kb in intermediate, and 150-200 Kb in microchromosomes. The average LD between adjacent SNPs in all autosomes was 0.37 and ranged from 0.38 to 0.43, 0.36 to 0.40, and 0.29 to 0.41 in macrochromosomes, intermediate chromosomes, and microchromosomes, respectively. The *Ne* from LD data showed that the ancestral population of 200 generations ago was much higher (548 animals) than the recent population of 5 past generations (157 animals). The LD generally decayed rapidly while the distance increased; however, there were differences in the persistence and extent of LD in different classes of chromosomes. The LD information is an important measure to characterize the broiler population and essential for other genomic analyses.

Key Words: animal breeding, genetic markers, genomics, poultry