

Topic: **Genomics, Evolution and Phylogeny**PI: **GEP08****LINKAGE DISEQUILIBRIUM PATTERNS IN DAIRY GYR BREED**Muniz M N M^{1,3}, Andrade L G D³, Guedes E³, Tagliatti R F³, Machado M A², Verneque R D S²,
Guimarães M F M², Arbex W A^{1,2}, Silva M V G B D^{1,2}¹*Núcleo de Bioinformática de Juiz de Fora - Universidade Federal de Juiz de Fora/Embrapa Gado de Leite - MG - Brazil*²*Embrapa Gado de Leite - MG - Brazil*³*Laboratório de Bioinformática e Genômica Animal - Embrapa Gado de Leite - MG - Brazil*

For using single nucleotide polymorphisms (SNPs) markers in a livestock breeding program they should be in linkage disequilibrium (LD) with the targets regions. Haploview software was used to perform the calculation of LD (r^2) between SNPs located on the same chromosome. It performs calculations based on genotypic data. This study presents a first generation of LD map statistics for the genome of indicine (*Bos indicus*) cattle, the Dairy Gyr breed. DNA samples from 379 Gyr breed genotyped by Illumina BovineSNP50 Bead Chip (Illumina Inc., San Diego, CA). Only SNPs with MAF > 0.03 (minor allelic frequencies) were included in the LD analysis, totalizing 26,094 SNPs (46.4% of the total SNPs available). The pairwise r^2 statistics of SNPs up to 5 Mb apart across the genome was estimated. For the pairwise distances of < 25kb, it was observed a mean value of $r^2 = 0.18 \pm 0.26$ and it dropped to 0.16 ± 0.24 at 50-75 kb. The proportion of SNPs in useful LD ($r^2 \geq 0.25$) was 20.2% for the distance of 50 and 75 kb between SNPs. LD structure is best described using a haplotype block model, which is defined where 95% of combinations of SNPs within a region are in very high LD, demonstrating historical recombination. A total of 440 haplo-blocks spanning 71,949.092 kb (2.8%) of the genome and containing 1,577 SNPs (6%) were detected. The mean and median block lengths were estimated as $2,481 \pm 1,429.06$ kb and 1,962.572 kb respectively. A set of tag SNPs has been identified, which will be useful for further fine-mapping studies. The number of haplo-blocks in Gyr cattle is lower than Holstein cattle. There are two hypotheses that can explain these findings. First, taurine breeds have a higher level of LD. Second, modern breeding programs increased the extent of LD in Europe and caused differences of LD between genomic regions.

Financial support: FAPEMIG, EMBRAPA, CNPq, CAPES