

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

LINKAGE DISEQUILIBRIUM AND EFFECTIVE POPULATION SIZE IN CUTTING AND RACING LINES OF QUARTER HORSE BREED EQUINES

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On the Quarter Horse breed, different selections goal led to formation of lines. Such lines have different capabilities, as ability to run or working with cattle. These distinct groups do differ on morphology, physiology and inbreeding. The aim of this study was to characterize the linkage disequilibrium ($LD - r^2$) on cutting and racing lines in Quarter Horses, with large scale SNP genotyping. Additionally, there was performed the effective population size (N_e) in the two populations (lines). Were used 408 Quarter Horses equines (both sexes), registered on the stood book of the Brazilian Horse Breeders Quarter Horse Association (ABQM), from both lines (61 – cutting horses; 347 – racing horses). All animals were collected on the Jockey Club of Sorocaba (Sorocaba/SP), but also in a dozen rural properties across São Paulo state. Were genotyped, on 2011, 177 horses (61 – cutting horses; 116 – racing horses) in 54K density of SNPs. All remaining animals ($N = 231$) were genotyped on 2015, in a density of 65K SNPs. Low density animals were imputed to 65K (55,114 imputed SNPs), so all analyses were performed over 43,117 and 55,114 SNPs, across cutting and racing, respectively. The average genomic r^2 between makers pairs was 0.22 for cutting line and 0.27 for racing line. On cutting line, the r^2 was less then 0.20 between 100 and 150 Kb, while the same threshold (0.20) was found between 300 and 350 Kd (racing line). The estimates of N_e were ranged from 60 and 50 effective animals on the last generation, for cutting and racing lines respectively. Large extensions of LD and smaller N_e in racing line may be explained by the population structure, which is more closed as a consequence of major rigor registration process and great influence of Thoroughbred horses in their formation.

Keywords: DNA polymorphisms, horse, molecular markers, SNP array, selections goal

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