

Linkage Disequilibrium and Haplotype Blocks Study from Two High-Density Panels and a Combined Panel in Nelore Beef Cattle

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Abstract : Genotype imputation has been used to reduce genomic selections costs. In order to increase haplotype detection accuracy in methods that considers the linkage disequilibrium, another approach could be used, such as combined genotype data from different panels. Therefore, this study aimed to evaluate the linkage disequilibrium and haplotype blocks in two high-density panels before and after the imputation to a combined panel in Nelore beef cattle. A total of 814 animals were genotyped with the Illumina BovineHD BeadChip (IHD), wherein 93 animals (23 bulls and 70 progenies) were also genotyped with the Affymetrix Axion Genome-Wide BOS 1 Array Plate (AHD). After the quality control, 809 IHD animals (509,107 SNPs) and 93 AHD (427,875 SNPs) remained for analyses. The combined genotype panel (CP) was constructed by merging both panels after quality control, resulting in 880,336 SNPs. Imputation analysis was conducted using software FImpute v.2.2b. The reference (CP) and target (IHD) populations consisted of 23 bulls and 786 animals, respectively. The linkage disequilibrium and haplotype blocks studies were carried out for IHD, AHD, and imputed CP. Two linkage disequilibrium measures were considered; the correlation coefficient between alleles from two loci (r^2) and the $|D'|$. Both measures were calculated using the software PLINK. The haplotypes' blocks were estimated using the software Haploview. The r^2 measurement presented different decay when compared to $|D'|$, wherein AHD and IHD had almost the same decay. For r^2 , even with possible overestimation by the sample size for AHD (93 animals), the IHD presented higher values when compared to AHD for shorter distances, but with the increase of distance, both panels presented similar values. The r^2 measurement is influenced by the minor allele frequency of the pair of SNPs, which can cause the observed difference comparing the r^2 decay and $|D'|$ decay. As a sum of the combinations between Illumina and Affymetrix panels, the CP presented a decay equivalent to a mean of these combinations. The estimated haplotype blocks detected for IHD, AHD, and CP were 84,529, 63,967, and 140,336, respectively. The IHD were composed by haplotype blocks with mean of 137.70 ± 219.05 kb, the AHD with mean of 102.10 kb ± 155.47 , and the CP with mean of 107.10 kb ± 169.14 . The majority of the haplotype blocks of these three panels were composed by less than 10 SNPs, with only 3,882 (IHD), 193 (AHD) and 8,462 (CP) haplotype blocks composed by 10 SNPs or more. There was an increase in the number of chromosomes covered with long haplotypes when CP was used as well as an increase in haplotype coverage for short chromosomes (23-29), which can contribute for studies that explore haplotype blocks. In general, using CP could be an alternative to increase density and number of haplotype blocks, increasing the probability to obtain a marker close to a quantitative trait loci of interest.

Keywords : Bos taurus indicus, decay, genotype imputation, single nucleotide polymorphism

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