

**P0540****Accuracy of Genotype Imputation in a Nellore Cattle Population in Brazil**

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Room: Grand Exhibit Hall

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Genome-wide association studies (GWAS) generally require large numbers of individuals that are both phenotyped and densely genotyped for markers across the genome. However, genotyping many animals with a high-density marker panel can be expensive and economically unfeasible. An alternative in this context is to use a lower density marker panel on a larger number of animals, and impute the missing genotypes. Our objective was to evaluate the accuracy of imputation in a Nellore cattle population, using different panels of low-density (3K and 6K) and moderate-density (50K) markers. The data included 755 Nellore males belonging to 34 half-sib families born between 2007 and 2009 at experimental farms of Embrapa Cattle-Southeast and Embrapa Beef Cattle, and three additional farms in the State of Mato Grosso do Sul, Brazil. These paternal half-sib families represented Nellore bulls widely used in several breeding programs in Brazil. Genotyped animals were split into reference panel and study sample, comprised of 34 bulls and their 755 calves, respectively. All animals were genotyped using the BovineHD BeadChip (770K markers). The study sample had markers from the high-density marker panel masked in order to obtain low-density and moderate-density panels. Imputation from 3K, 6K and 50K up to 770K markers was performed using AlphaImpute. The mean proportions of correctly imputed genotypes were 0.74, 0.77 and 0.83 for the 3K, 6K and 50K panels, respectively. Imputation accuracies across chromosomes ranged between 0.60 and 0.81. The imputation resulted in reasonable accuracies, indicating its potential as an alternative strategy for GWAS with Nellore cattle.

Key words: imputation, beef cattle, SNP, Nellore, GWAS

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