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Correlation between the concentration of DNA and the call rate of genotyping of bovine embryos biopsied samples**Júlia Martins¹, Carolina Capobianco Romano Quintão¹, Luiz Sérgio de Almeida Camargo¹, Luiz Altamiro Garcia Nogueira², Clara Slade Oliveira¹**¹Embrapa Gado de Leite, Valença, RJ; ²Universidade Federal Fluminense, Niterói, RJ.

The use of embryos in genomic selection has been discussed through the application of high density marker genotyping panels. This possibility arose from the evolution of the techniques of genotyping and pre-amplification of small samples that made the use of the whole-genome amplification (WGA). The objective of the present study was to evaluate the DNA quality of the amplified biopsy sample and to associate it with the call rate obtained after genotyping. The call rate is a quality parameter of the genotyping, which indicates the fraction of SNPs found in relation to the total SNPs tested in each sample. For this, biopsies were removed from PIV blastocysts (d7) by the manual section of the trophoctoderm fragment (10-20% of the embryo, Bioniche blade). The samples were frozen in nitrogen, and subsequently the DNA was extracted and amplified using the Single Cell GenomiPhi DNA Amplification kit (Illustra, Buckinghamshire, United Kingdom). The quality of the amplified material was analyzed by the 2100 Bioanalyzer instrument (Agilent Technologies, Santa Clara, CA, USA). Twenty-two biopsy specimens were analyzed. The criteria of total DNA concentration and concentration of DNA fragments greater than 7,000 bp prior to genotyping were adopted. According to the Bioanalyzer, the total DNA concentration reached the minimum value of 3.58ng/ul and the maximum of 726.03ng/ul, average of 25.26 and standard deviation of 155.01. Regarding the concentration of DNA fragments higher than 7,000 bp, the minimum value was 0.98 ng/ul and the maximum was 53.62 ng/ul, the average was 4.98 and the Standard deviation was 12.19. The samples were sent for genotyping using the Bovine SNP50k assay. After the genotyping, the average call rate of each sample was compared with the DNA quantification parameters obtained in the Bioanalyzer. Regarding the call rate, a range of 0.41 to 0.96 (minimum and maximum, respectively) was obtained, an average of 0.79 and a standard deviation of 0.23. The correlation analysis between the total amount of DNA in the Bioanalyzer and the call rate was not significant ($R = -0.19$ and $P = -0.36$, Spearman). Similarly, there was no correlation in the parameter concentration of fragments greater than 7,000 bp and the call rate ($R = -0.04$ and $P = 0.85$, Pearson). Thus, we can conclude that high total concentration or fragments greater than 7,000 bp of DNA in samples of amplified embryonic biopsies does not suggest that the sample will present a high call rate after genotyping.

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