GENOMIC ASSOCIATION FOR BUFFALOES WITH WILMINK'S LACTATION CURVE VIA BAYESIAN INFERENCE

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A genomic association study was proposed for lactation curves in buffaloes based on a Bayesian hierarchical model. Under the proposed hierarchical approach, the individual lactation trajectories were modeled using Wilmink's nonlinear function: $a + tb + ce^{-t0.05}$, where a, b, and c are parameters, and t is time-dependent variable. This procedure consisted of a joint analysis, in order to the parameter estimates were considered to be affected by the polygenic additive, systematic and SNP markers effects. Therefore, obtaining simultaneously lactation curve parameters (co)variance components and breeding values. The data were composed of 286 first lactations of genotyped Murrah buffaloes (90k Axiom Buffalo Genotyping (Affimetrix®, Santa Clara, CA)) from Rio Grande do Norte State, Brazil. Heritability estimates varied from 0.27 to 0.62 for the parameters, initial milk yield (**a** = 0.27), ascent to peak (**b** = 0.62) and descent from peak (**c** = 0.50). Genetic correlations of moderate magnitudes positive and negative among the parameters were found (**a** and **b** = 0.50), (**a** and **c** = -0.54) and (**b** and **c** = -0.53). Heritability values for the estimates of the initial milk yield (**a**), ascending (**b**) and descending (**c**) parameters of the curve indicated that these traits may be a viable alternative for breeding programs that aim to change the shape of the lactation curves in breeding programs. Moreover, a useful selection objective could involve a reduction of the parameter **b** and **c** to obtain flat lactation curves, which avoids problems related to high lactation peaks and reduces high feeding costs providing a more efficient milk production.

Keywords: hierarchical model, nonlinear function, SNP markers