



# Water buffalo (*Bubalus bubalis*) milk-related features using single-step genomic linear unbiased prediction

W Carve\*

Department of Animal Sciences, Yale University, New Haven, Connecticut, United States

\*Corresponding author. E-mail: [williamcar@gmail.com](mailto:williamcar@gmail.com)

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## DESCRIPTION

Numerous livestock breeding programmes now routinely use genomic selection, but it is still in its early stages in the case of buffalo. Therefore, the purpose of this study was to estimate variance components using genomic information in Murrah buffalo, evaluate the effectiveness of genomic prediction for traits related to milk using single- and multitrait Random Regression Models (RRM), as well as the Single-Step Genomic Best Linear Unbiased Prediction (ssGBLUP) approach, and estimate longitudinal SNP effects and candidate genes potentially related to time-dependent variation in milk, fat, and protein yields, as well as somatic mutations. Due to the fact that buffalo milk and other dairy products are consumed by millions of people worldwide, the global population of buffalo (*Bubalus bubalis*) has increased to over 234 million animals. Compared to milk from other typical dairy animals, buffalo milk is higher in fat, protein, and Carbohydrates. As a result, buffalo milk is economically appealing for producing high quality dairy goods like ghee and mozzarella cheese. Dairy buffalo individual productivity is still much below desired levels, but it can be raised through genetic and genomic selection as well as improved management techniques.

The dairy buffalo industry's primary breeding objectives are to increase milk yield and quality while also improving lactation persistence and udder health. It is crucial to assess the lactation curves' shape in addition to the total milk efficiency for every milk production because bigger lactation peaks are frequently linked to a higher prevalence of metabolic disorders and call for distinct management strategies. In order to reflect the physiological changes that occur throughout the production phase, lactation curves can be physically characterised. Test-day records and random regression models are the two most popular techniques for genetically assessing milk-related characteristics. Several dairy species, including dairy goats, dairy cattle, dairy sheep, and dairy buffalo, have been subject to the RRM.

RRM are particularly intriguing in multiple-trait contexts because they make it possible to pinpoint the times of year that produce the genetic responses that are most closely associated.

Compared to other livestock species, the application and availability of genetic data for buffalo remains in its infancy. The single-step genomic best linear unbiased prediction method is a promising one because it allows for the simultaneous integration of phenotypic records, pedigree information, and genomic information to produce more precise predictions of genomic estimated breeding values. Numerous species, including dairy cattle, poultry, pigs, beef cattle, and small ruminants, have been tested to determine how well ssGBLUP performs. Studies examining the viability of Genomic Breeding Values (GEBV) genomic prediction in buffalo, particularly for longitudinal characteristics, are still lacking. Dairy buffalo and dairy cow breeding are comparable therefore it stands to reason that the benefits of genomic selection shown in dairy cattle will also be seen in dairy buffalo. However, due to the small number of genotyped animals worldwide, there aren't many studies in the literature examining the effectiveness of genomic predictions in dairy buffalo.

Additionally, genomic RRM offer the chance to identify the genomic areas and potential genes linked to attributes of interest at particular time periods that may have influenced particular lactation stages for milk qualities in buffalo. The statistical power for identifying time-dependent and, subsequently, candidate genes influencing characteristics at particular lactation stages can be increased by the use of statistical models that take into account all the variability from repeated data. Nevertheless, there aren't many studies on genetic RRM for dairy buffalo. The primary goals of this study were to evaluate genetic characteristics of traits evaluated throughout lactation in Murrah dairy buffalo using RRM and ssGBLUP, investigate the accuracy and bias of GEBV predicted using the ssGBLUP technique, estimate

the time-dependent impacts of SNPs linked with milk-related qualities, and identify candidate genes and metabolic pathways potentially associated with the analysed traits across parities in Murrah buffalo. The genetic correlation estimates ranged from low to high, which suggests that during breastfeeding, attributes are genetically connected in the same general direction but at varying degrees. Due to the increased number of records per animal and genetic association across traits, the estimations produced through multiple-trait analyses were more accurate than those obtained through single-trait studies. Additionally, we were able to comprehend

the link between several Test Daily (TD) for various qualities and lactations because the multiple-trait analysis. Our findings also show that tuning parameters have a minor impact on the precision of ssGBLUP's predictions of GEBV for the TD based on the RRM for Murrah buffalo, but have a larger impact on the bias of the EBV when compared to the pedigree. Nevertheless, ssGBLUP offers a good and simple genetic evaluation option and produces outcomes that are on par with those of the conventional models.