

Genomic Breeding Values – a tool to select buffaloes to achieve faster genetic progress in the herd

Why does selecting buffaloes based on their breeding values ensure a progressive increase in performance in a herd?

Buffaloes' milk production and their performance on other traits such as fat percentage, protein percentage, age at calving, fertility, mastitis resistance, etc. depend on both their genetics and environmental factors that affect these traits. Breeding values reflect the genetics animals carry, independent of environmental factors that affect their performance. Knowing the genetic potential of animals is important as animals pass on only their genetics to their progenies and not the influence of environmental factors. Therefore, focusing solely on an individual's yield can be misleading, as a high yield doesn't always mean superior genetics. The genetic worth of animals in terms of what they can transmit to their progenies is expressed in terms of breeding values (BV).

Breeding values are expressed as a difference from the mean of the population. For example, one bull's breeding value for 305-day lactation yield is + 1000, and that of another bull is +500. This means that the average yield of daughters of the first bull will be 500 kgs more than the average of the population, and the average yield of daughters of the second bull will be 250 kgs more than the population mean. In other words, the difference between the average of the daughters of these two bulls will be 250 kgs. Likewise, if one she buffalo's breeding value for 305-day lactation yield is +100 and that of another she buffalo is -150, then the difference between the average production of daughters of these two buffaloes will be 125 kgs. $(50 - (-75) = 125)$.

How are breeding values estimated?

As stated above, an animal's performance is influenced by its genetic makeup and environmental factors such as herd, village, year of calving, season of calving, age of animal, etc. For estimating the genetic worth of an animal, performance records for different traits are first corrected for such various environmental factors. After correcting for environmental factors, relationships among all animals are used to calculate their breeding values. Breeding values thus estimated for different traits are referred to as traditional breeding values (BV). Along with estimating breeding values, their reliabilities are also estimated. Reliability provides the confidence that one can place in the estimate of breeding value. With higher reliability, the confidence in its estimate increases. The reliability of breeding value increases with the use of a larger number of pedigree and progeny records of an individual.

When, along with performance records and pedigree data, genotype data of animals are used in estimating breeding values, the estimated breeding values are referred to as Genomic Breeding Values (GBV). With the given set of performance and pedigree data, the addition of genotype data increases the reliability of GBV. For example, the reliability of genomic breeding values of young male or female calves will be higher compared to their traditional breeding values when only pedigree data are used. In other words, one can predict the future performance of animals with higher confidence with genomic breeding values compared to traditional breeding values. With genomic breeding values, farmers can predict the future performance of their female calves and make an appropriate decision on keeping or selling

the calf very early avoiding the cost of rearing unwanted calves. Having GBV for a heifer also gives an advantage in price negotiations while selling it.

How can farmers get GBV for their buffaloes and bulls?

The National Dairy Development Board has established a genotyping laboratory at its headquarters in Anand. One can send a blood sample of a male or female calf or of an adult buffalo to this laboratory and get GBV for the sample sent. NDDB charges a nominal fee for the genotyping service offered. To know the current fee charged for the genotyping service, one can visit the NDDB website (www.nddb.coop) or send an email (anand@nddb.coop) or call (Tel No.: 02692 260148). For carrying out genotyping of blood samples of buffaloes, NDDB, in collaboration with ICAR-NBAGR, NIAB, and BAIF, has developed a chip called MAHISHCHIP. It has also built a reference population of recorded buffaloes through its progeny testing and pedigree selection projects implemented under the Rashtriya Gokul Mission a central sector scheme funded by the Government of India. Using MAHISHCHIP and the buffalo reference population, GBV is estimated for any blood sample of buffalo received by the laboratory.