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GENOMIC TOOLS AND GENETIC IMPROVEMENT OF CROSSBRED FRIESIAN CATTLE

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ABSTRACT

Any genetic improvement in dairy cattle requires information on productive and reproductive performance in the given population. Animals have been selected to improve their productivity in order to increase the profitability to the farmer. As a result, selection of animals is made for higher production and a shortened productive life. The reproductive performance of Friesian cows under intensive and semi-intensive management system in Bangladesh is poor. Animal selection has historically been based on production traits, and not much attention was given to AI recording. Many attempts were taken scatterly to increase productive and reproductive potential of Bangladeshi cattle for different periods with variable achievements. Therefore, in this review article we have addressed the new tools and information that could be used to determine the level of productive and reproductive performance and to evaluate genetic factors using admixture analysis of cows bred by AI sires which affect reproductive traits of crossbred Friesian dairy cows reared in selected areas in Bangladesh.

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INTRODUCTION

Genetic improvements have been achieved in several species by combining within breed selection with reproductive technologies (such as artificial insemination and embryo transfer) to more effectively disseminate elite genomes. Moreover, the poor reproductive parameters will be leading to a substantial economic loss because of prolonged calving intervals, increased insemination and veterinary costs, higher culling rates and excessively late age at first calving which can result in reduced lifetime milk yield and increased replacement costs (Andersen et al., 2003; Kadarmideen et al., 2003). Bangladesh is known for its huge livestock population and is estimated to have 24.24 million heads of cattle (DLS, 2018-19). Although cattle population size in Bangladesh is satisfactory but their productivity is very low compared to exotic dairy animals. Milk and milk products of some countries may still be contaminated by radioactive substances that have an unsafe impact on public health particularly for youngsters. The sustainability and profitability of Local × Friesian × Friesian (L×F×F) crossbred cows seemed to be more suitable for dairy farming under rural context in Bangladesh. This is why the number of crossbred cattle is expanding day to day with the extent of artificial insemination (AI) practices all around the country (Rahman et al., 2016). Livestock farmers usually rare cows of indigenous, cross-breed (particularly between indigenous and exotic) and exotic breed types (Marshall, 2014). Genetic merit has a substantial impact on biological efficiencies of dairy cows (Khaton et al*.,* 2015). For the improvement of dairy production genetic merit and/or animal husbandry practices should be improved but often reproduction is neglected (Rahman, et al*.,* 2016; Plaizier et al., 1998).

Genetic potential of animals enhances livestock development. To achieve this genetic potential, optimum nutrition, disease control and managemental practices should be scheduled (Ansell, 1985). Records of the productive and reproductive traits are crucial factors determining the profitability of dairy industry (Sarder et al*.,* 2007; Lobago et al., 2007). Productive and reproductive performance and poor genetic merit of cattle are considered as the major constraint against growth in dairy industry in Bangladesh. To overcome this constraint, AI has been practiced as a breeding tool to improve genetics of adopted indigenous cattle by using semen of exotic bulls from temperate countries since 1960s. But the success of AI remained far beyond stakeholders' expectations. Due to haphazard breeding evidenced by insemination of cows without keeping proper records, selection of future dam and sire has become difficult for improvement of dairy sector. About 6.0 million AIs were performed in cattle in Bangladesh in 2016-17 by the Department of Livestock Services (DLS), NGOs, cooperative unions and private organizations. It is generally found that about two services are required for one conception. On the other hand, average calving interval ranged from 365-536 days and average postpartum service period is ranged from 103-161 days among the indigenous and crossbred Friesian cattle (Kamal, 2010; Shamsuddin et al*.,* 2006).

Furthermore, there is inadequate identification of animals and record keeping on production traits in Bangladesh. Considering the above mentioned facts, it is important to identify the best crossbred Friesian dam and sire with respect to performance traits using genomic tools (Genomics uses recombinant DNA technology to analyze the structure and function of the complete set of DNA within an organism. This includes using electrophoresis and purification systems to isolate DNA templates, PCR and sequencing to determine the sequence and map of the DNA base code, microarrays-Low-density SNP assays (Mrode et al*.,* 2016*)*) and genotyping to determine the similarity and differences between sequences, mass spectrometry for analysis of oligonucleotides and next generation sequencers to analyze whole genomes. The beginning of most assays require a clean, good quality DNA template (Wikipedia/www.biocompare.com)) for improvement of dairy sector Bangladesh. The population of Friesian crossbreds is increasing in many countries in tropics including Bangladesh, as the Friesian crossbred cows produce high amount milk in their lactation and sustainability of this breed in Bangladesh is also satisfactory in such a temperate climate**.** It is essential to have knowledge of genetic correlation with performances of the population to predict gains from breeding programmes and to predict breeding value of the Friesian crossbreds (Ashutosh et al., 2013). Considering the above mentioned facts and circumstances, the objectives of this review are to evaluate the parameters for productive and reproductive performances and how genomic tools will affect genetic progress in Friesian crossbred cattle for the selection of best father and mother to be used in AI programmes resulting in sustainable dairy development in Bangladesh.

Productive and reproductive performances

The reproductive and productive traits of performance, i.e., age at maturity, age at first conception, age at first calving, days open, service per conception, Calving to first Service Interval (CFSI), calving interval, lactation length, dry period, lactation milk yield and parity are important to find out the actual efficiency of performance (Sattar et al.,2005, Abdel and Alemam, 2008, Tadesse et al., 2010, Alemayehu and Moges, 2014, Haftu Kebede, 2015, Mamun et al., 2015, Mengistu and Wondimagegn, 2018).

Reproductive Traits

Age at maturity

Sexual maturity is the age when heifer for the first time shows signs of oestrus which subsequently and continuously is displayed in regular cycles. Time of sexual maturity depends not only on age but also is result of the effect of numerous genetic (process of sexual maturation, display of sexual maturity) and environment factors (nutrition, climate, rearing, housing, care, etc.). After reaching sexual maturity, animals require an adequate period for further body development in which necessary breeding maturity of the animal will occur. Beginning of the breeding maturity is variable and depends mainly on the body weight of animals (Smiljakovic et al., 2007, Novakovic et al., 2011). In case of heifers of high yielding breeds, sexual maturity is reached at the age of 9-11 months and average body mass of 250-280 kg (Sejrsen and Purp, 1997). Most of the recommendations refer to first insemination of heifers at the age of 14 to 15 months and body mass of ≥ 350 kg, in order to achieve age at calving of 24 months (Antov et al., 1998).

Age at first conception

Age of dairy cattle at first conception is one of the major reproduction properties. Age of calves at first calving depends mainly on age at first conception. Age at first conception is determined by the date of birth and date of first conception (Novakovic et al., 2011). Age at first conception includes the period from the birth of the heifer to first insemination at the age when the animal has reached breeding maturity enabling it normal gravidity. Age when animal reaches sexual and breeding maturity has for long time been in the center of attention of expert and scientific public in regard to the possibility for shortening of the generation interval. Age at first calving is an important factor influencing the yield and composition of milk (Pirlo et al., 2000). Age at first conception is one of the most important fertility properties in dairy cattle. It has a direct impact on age at first calving since duration of gravidity has physiologically constant value. There is a positive relation between the body mass at first calving and milk yield in the first lactation. This relation is an important basis for defining levels of body development and age of heifers at first conception/calving. Age at first conception is determined within defined time limits. Bottom limit is date of birth, and top limit date of conception (Novakovic et al., 2011).

Age at first calving (AFC)

It is defined as the beginning of a cow’s productive life. Generation interval is closely related to age at first calving which influences response to selection. Friesians of temperate regions attain their puberty earlier than in the tropics (8-9 months as compared to about 20 months in the tropics) and their age at first calving is between 17-20 months compared to about 30 months in the tropics (Zaied, 1995, Ajili et al (2007), Rahman and Aleman, 2008,) reported that the mean age at first calving is higher than 29.3 months in Tunisian Friesian-Holstein cows; 823 days (27.2 months) in Holstein Friesian cows in Pakistan Niazi and Aleem (2003). On the other hand, Sattar et al*.*, (2005) reported that the age at first calving of Holstein Friesian cows in Pakistan was 988±9.81 days (32.7 months). The prolongation of age at first calving in HF cows could be attributed to factors such as poor nutrition and management practices including poor heat detection at the time of mating the heifers. In the same way year, season and breed of the sire significantly affected age at first calving (Abuzaid, 1999). It is expected that heifers would exhibit fast growth and attain higher weights at comparatively younger ages (Tadesse et al., 2010).

Days open (DO)

Days open is the part of the calving interval, longer days open associated with decreased profitability in the dairy farm. The mean days open was highest at short rainy season, while there was no significant difference between long rainy season and dry season. On the other hand, the mean days open significantly decreased from 1st to 5th parity, increased at 6th parity while decreased again after parity seven (Mengistu and Wondimagegn, 2018). Cows in the first parity dad significantly longest DO, while shortest at 7th parity (Peters, 2007). The longer days open of cows calved in parity one and decreasing trend of days open with advancement in age (Asimwe and Kifaro, 2007).

Service per conception (SPC)

Reproductive efficiency is measured by service per conception (SPC). It is one of the tools for measuring SPC. It expresses the fertility level of dairy herds. It is simple and easy to calculate and understand. Although it is a good measure of reproductive status, but still, it usually does not indicate the reasons behind it in heifers and cows that fail to conceive. However, the breeding system largely influences the SPC. It is higher uncontrolled natural breeding and low where hand-mating or artificial insemination is used. Herd, season, placenta expulsion time, lactation length and milk yield affect the

SPC significantly (Esslemont et al., 1985, Rahman and Alemam, 2008).) defined the term SPC as the total number of services given to a group of cows over a defined period divided by number of services which results in a diagnosed pregnancy not less than 42 days after service to culled cows included.

Calving to first Service Interval (CFSI)

Calving to the next service is defined as calving to the first Service Interval. Optimum level service period (SP) consistency indicates regularity and stability of the reproductive status of the animal, especially the oestrus cycle (Rahman and Alemam, 2008). The average CFSI is similar to the value of 111 days and lower than 170 days respectively in HF breed in Turkey and Tanzania (Kifaro,2007, Cilek, 2009) and 142 days in Ethiopia (Shiferaw et al., 2003). The longer than the ideal interval of 60-90 days could be attributed to different factors (Berry et al., 2003). The delaying in interval to first service is due to greater negative energy balance in modern dairy cows was suggested by many researchers. Negative energy balance also delays the resumption of ovarian activity (Butler and Smith, 1989). A variety of environmental factors delay ovulation and estrus after calving (Rhodes et al., 2003). Limited energy intake, lower body reserves, increased partitioning of energy to milk production are the main factors for delaying calving to first service interval. On the same way parity also influences CFSI (Tedesse et al., 2010, Elgaj, 2003). The greater nutritional stress being imposed on younger cows due to requirements for growth as well as lactation is reflected by the significantly longer CFSI obtained in parity.

Calving Interval (CI)

Calving interval is that period of time between calvings that is measured in months. It is additionally outline that the quantity of time (days or months) between the birth of a calf and therefore the birth of a subsequent calf, each from identical cow. It is in all probably the most effective index of a herd's fruitful reproductive efficiency. Recommencement of ovarian activity within the postnatal does not essentially result in conception and ways of stimulating oestrus should be thought in relevance to their effect on conception (Holness et al., 1980) and indirectly on calving intervals. The Calving interval (CI) was considerably palgued by genotype, year, season, poor nutrition, poor housing, failure to detect heat by the farmer, age and alternative factors like sex of the calf, placenta expulsion time and womb pathology (Choudhuri et al., 1984, Britt et al., 1986, Msanga et al., 1999, Hammoud et al., 2010, Haftu Kebede, 2015). In temperate regions, calving interval typically ranges between twelve to 13 months (Spike and Mcedows 1973; Barr, 1975). The mean calving intervall of foreign and locally born Friesian cows in Sudan was 16.0 and 15.9 months, respectively. There is general agreement that the calving interval isn't but 14 months (Abuzaid, (1999)). The birth intervals of Holstein Friesian are twenty six days lesser than native cows (Mamun et al., 2015). Poor management of the present farm as well as poor breeding management has vital result on calving interval particularly within the tropics (Mengistu DW and Wondimagegn KA, 2018).

Productive Traits

Lactation length

Lactation length is defined as the period between two consecutive calvings during which cows are capable of producing milk or lactating. Many researchers in tropical countries have reported the mean of lactation length (Abdel Rahman and Alemam, 2008). Hatfu Kebede, 2015 reported that the lactation length in his study was shorter than the optimum value of 305 days required to maintain the optimum calving interval of 12-13 months. The shorter lactation length may be due to factors such as improper feeding regimes, inadequate dry period and prevalence of diseases.

Dry period

It is the period of off milking. Smith (1959) stated that dry period is necessary in order to accomplish one or more of the following**:**

a) To refresh the body with nutrients those were depleted during lactation.
b) To repair and regenerate the alveolar system.
c) To gain new stimulation for lactation as the result of parturition following gestation.

Thus an optimum dry period is essential for maximum production of milk in subsequent lactation. The standard length of dry period is a period of 60 days (Rahman and Alemam, 2008). Dry period of indigenous cows was higher than HF cows which in turn increased lactation length in HF cows (Nahar, 1987, Mamun et al., 2015).

Lactation milk yield (LMY)

The production of milk during a lactation amount is popularly known as lactation yield. Duration of calving, parity, interaction between parity, season of birth, parity and herd considerably (p <0.001) influenced lactation milk yield (LMY). On the contrary, the effect of season on birth and herd of cow weren't noteworthy (Tadesse, 2010). Improved management, adaptation of Holstein Friesian breed to the surroundings through time or both will increase the trend in lactation milk yield over the period of calving. Mean lactation milk yield flourished from parity one to parity 3rd. The increased trend in lactation milk yield (LMY) up to third parity and decreased trend thereafter is similar to the results reported in Holstein Friesian cross in Sudan (Ahmed et al*.,* 2007). The age variation (i.e. difference of lactation number) is one among the necessary non-genetic sources of variation in milk yield (Martinez et al., 1988).

Dairy farming and reproduction

The reproductive performance of the dairy cattle influences the efficiency of dairy farming (Peters and Ball, 2004). Reproduction in livestock is decisive for production of the necessary replacement stock, for reducing unproductive periods, for initiation of milking, for increasing period of milk production and income (Das et al., 1986). Poor reproductive efficiency of a farm losses the farm in various ways include fewer calves being born due to longer calving intervals, increased veterinary expenditures due to more problematic cows, increased number of services to achieve conception as a result of poor heat detection, and increased number of replacement heifers needed for non-voluntary reproductive culls. In this study, it reveals that the overall reproductive and productive performance of Friesian dairy cows kept at Kitulo Livestock Multiplication Unit (Kitulo LMU) is low to moderate. To achieve the better results in reproductive and productive efficiency of Bos taurus cows in tropical environment, proper management of the animals through various phases of life from calving to maturity is necessary to ensure their early age of service and calving, better conceivability, decrease calving interval and increase milk yield. Therefore, for better reproductive and productive performance of the herd, management practices at the farm need to be improved (Kashoma et al*.,* 2015).

Broadly, Indigenous and crossbreds types of dairy cattle are available in Bangladesh. The mean production per day of indigenous and crossbred cows is 1.5 L and 2.5 L respectively (Saadullah, 2001). On the other hand, Islam et al., (2014) found that the average milk production of Holstein Friesian crossbred cows ranges from 2.5-8.5 L and which was 2.5-5.8 L in Indigenous cows. Biologically, potentiality of milk production enhances by the age at puberty, early first calving, number of parity and shorter calving interval and milk yield. The genotype of breeds and parities differs the intensity of production traits (Djemali and Freeman, 1987; Rahman et al., 1987). In Bangladesh, the productive and reproductive performance in dairy cows at both subsistence and semi-intensive or intensive farming system had been subjected to several studies (Shamsuddin et al., 1987, Alam and Ghosh, 1988; Ghosh et al., 1988) where delayed puberty, long post-partum intervals with or without uterine disorders had been predicted. Although the crossbred cows are capable to produce higher quantity of milk but they are susceptible to diseases and their veterinary cost is also higher. For this genetic merits can be developed through selection, crossbreeding and upgrading for better production and profit. In Bangladesh, cattle population size is satisfactory but their productivity is not satisfactory when compared with exotic dairy animals like Friesian cows.

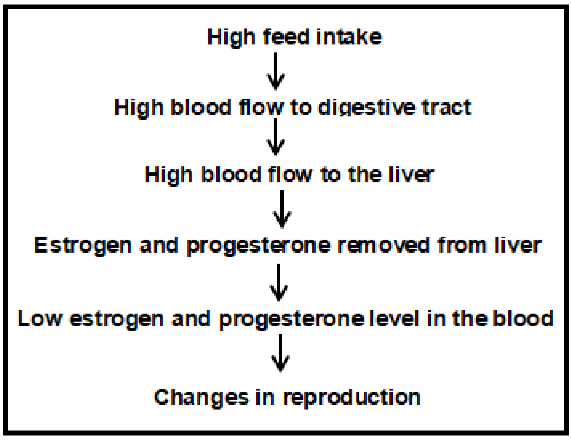
Moreover, management practices in dairy farms vary from areas to areas, which have profound effects on production and reproduction (Mamun et al*.,* 2015). Accurate quantitative knowledge of factors affecting productive performance of animals is the pre-requisite for effective management of dairy farming (Bagnato and Oltenacu, 1994). But the pure exotic breed (e.g. Holstein Friesian) is not so suitable in context of Bangladesh in relavent of environmental conditions because pure breed may require low temperature, better feeding and management. The disease prevention capacity in pure breed is also lower than that of native cattle. On the other hand, the native cattle are well adapted as well as high disease resistance than exotic pure breed. The crossbred cattle performed better than that of exotic and native cattle in terms of adaptability and production (Rahman et al., 2017). However, fertility rate of crossbred dairy cattle suffered from genetic performance, poor reproduction, and lower level of management, poor inception rate, long post-partum anestrus and calving interval (Kiwuwa et al*.,* 1983, Madalena et al*.,* 1990; Mengistu and Wondimagegn, 2018). Genetic, environmental/management factors or both could be related with lower reproductive performance. Consequently, it is essential to evaluate the reproductive performance of dairy cattle and factors affecting their performance periodically (Tadesse et al*.,* 2010). Many environmental factors affect the performance of dairy animals. The animal's true genetic ability and create a bias in the selection of animals may suppress by these environmental factors (Lateef et al., 2008, Tadesse et al*.,* 2010).

Environmental impact on production

The most effective route to reduce the harmful environmental impact of livestock is to extend productivity: the carbon footprint of one kilo dairy farm trade was reduced by forty one percent over the identical period despite the 250% increase in total milk production (Capper et al., 2013). However, exclusive stress on production has junction rectifiers to harmful correlative responses in of milk created within the U. S. in 2007 was thirty seventh of that in 1944, and also the carbon footprint of the whole U.S.A. different traits, notably those related with fitness. For instance, though selection of milk production in dairy cattle was very palmy, there was a considerable unsought decline in fertility over the identical period (Pryce et al., 2004). Thus, selection schemes now progressively attempt to balance animal health, fertility, production and environmental impact (Georges et al., 2018). The productive and reproductive performances under the existing management system need to be monitored regularly for the success of dairy production namely periodical evaluation. For future planning and managemental strategies to develop the sector, the periodical evaluation of factors affecting productivity of animals is very important (Kebede, 2015).

Effects of nutrition on reproduction

The aim of a dairy farm is to get one calf from a cow once year (Shamsuddin et al*.,* 2006a), Nutrition plays a vital role to initiate puberty and reproductive potency in all animals (Shamsuddin et al*.,* 2006a and Bindari et al*.,* 2013).The topmost priority is to be given on energy and protein to optimize reproduction in dairy cows. Minerals and vitamins should even be balanced within the diet. Overfeeding of nutrients might also impair the reproduction (Yugal Raj Bindari et al*.,* 2013). Nutrition and reproduction have the interaction for the implications of reproductive performance (Smith et al*.,* 2010). In puberty, heifers manifest estrus signs and ovulate for the first time. Inadequate nutrition in mature cows delays puberty in heifers and as well as prolong the calving interval. Crossbred heifers, especially Friesian are often bred at 15-18 months with good nutritional management. The age at puberty varies from 24-36 months in South Asian zebu cattle (Mukasa, 1989). Calves of 8-12 months of life are usually fed poor quality milling byproducts when the reproductive organs are developing. Replacement heifer management programs are rare in several countries like Bangladesh. Heifers are often fed surplus dairy cows feed. Parasitic infestation or poor nutrition causes anemia that delays sexual maturity in heifers (Kamal, 2010). Under nutrition leads to loss of body weight and body condition, delays the onset of puberty, will increases the post-partum interval as well as post-partum conception, interferes with normal ovarian cyclicity by decreasing gonadotropin secretion and will increase infertility (Capuco et al., 1990; Boland et al., 2001).



- Decreased duration of estrus (Standing heat)
- Increased double ovulation rate (Increased twining)
- Decreased conception rate
- Increased Pregnancy loss

Figure 1. Schematic representation of the potential physiological pathway that may produce the changes observed in high-producing lactating dairy cows [Thomas et al*.,* 1997]

Growth of heifers and first birth age are delayed by these factors (Shamsuddin and Aryal, 2009). Poor body condition score (BCS) usually leads to anestrus for a few years, that prolongs the interval from birth to first service and after to subsequent birth. Lower BCS cows had longer intervals from birth to first ovulation and fewer detected estrus than cows with a better BCS (Siddiqui, 2008; Shamsuddin et al*.,* 2001). Higher energy diet on the breeding day of cows will have a few chances of conception and high levels of glucose within the blood at the time of early embryo development may be detrimental to embryos (Siddiqui et al*.,* 2002).

Genetic evaluation

Rankings of animals which will generate progress on a breeding objective are supported by the genetic analysis system. For genetic analysis, animal models are used for many of the traits. During this model, solely the phenotype of a specific cow is taken into account as a function of her own additive genetic merit. On the contrary, in the sire model, solely the genetic contribution of the cow's sir is taken into account. Animal and sire models are special cases of mixed linear models (Henderson, 1984) whereas genetic effects are thought-about as random. Best linear unbiased prediction (BLUP) is the favourite estimation procedure (Henderson, 1963, 1984). This suggests that the environmental effects are calculable only from the data, whereas the genetic effects are calculable (or predicted) combining information from data with prior knowledge of pedigree relationship between animals. The BLUP model most ordinarily used which might be created and solved comparatively simply (Ducrocq V and Wiggans G, 2015). Current limitations in genetic improvement of cattle by AI in Asian countries like Bangladesh are poor animal identification, lack of pedigree and performance data aggregation for sire and bull mother. In smallholder cows, the post-AI conception rate was reported to be fifty one percent (Siddiqui et al*.,* 2013). In conjunction with the skill of the AI technicians, the conception rate varied widely (Siddiqui et al., 2013). Poor heat detection was additionally detected as a vital limiting factor for conception.

In another study using progesterone RIA, Shamsuddin et al,. (2006) determined that oestrus was accurately detected in at most thirty percent of cases. Another thirty percent of cows were detected as in oestrus after they weren't (false positive) and forty percent cows remained unobserved after they were in oestrus (false negative). Banu et al*.,* (2012) detected poor estrus in buffaloes, wherever the cyclicity was evaluated by determining progesterone in milk using ELISA. Moreover, the AI technicians usually do not follow the breeding policy for using semen for AI that must be strictly regulated by the Directorate of Livestock Services (DLS). Further, identification of animals and record keeping on production traits in Bangladesh is inadequate. Considering the above mentioned facts, it is important to identify the best crossbred Friesian dam and sire with respect to performance traits using genomic tools for improvement of dairy sector Bangladesh.

A comprehensive storage and management of genomic and performance data would assist Artificial Insemination(AI) centers to establish a data flow system and increase interactions with farmers for choice of best sire in future. Now a days science offers many opportunities whose conjunct applications would bring positive changes in conventional animal breeding, particularly in developing countries. For examples, (1) application of AI conjoined with Radioimmunoassay (RIA or ELISA) of hormones to confirm successful mating and therefore to extend manifolds the dissemination of desired genetics, (2) nuclear and nuclear-derived molecular techniques for genetic characterization of animals and identification of marker(s) that drives favourable traits from parents to offspring and (3) database applications and software system to manage, analyze and create report from massive datasets involving genomics, phenotypes and their attainable interactions. Application of recent technologies permits the characterization of the genome with markers at a decreasing price. In developed countries the utilization of genomic tools is quickly increasing and leading to economical genetic improvement programmes. It is time to coalesce tested tools and strategies for the validation of technologies through adaptive research to the requirement of developing countries like Bangladesh for a speedy, vertical growth in animal productivity. Low price genomic tools for parentage testing are accessible and may be reconciled for use in developing countries like Bangladesh, and are needed for genetic improvement programmes. Moreover, it is attainable to develop low price genomic tools for measuring breed composition of crossbred animals, verify purity of purebred animals and match information with applicable genetics to pick out superior stocks for breeding. Correct parentage and breed composition will be combined with performance data to elevate the selection process**:**

Within-breed selection

A process by which sires and dams that above average breeding values are selected as parents to produce the next generation of animals.

Genetic gains

It means differences in the average breeding values of the population before and after selection. Genetic gain is a function of the amount of genetic variance, the accuracy of selection, the intensity of selection and the generation interval.

Quantitative trait loci (QTL)

Regions in the genome that encompass genetic variants with an effect on a quantitative trait of interest.

Genome- wide association studies (GWAS)

Scan of the entire genome to identify genetic variants for which variation in genotype is associated with variation for one more phenotypes of interest.

Genomic selection (GS)

An ensemble of methods to estimate the breeding values of individual animals on the basis of genome-wide-single nucleotide polymorphism genotype information.

Single nucleotide polymorphism arrays (SNP arrays)

Microarrays used to determine the genotype of individuals for hundreds to millions of SNPs at once.

Progeny testing (PT)

An approach by which the breeding value of an animal is estimated from phenotypic measures made on its progeny.

Genetic architecture (GA)

The description of the number, location and effects of the genetic variants that affect a phenotype of interest.

Genotype imputation (GI)

The in silico prediction of the genotype of an individual for non genotyped variants on the basis of known genotypes at neighbouring variants and a reference population with genotype information for all variants imputation exploits the nonrandom association of alleles at neighbouring variants, referred to as linkage disequilibrium.

Epigenome

The combination of chemical modifications of the DNA sequence (such as cytosine methylation) or nucleosomes (such as methylation of Lys 27 of histone H3) that mark functionally distinct segments of the genome (such as active enhancers) and are inherited mitotically and/or meiotically (Georges et al., 2019).

Haplotypes

It means combination alleles at multiple variant positions transmitted by a gamete. The term is often used to describe variants that are located close to each other in the genome. Estimation of the proportional contributions of ancestral populations in admixed (crossbred) individuals is important to clarify the population structure, historical background and pattern of admixture along the genome of admixed individuals (Khayatzadeh, 2017). Recent advances in high-throughput genotype sequencing technology have provided unprecedented opportunities to learn about the evolutionary history of admixed populations at both global and local levels.

- Global genetic ancestry establishes ancestral proportions averaged across the genome of an individual.
- Local genetic ancestry is the identification of the ancestral origin of distinct chromosomal segments within an individual genome.

There is a growing concern in association studies about confounding effects, due to considerable discrepancy between the allele frequencies in the cases and the controls. An accurate inference of locus-specific ancestry in admixed populations has improved the genetic disease (Parkinson, Diabetic disease, Alzheimer and other diseases) association studies in human genetics (Sankararaman et al*.,* 2008; Rosenberg et al*.,* 2010; Seldin et al*.,* 2011; Hu et al*.,* 2013).

Genetic admixture

Genetic admixture is that the presence of DNA in a personal species, as a results of interbreeding between populations or species that are reproductively isolated and genetically differentiated. Admixture leads to the introduction of recent genetic lineages into a population. For autosomal DNA test, admixture analysis is one of the components (Wikipedia). To estimate the ancestry and therefore the genetic structure of the cattle population, one ought to use admixture software (a software tool for optimum likelihood estimation of individual ancestries from multilocus SNP genotype datasets) eg. version 1.3.0 (Alexander et al*.,* 2015). Genomic ancestry of a specific breed is going to be fixed in genomic regions of native breeds or crossbreds once it's advantageous for survival or production in harsh environments.

To look at this situation, twenty five Friesians and 162 local cattle made by crossbreeding of milch breeds in Kenya were sampled and genotyped utilizing 50K SNPs. Utilizing principal component analysis (PCA), the admixed native cows were found to contain many foreign breeds, namely Guernsey, Norwegian Red, and Holstein. Local ancestry mapping was performed based on the similarity of haplotypes to understand the influence of parental breeds on genomic regions. As a consequence, it seems that no genomic region has been below the entire influence of a specific parental breed. Nevertheless, in most genomic regions (>80) the ancestry of Holstein-Friesian was substantial. The analysis of native ancestry could be a useful approach to realize the whole genomic structure and should reveal regions of the genome needed for specialized adaptation once combined with methods for looking for the recent changes of haplotype frequency in an admixed population (Kim et al*.,* 2014). To estimate the ancestry and also the genetic structure of the Iraqi cows population, admixture version 1.3.0 and Genesis software (version 0.2.6b) (http://www.bioinf.wits.ac.za/ software/genesis/) ware used. The analysis was conducted at genome-wide autosomal level, first with Iraqi breeds and four reference breeds (Holstein-Friesian, N'Dama Guinea, Sheko, and Nellore) and then including the entire set of breeds (Alshawi et al., 2019).

Principal component analysis (PCA) and discriminant analysis of principal components (DAPC) were used to examine the admixture in the Kenyan cattle population. DAPC is a method which optimizes the segregation of individuals into default groups utilizing a discriminant function of principal component (Jombart et al., 2010). Membership probability was obtained to present the overall genetic background of an individual on the basis of DAPC. Western breeds, namely Holstein, Guernsey, and Norwegian Red cattle as well as two Kenyan cattle populations were included for this analysis. To measure differentiation of populations single marker F_{ST} (Wright, 1951) across the genome was estimated. In the same way, to analyze population admixture and F_{ST} (Jombart and Ahmed, 2011) the software package adegenet in R was used. The genome of crossbred (admixed) individuals could be a mosaic of ancestral haplotypes formed by recombination occurring at each generation (Sankararaman et al*.,* 2008; Price et al*.,* 2009a). In a very recently crossbred population, ancestral populations are mixing for a comparatively tiny number of generations, leading to a brand new population with totally different proportions of the initial populations.

Moreover, admixed populations give the special chance for learning recent selection signatures happened after admixture. The genetic admixture of Friesian was the highest relating predominant individual breed characteristics followed by Jersey and Sahiwal with local cows (mainly Pabna cattle). One amongst the vital reasons of this admixture is random and unplanned breeding and such scenario originated from non/zero-record keeping system Shahjahan et al*.,* (2017). Knowing on top of mentioned facts, application of genomic tools to assist for the selection of animals with increased productivity traits has been in practice in several developed countries. Low density single nucleotide polymorphism (SNP) marker will be used for analyses of diversity, genetic structure of sires and breedable females, admixture analysis of breedable males and females based on genotypes originated from low density SNPs. Analyses of genome-wide SNP knowledge from cattle breeds give the chance to analyze gene flow and admixture processes that have contributed to the evolution of domestic cattle. Use of high-density genome-wide SNP markers can investigate genetic origins, admixture patterns and demographic histories of cattle populations (Upadhyay et al*.,* 2016). Moreover, association between the amount of admixture and performance data of crossbred Friesian cows are determined. Generally, females, either as herd replacements or bull dams are measured with lower accuracy info than their bull counterparts. For instance, bulls are also a part of a post-weaning growth test with feed potency and ultrasound measures wherever females are also restricted to weight traits solely.

Females are similarly deprived in terms of progeny numbers where a 3-year previous female can have one progeny record, wherever a 3-year previous bull will have twenty or a lot of. Although some females will have several records, this typically coincides with older cows and longer generation intervals, which might be counter-productive. Genomics can greatly increase the accuracy of selection in cows and can contribute to improved progress through this selection pathway. Moreover, with a genomic test at low value, thousands of choice candidates are often genotyped followed by greatly increasing the choice intensity.

Genetic parameters estimation

Genetic parameters quantify the rate of genetic change that it is possible to achieve. Genetic parameters are required for estimation of genetic merit. Of these parameters, the heritability is one of them. Other genetic parameters include the effects of dominance, individual genes, breed, inbreeding and heterosis (crossbreeding) (Ducrocq et al*.,* 2015). Estimation of genetic parameters such as heritability and genetic correlation is the pre-requisite for the assessment of genetic worth of animals (Das et al., 2013). Estimation of heritability and genetic correlation of economic traits will help in planning further genetic improvement programme of any breed. Accordingly, heritability of production and reproduction traits such as lactation milk yield, lactation length, peak milk yield, dry period, age at first service, age at first calving, post-partum onset of heat, services per conception and calving interval (Aaron et al*.,* 1987, Deb et al., 2008, Verma et al*.,* 2018). Moreover, genetic parameters of Holstein crossbred cows were evaluated in commercial dairy farms in Bangladesh (Das et al., 2013). However, Das et al., (2013) used a traditional method for genetic evaluation of heritability in crossbred cows and genome based method will be used in the present research work.

Genomic tools have been used to determine the animal's breed composition, verify parentage and coat colors in community managed dairy cattle and sheep breeding (Mrode et al., 2016; Muniz et al., 2016). It is now well accepted that the best way to implement genomic information into genetic improvement programmes is simply to allow the genomic information to contribute to the animal genetic evaluation. Research is continuing to develop the best methods to incorporate genomic information into traditional genetic evaluation programmes (Kachman et al., 2008). As genomics will allow the identification of elite females that is not possible previously, it will bring new opportunities for improvements in reproductive technologies. By identifying elite cows by application of genomic tools will help rapid generation of elite cows by embryo transfer and in-vitro embryo production programme. With increased accuracy of selection in females by using genomic tools, the genetic merit of the resulting embryos can be increased. Embryo transfer can also be combined with sexed semen technology that is now available to change the way bulls are developed.

Genomic selection (GS)

Genomic selection is a very recent innovation. For genomic selection, genomic tools are now available and are routinely used for most livestock species. One of them is reasonably priced low-density SNP technology in the selection of females (Boichard et al., 2012, Clay, 2012 and Ponsart et al., 2014). Strong evolutions have started, including reduction in genotyping costs, phenotyping strategies for new traits, approaches for the creation or the replacement of reference populations, increase in robustness and persistency of genomic predictions using causal mutations identified from genome sequences, or genomic prediction of genetic environment interactions (Dekkers, 2012 and Boichard et al., 2016). Genomic selection for yield alone increases feed intake but also results in a larger negative energy balance (EB) and more body tissue mobilization during lactation. This follows from the size of the genetic correlation between yield and feed intake (i.e., the expected correlated response in feed intake from selection on yield alone cannot completely cover the extra requirements for the increased yield) and is also illustrated by the negative genetic correlation of yield with 1) measures of EB, 2) BW (Veerkamp, 1998). Even though a negative EB during early lactation is normal for mammals (Robinson, 1986), magnitude and duration of the negative EB are generally related to reduced health and fertility (Treacher et al., 1986; Harrison et al., 1990; Waltner et al., 1993; DeRouen et al., 1994). For example, bulls with a very high EBV (Estimated Breeding Value) for dairy form (low BCS) had daughters with more reproductive problems (Rogers et al., 1999) and a more positive EB, a higher BW during lactation or BW gain all had a favorable genetic correlation with days until first luteal activity (−0.40 to −0.80) (Veerkamp et al., 2000).

SNP chips for genomic selection

The current, most practical approach to detect SNPs is the SNP chip. SNP chip is a small piece of plastic or glass with dozens to hundreds of thousands of small dots on it that bind DNA. Each dot corresponds to a specific SNP and a small bit of adjacent DNA, and for a given animal, the SNP can be present in zero, one, or two copies, corresponding to having been inherited from neither, one, or both parents (https://www.illumina.com/products-Illumina. Inc. San Diego,CA).
The genomic era (Genomic selection) for dairy cattle began in 2007 with the event of assays which will be accustomed to genotype large numbers of SNPs at low price (Matukumalli et al., 2011). Since then it's become potential to get genomic evaluations of adequate accuracy as shortly as a DNA sample is processed (Meuwissen et al., 2001). The last decade has seen exponential growth within the development of genomic tests for economically necessary traits in beef cattle improvement. What started as small SNP markers for beef quality traits has developed into a variety of panels of SNPs for a variety of traits within the half decade. A lot of this enlarged development output will be attributed to rapidly changing technology and also the sequencing of the bovine genome (Elsik et al., 2009) leading to dramatic reductions in genotyping expenditure. In 2005 genotyping took a major breakthrough with the first large SNP panel for cows, the ParAllele 10K chip

(Barendse et al., 2007; Sargolzaei et al., 2008). After the very fruitful Bovine SNP50 BeadChip® (The most common SNP *chip* used for cattle is from the company Illumina (Illumina Inc., San Diego, CA). This *chip* has around 50,000 SNPs and thus is called a 50K SNP chip, but only about 40,000 of these are reasonably useful for a variety of reasons; for example, some SNPs provide redundant or ambiguous information), the illumina company discharged two additional genotyping chips in 2010**:** a low density chip (Bovine3K®) with 2900 SNPs and a high-density chip (BovineHD®) with 777,962 SNPs. The Bovine3K reduced the value of genotyping, thereby increasing application to females (Ducrocq et al., 2015). Following this the Illumina Bovine SNP50 bead chip was discharged, greatly bringing down the value per genotype and substituting the 10K. The 50K SNP chip provides useful markers for most alleles of genes affecting phenotypes of cattle. Especially important is that essentially all phenotypes, from docility to protein content of milk can be evaluated (Lee et al*.,* 2008).

Figure 2. BovineSNP50 v3 BeadChip

The BovineSNP50 v3 BeadChip microarray kit contains 53,218 highly informative SNPs uniformly distributed across the entire genome of major cattle breed types, empowering applications such as genome-wide enabled selection, identification of quantitative trait loci, evaluation of genetic merit of individuals, and comparative genetic studies (https://www.illumina.com/products).The results of the bovine SNP50 array are quite promising in dairy cattle and it is clear that genomic selection is beyond question operating with outstanding results among breed (Cole et al., 2009; Hayes et al*.,* 2009; Schenkel et al., 2009). Recently, Park et al., (2015) identified the dramatic improvement of British aurochs alleles in north European bovine breeds utilizing genome-wide single nucleotide polymorphisms (SNPs).

BovineHD DNA Analysis Kit

The BovineHD BeadChip is a comprehensive genome-wide bovine genotyping array, providing the power to interrogate genetic variation across any breed of beef and dairy cattle. Illumina developed this product in collaboration with major bovine agricultural thought leaders, including USDA-ARS, UNCEIA-INRA, Pfizer Animal Genetics, and the University of Missouri.

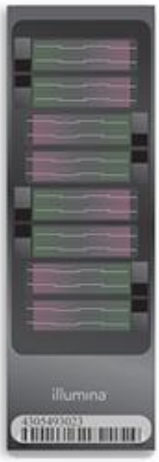


Figure 3. BovineHD DNA Analysis Kit

BovineLD BeadChip

The BovineLD BeadChip microarray kit enables accurate genotyping to understand the impact of genetics on milk production, reproduction, health, and more. Delivering scalable, expert-selected content at an economical price, it allows you to extend genomic selection to the entire herd.

Figure 4. BovineLD v2.0 BeadChip

The BovineLD v2.0 BeadChip, together with the Infinium BovineSNP50, Infinium BovineHD, and iSelect Custom BeadChips, creates a broad genotyping portfolio that breeders can rely on to characterize genetic variation and accurately estimate genomic breeding value. While the BovineHD and BovineSNP50 BeadChips provide power to interrogate genetic variation in high-value animals and support genome-wide studies, the BovineLD v2.0 BeadChip enables the cost-effective genotyping of lower-value animals (https://www.illumina.com/products).

With the execution of genomic selection in dairy cattle there has in addition been a noteworthy change in breeding program design and structure. Firstly, highly proven sires were affected very little through the inclusion of genomics into breeding worth prediction as their proofs were already highly accurate. However, genomics had a phenomenal impact on the ranking of cows. Not like sires that have very correct proofs supported many daughters evaluated across a variety of numerous herds, cow evaluations are measured on a restricted range of lactation records which can be instigated by environmental factors like superior treatment of targeted cow families.

Once choosing dams of sires, genomics has elucidated a lot of clearly the true genetic difference between selection candidates. Admixture levels were determined by Freeman et al., (2004) employing a type of methods- Ancestry informative or population associated alleles (PAAs) were selected using population from India, the Near East and Europe. Statistical methods like multivariate analysis, the admix program and model-based Bayesian admixture analysis approaches were also used. Therefore, genomic selection has been very successful in cattle as a result of it provides a lot of genetic gain at a similar or lower price. However other necessary and sometimes consequences are the large opportunities it offers for traits tough to select, for traits not yet designated, however necessary for sustainable production, and for a much better management of the genetic variability in the future. Veerkamp et al., 2001, reported that there were genetic correlations among body condition score (BCS), milk yield, and fertility in first-parity cows. A better genetic merit for milk yield has unfavorable effects on fertility; however the genetic correlation suggests that BCS (at some stages of lactation) would possibly facilitate to alleviate the unfavorable result of selection for higher yield on fertility. Heritability and genetic correlation was estimated by Becker (1985) using paternal half sib method.

Genetic Correlation (rg)

Genetic Correlation is the correlation between an animal’s genetic value for one trait and the same animal’s genetic value for the other trait (Searle, 1961). This is a measure of genetic factors shared between two traits. Once two traits are extremely genetically correlated, the genes that contribute to the traits are typically co-inherited (Lynch & Walsh, 1998). Whereas traditionally used in animal breeding (Lynch & Walsh, 1998), in a very broader three research context, genetic correlations contribute to understanding the progress and pathways of traits, population level gene flow and therefore the co-occurrences of traits (Via & Hawthorne, 2005).

For this reason, genetic correlations play a crucial role in evolutionary biology, and estimates of genetic correlations are also employed in theoretical modeling of human populations. Calculation of genetic correlations (rg) depends on the additive genetic variance and covariance between traits.

Genetic Correlation (rg)

$$rg(xy) = \frac{Cov\ s\ XY}{\sqrt{\sigma s2\ (X)\ \sigma s2\ (Y)}}$$

where,

X and Y are two different traits
Covs XY is the sire component of covariance between traits X and Y.
σs^2(X) and σs^2(Y) are the sire component of variance for trait X and Y respectively (Verma et al., 2018).

Phenotypic Correlation (rp)

Phenotypic Correlation is the correlation between records of two traits on the same animal and is usually estimated by the product- moment correlation statistic (Searle, 1961).

Phenotypic correlation is calculable as-

$$rp(xy) = \frac{Covs(XY) + Cove(XY)}{\sqrt{[\sigma s2(X)\ +\ \sigma e2\,(X)][\sigma s2\,(Y)\ +\ \sigma e2\,(Y)]}}$$

Where,

Covs (XY) is that the sire element of variance between traits X and Y
σe^2(X) and σe^2(Y) are unit the error element of variance for traits X and Y, severally (Verma et al., 2018).

Therefore, the estimation of genetic correlation among BCS, fertility, milk yield, day's open and other traits of performance of crossbred Friesian cows is of essential for dairy development. Traditionally genetic correlations area unit calculated from pedigree information victimization applied mathematics strategies to partition phenotypic (co)variance into genetic variance and genetic co-variance (Henderson, 1986). Newer strategies create use of genome-wide single nucleotide polymorphism (SNP) information and therefore the terribly little coefficients of relationship between terribly massive numbers of unrelated individuals as to calculate these parameters (Lee et al., 2012). This approach assumes that the genetic correlation is the same across the gene frequency spectrum. In addition, as genotyping becomes cheaper, genome-wide SNP information is turning into additional promptly and widely accessible than pedigree information (Bulik-Sullivan et al., 2015a; Ni et al., 2017).

CONCLUSION

Proper management of the animals from birth to maturity is important to confirm their early age of service and borth, higher possibleness, lower birth interval and high milk yield. Management practices at the farm need to improve for higher reproductive and productive performance of the herd. Therefore, the estimation of genetic correlation among BCS, fertility, milk yield, day's open and different traits of performance of crossbred Friesian cows is of essential for dairying. In this discussion it's discovered that unplanned breeding between or among breeds that affect the performance of cows' population. To beat the prevailing problem, research ought to be done on breed composition to clarify existing genetic makeup and specific breed results on the variation of production. Based on performance, specific breed ought to be used for insemination or controlled natural/sexual activity by superior breeding bulls of that breed to scale back genetic admixture and increase performance.

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CONFLICTS OF INTEREST

The authors have not declared any conflict of interests.

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