

We are IntechOpen, the world's leading publisher of Open Access books Built by scientists, for scientists

6,900

Open access books available

186,000

International authors and editors

200M

Downloads

Our authors are among the

154

Countries delivered to

TOP 1%

most cited scientists

12.2%

Contributors from top 500 universities



WEB OF SCIENCE™

Selection of our books indexed in the Book Citation Index
in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?
Contact book.department@intechopen.com

Numbers displayed above are based on latest data collected.
For more information visit www.intechopen.com



Genetic and Breeding Aspects of Lactation

Vijay Kumar

Additional information is available at the end of the chapter

<http://dx.doi.org/10.5772/66179>

Abstract

Animal breeding is the most important tool to improve milk productivity in dairy animals. Identification of better animals as parent for the next generation is the approach to generate high-producing animals. Genetic disease is the main problem in livestock sector. Complex vertebral malformation (CVM), bovine leukocyte adhesion deficiency (BLAD) syndrome, bovine factor xi deficiency, deficiency of uridine monophosphate synthase (DUMPS), and bovine citrullinemia are some of the main genetic disorders, which should be studied in Holstein and its cross. Recent developments in biotechnology have made it feasible to reveal a large number of genetic polymorphisms at the DNA level. As a result, researchers have been encouraged to use them as markers in order to evaluate genetic basis for the observed phenotypic variability. The selection of genetically superior sires is of utmost importance for any successful breed improvement program as semen of sires is disseminated in various herds under progeny testing program. The investigations on mode of genetic improvement around the world indicated that proper genetic evaluation and selection of bulls bring about more than 75% of the actual genetic improvement.

Keywords: molecular markers, genetic disorder, part-lactation milk yield, test-day milk yield

1. Introduction

Lactation is one of the most important economic characters of dairy animals. Genetic aspect of lactation includes those concepts, which are important for milk production in an individual animal. On the other hand, breeding aspect is important for improvement in milk production in a population of dairy animals. Milk production is largely affected by a combination of factors, namely, genetic makeup, a favorable nutritional environment and improved managerial practices. Consequently, genetic makeup of dairy animals plays a great role in the variation of milk yield and composition. Lactation is, therefore, a factor of genotype-environment interactions. Animals are subjected to constant improvement for this trait, which is based on

phenotypic observations of cattle and evaluation of the progeny and kins. These processes are both time-consuming and expensive. With the observed advances in molecular genetics, one may presume, however, that this may dramatically accelerate genetic improvement of dairy cattle, especially due to genotyping of young animals. Identification of various genetic factors involved in regulating the lactation and involution in farm animal would enable to reveal the molecular basis of milk production. This would serve as a platform to direct future research to enhance the productivity of cattle. The identification and characterization of these factors will pave the way to design appropriate approach to ameliorate the problem of lactation. The availability of fully sequenced genomes and further development of DNA sequencing techniques allowed gaining of complex genomic data from a number of animals and promises to overcome traditional problems with understanding of fragmented genomic data provided by other genomic techniques. Association studies using whole genome sequence from animals with different phenotypic performances will permit identification of genomic regions with significant effect on main economic traits. Genetic improvement includes selection of excellent animals from a population to produce higher yields in future generations. Since long back, livestock breeders have used genetic evaluations to identify best animals. Selective use of these livestock improved phenotypic measures for milk production and milk components.

2. Molecular markers and milk production

Recent developments in biotechnology have made it feasible to reveal a large number of genetic polymorphisms at the DNA level. As a result, researchers have been encouraged to use them as markers in order to evaluate genetic basis for the observed phenotypic variability. The distinctive genetic properties as well as methodological advantages of molecular markers make them helpful and amenable, to a greater extent, for genetic research than other genetic markers. Nowadays, molecular markers are being identified on a vast variety of genes of economic importance and are widely accepted. Association between DNA polymorphism and milk production traits has been studied for a number of genes, including prolactin; leptin; diacylglycerol acyltransferase (DGAT1); bovine leukocyte antigen (BoLA)-DRB3, growth hormone receptor gene, ATP-binding cassette, and protease inhibitor gene; proliferator-activated receptor gamma and coactivator (CoA) 1 α gene; growth hormone (GH) gene; signal transducer and activator of transcription (STAT)1; thyroglobulin gene; β -lactoglobulin gene; STAT5A; and stearoyl-CoA desaturase. Out of the different marker studies, molecular markers for prolactin, leptin, and DGAT1 show their association with milk traits.

2.1. Pit-1 transcription factor

Pit-1 transcription factor regulates the expression of growth hormone and prolactin in the anterior pituitary gland [1]. The bovine Pit-1 gene is located in centromeric region of chromosome 1 in bovine [2]. Bovine Pit-1 is a 291 amino acid protein. This gene is a candidate for lactation yield because of its role in regulating expression of bovine growth hormone (bGH) and the prolactin genes. Association studies have shown that Pit-1 is associated with milk production in domestic animals. Pit-1 was found to be related to birth weight weaning and average

daily gain. Quantitative trait loci (QTL) detection revealed that the region surrounding POU domain, class 1, transcription factor 1 (POU1F1) on cattle, 1q21–q22, had an effect on animal production. POU1F1 gene is also a possible candidate for growth traits. In cattle, Pit-1 was found to be associated with milk production traits. *Hinf1* polymorphism has been reported in exon 6 of the bovine Pit-1 gene by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) technique. This single nucleotide polymorphism (SNP) was found in the coding region of the bovine Pit-1 gene. Moreover, four intronic polymorphisms were also reported: two located in intron 3, one in intron 4, and the last in intron 5.

2.2. Growth hormone receptor (GHR)

The growth hormone plays a critical endocrine role controlling nutrient metabolism in dairy cattle. In the liver, growth hormone receptor (GHR) is dynamically regulated by lactation and energy balance. GH receptor is determined by a single gene with a length of 110 kbp, consisting of ten exons, located on chromosome 20 of cattle [3]. The gene of this receptor (*GHR*) is characterized by the existence of numerous exons whose transcripts undergo alternative splicing. Growth hormone activity depends on the receptor, and consequently its gene may be a potential candidate gene.

2.3. Insulin-like growth factor 1 (IGF-1)

Insulin-like growth factor 1 (IGF-1) is produced in the liver and body tissues. Important role for IGF-1 is to promote cell growth and division. The bovine *IGF-1* gene is located on the long arm of chromosome 5. It contains seven exons, separated by long introns. As stated, IGF-1 regulates cell growth, development, and division; it can stimulate growth in both normal and cancerous cells. Even small increases in serum levels of IGF-1 are associated with increased risk for several common cancers.

2.4. Diacylglycerol acyltransferase 1 (DGAT1)

DGAT1 is the main enzyme for the synthesis of triacylglycerols, the major fraction of milk fat compounds. Bovine *DGAT1* locus is found on chromosome 14. Milk is the main source of saturated fatty acids, which are a valuable source of nutrients. Recently, a dinucleotide substitution located in the exon 8 of the gene coding for acyl-CoA, diacylglycerol acyltransferase 1 (DGAT1), that modifies the amino acid order from a lysine to an alanine (Lys232Ala) in the mature protein was shown to have an immense effect on milk fat content in some cattle breeds. The frequency of polymorphism in *DGAT1* gene has been found to be very high in dairy cattle. The attention in the bovine *DGAT1* gene has increased during the previous few years. *DGAT1* is also important for the physiological processes involving triacylglycerol metabolism such as intestinal fat absorption, adipose tissue formation, and lactation.

2.5. Leptin (LEP)

Leptin is a 16-kDa protein secreted from white adipocytes, which is involved in regulation of feed intake, milk yield, energy balance, fertility, and immune functions in animals. Leptin is considered as a powerful biomolecule for enhancing productivity in farm ani-

mals. Its role in lactogenesis, colostrum secretion, galactopoiesis, and immunity to mastitis has made it an important candidate gene for genetic studies. Since the bovine leptin gene has been recognized on chromosome 4, several SNPs have been in the past identified in introns and exons of leptin among different breeds of cattle. Several investigations have revealed that polymorphisms were associated with lean and fat cattle [4, 5] and with the fat contents and feed intakes [6–8]. Important profitable factors for livestock production may be affected by leptin including feed conversion competence and intramuscular fat, which is considered to improve meat quality [9].

Nutrition is a main determinant of productive potential in cattle and other mammals. Therefore, responses of the productive system to changes in nutrition and metabolic status influence reproductive and economic efficiency of food-producing species in a variety of contexts. As the hormone leptin is involved in regulation of nutritional status and reproductive function, this hormone is an interesting protein to investigate during the periparturient period in dairy cattle. Leptin may help regulate ovarian development and steroidogenesis and serve as either a primary signal initiating puberty or as a permissive regulator of sexual maturation. Leptin is supposed to be necessary by the mammary growth, development, and function, when mammary fat cell leptin expression requires prolactin which then cooperates with leptin to influence mammary activity. The ruminant mammary epithelial cells also synthesize leptin during pregnancy and during established lactation. In dairy cattle, the increase in milk yield has been accompanied by a more negative energy balance during early lactation and a decrease in fertility. The polymorphism in LEP gene was associated with milk performance and increased perinatal mortality in dairy calf birth and weaning weights in beef and dairy and reproductive performance in dairy cattle. Exogenous administration of leptin in ob/ob mice leads to a significant improvement in reproductive and endocrine status as well as reduced food intake and weight loss.

2.6. Prolactin

The bovine prolactin gene (*bPRL*) is regarded as a good candidate gene for marker-assisted selection (MAS) for milk production parameters. Bovine prolactin spans approximately 9.4 kb and consists of five exons and four introns, which encode a mature protein with 199 amino acids first mapped it on the bovine chromosome 23. Prolactin gene disruption experiments proved its important roles in mammary gland development (mammary gland development), lactogenesis, maintenance of milk secretion (galactopoiesis), and expression of milk protein genes [10]. It is also chiefly accountable for synthesis of lactose, lipids, and all other major components of milk [11]. Consequently, the bovine prolactin gene seems to be an outstanding candidate for linkage analysis with quantitative trait loci (QTL) affecting milk production traits. Prolactin is a polypeptide hormone and plays crucial roles in mammary gland development, initiation, and maintenance of lactation, which is synthesized in lactotroph cells of the anterior pituitary gland of vertebrate. Prolactin is a protein hormone primarily, but not solely produced by lactotroph cells of the anterior pituitary. Its role in maintenance of milk secretion is well demonstrated. As a result, the gene encoding prolactin is assumed to be one of the key links in constituting the hereditary component of milk productivity. Therefore, the bovine prolactin gene seems to be an excellent candidate for quantitative trait loci (QTL) affecting milk production traits.

3. Genetic disorders and animal selection

Apart from selection of bulls on the basis of milk production and reproductive abilities, some of the genetic disorders should also be taken care of. Chromosomal abnormalities in domestic animals are one of the very important causes of reproductive impairment. The impairment in reproduction leads to loss of germplasm, and there is every possibility that these chromosomal aberrations are transmitted from one generation to another. Several centric fusions, i.e., *Robertsonian* translocation, have been reported in cattle. The animals carrying this translocation are phenotypically normal but have reproductive problems. In this translocation, two nonhomologous chromosomes break at the extreme end at the short arm. These small segments are lost, and the large segments fuse at their centromeric region and produce a new large metacentric or submetacentric chromosome. The exchange of segment between two nonhomologous chromosomes is a type of structural variation called a reciprocal translocation. In this, the genetic information is neither lost nor gained rather there is a rearrangement of genetic material. The least complex way for this event to occur is for nonhomologous chromosome arms to come close to each other so that an exchange is facilitated. For this type of translocation in which the ends of chromosomes are involved, only two breaks are required. Heterozygous homologues for a reciprocal translocation undergo unorthodox synopsis during meiosis, resulting in a cross-like configuration. By whatever mechanism produced, the translocated region may nevertheless act normally with respect to homologous pairing. Thus, a translocation homozygote forms the same number of homologous pairs as the normal homozygote as long as centromeres are not lost. In several countries, there is restriction on the export and import of semen from bulls without normal karyotype. In the United Kingdom, all the bulls used for artificial insemination are subjected to routine screening for cytogenetic abnormality.

Selection is based on genetic markers and also universally checking up of the breeding bulls for heritable diseases. Many heritable mutations and diseases have been traced to autosomal chromosomes of different cattle breeds; most of these mutations are lethal or bring about deficiencies in the defense mechanism if they occur in the homozygous recessive manner. Moreover, due to coverage of wild-type allele on mutant allele in heterozygotes, carrier animals may not show any phenotypic abnormality but are most likely to transmit the mutant alleles to the next generation. The same problem may assume catastrophic significance if the carrier is a bull intended to be used in artificial breeding programs.

3.1. Complex vertebral malformation

The complex vertebral malformation (CVM) is a recessively inherited congenital disorder leading to frequent abortion of fetuses or vertebral anomalies and prenatal death [12–14]. It is characterized by growth retardation and bilateral flexure of the carpal and metacarpophalangeal joints along with rotation of the digits. In stillborn, aborted, and preterm calves, CVM has been characterized by shortened cervical and thoracic regions of the vertebral column and symmetric arthrogryposis. Multiple hemivertebrae, scoliosis, and synostosis and fused and misshaped vertebral column have also been described. The syndrome was first

discovered in the Danish Holstein population in 1999, but, shortly thereafter, its occurrence was reported in the Netherlands, in the United States, in the United Kingdom, and in Japan.

Studies of Danish Holstein showed that the extent of fetal mortality was approximately 77% prior to gestation day 260. This is reflected in a significantly reduced ratio of CVM-affected calves in breeding studies. Through increased fetal mortality, the status of the fetus has a significant effect on calving interval and involuntary culling of cows. The symptoms of the defect have not been observed in carriers of CVM. No productive and reproductive differences between carrier and noncarrier animals have been reported. The only difference which is very important was increase in the rate of intrauterine mortality. The risk of return to service was higher in carrier animals.

When studying the postpartum recommencement of ovulation—the carry-over of ovarian cycles after the birth of one calf—the researchers recognized that there was no major difference in the rate at which resumption occurs in carriers as compared to Holstein cows that were not carriers for CVM. However, CVM carrier cows were recognized to have drastically lower conception rates than control cows, with the gap between calves observed at 463 days in carriers than 399 days for control cows, telling the possibility of heightened death of embryos in CVM carrier cows.

3.2. Bovine leukocyte adhesion deficiency syndrome

Bovine leukocyte adhesion deficiency (BLAD) syndrome is an autosomal recessive hereditary disease affecting young Holstein calves characterized by recurrent bacterial infections, progressive periodontitis, ulcers of oral mucosa, and impaired inflammatory responses [15, 16]. These clinical findings are associated with impaired neutrophil functions such as markedly decreased adherence, chemotaxis, and phagocytosis. In 1990, a lack of β_2 integrin molecules expressed on the leukocytes from affected animals was found in a calf with granulocytopeny syndrome, and this disease was termed bovine leukocyte adhesion deficiency, which was considered to be analogous to human leukocyte adhesion deficiency (LAD). BLAD causes immune deficiency in the early days of life. The affected animal is prone to all infectious agents which can cause death. BLAD was first documented in Holstein-Friesian cattle, and no study has reported the incidence of this disorder in other breeds. The affected cattle with BLAD was linked to common ancestral sires that had been documented to be carriers.

3.3. Deficiency of uridine monophosphate synthase

Deficiency of uridine monophosphate synthase (DUMPS) is a genetic disorder which interferes with pyrimidine biosynthesis. Uridine monophosphate synthase (UMPS) has a key role on the pyrimidine nucleotide synthesis, which is essential for normal growth and development for several ruminant and nonruminant species [17]. Inactivation of this enzyme is caused by an autosomal recessive heredity mutation, which takes place in the gene of uridine monophosphate synthase. The mutation (cytosine to thymine) leads to the loss of the restriction site of *Ava*I site at nucleotide position 405 of the gene. This disorder is named as DUMPS in the Holstein cattle and characterized by lowered blood activity of enzyme UMPS [17]. DUMPS

leads to embryonic death in the early stage of pregnancy. So some serious reproductive problems take place in dairy herds.

3.4. Factor XI deficiency syndrome

Factor XI (FXI) deficiency is an autosomal recessive disorder, with partial deficiency of FXI coagulant activity in heterozygotes and considerable deficiency in homozygotes [18]. One of the protein factors concerned in blood coagulation is a serine protease—factor XI. It is produced in the liver as a zymogen, and after alteration to a proteolytic enzyme. FXI deficiency has been recognized in humans and cattle. FXI gene is located on chromosome number 4 in human and on chromosome number 27 in cattle. FXI gene encodes coagulation factor XI of the blood coagulation cascade, and it is one of more than a dozen proteins involved in blood clotting.

In cattle, FXI-deficient animals may be asymptomatic or display several symptoms, like prolonged bleeding, anemia, greater prevalence of repeat breeding, or even lower resistance to pneumonia, mastitis, and metritis. *FXI* deficiency has been recognized in a number of species of mammals, including humans, dogs, and cattle. *FXI* deficiency possibly will result in delayed bleeding and anemia. Persistent bleeding from the umbilical cord is occasionally seen in affected calves. Delayed emission of blood following dehorning or castration may also be observed. Affected cows repeatedly have pink-colored colostrum.

3.5. Bovine citrullinemia

Bovine citrullinemia is a genetic disorder, which has been reported in Holstein cattle [19]. It has been established that bovine citrullinemia is a consequence of a deficiency of argininosuccinate synthetase (ASS), one of the enzymes of the urea cycle. A shortage of the urea cycle enzyme consequences in a lethal neurological disease in newly born calves. The urea cycle entails a series of biochemical steps in which waste product of protein metabolism is removed from the blood in the form of urea. The deficiency of ASS occurs when a calf inherits a copy of the mutant gene encoding for ASS from each parent. The gene is located on chromosome number 11 (BTA11). The mutation is caused by a transition of cytosine to thymine at codon 86 within exon 5 in the gene coding for ASS leading to impaired enzyme, which cannot participate in urea cycle. Calves affected with the disorder appear normal immediately after birth. However, by the second day of birth, they become depressed. By the third day, they are seen wandering or standing with their head pressed against a wall. Death usually takes place within 12 hours of start of these clinical signs. The clinical signs of citrullinemia are believed to be as a consequence of accumulation of ammonia in the brain of the affected calves.

4. Factors affecting milk production

The success of dairy industry is much dependent on productivity and efficient reproduction performance of animals. Genetic progress may be done by selection. The nongenetic

factors such as management, housing, feed, season, etc. also control production. The genetic improvement of growth of dairy animals is of great importance in the large ruminant industry.

4.1. Dry period

Dry period is an important economic trait which has the direct effect on lifetime milk production. There is a lot of variability observed in the dry period. It is the period from the date of drying to the next calving. Animals should be given proper rest, when they are in pregnancy, before the next calving to compensate for growth of fetus.

4.2. Growth

The genetic improvement of growth is of great importance in the large ruminant industry. The growth rate of a heifer calf until it matures to a cow is also a significant trait since it characterizes the adaptability and economic appropriateness of the animal. It is anticipated that animals growing faster may also begin physiological performance of reproduction and milk production earlier.

4.3. Age at first calving

Age at calving is an important trait because lower age at first calving (AFC) leads to shorter generation interval and hence increases genetic gain. AFC has a considerable influence on the total expenditure of raising dairy replacements. Older calving heifers are being more expensive to raise than younger calving heifers. Moreover, reducing AFC can also increase the profitability by increasing lifetime milk production and milk production per year of herd life. The most important drawback of reducing AFC is that it is commonly associated with a reduction in the first lactation milk yield. Regardless of this decline in the first lactation milk yield, production per year of herd life is characteristically increased by reduced AFC. In addition, while the first lactation may be affected by AFC, future lactations are absolutely not. Furthermore, stayability and health of cows are not affected by reduced AFC as long as the first calf heifers freshen at a sufficient weight.

4.4. Service period

Service period is the duration between date of calving and date of successful conception. The finest service period facilitates the animal to recover from the stress of calving and also for reproductive organs back to its usual shape. Usually for cattle the best service period is 60–90 days.

4.5. Calving interval

The interval between two successive calvings is referred to as calving interval (CI) which consists of two components—service period and gestation period. Among the traits of dairy animals, calving interval is the most important trait as it determines the number of lactations possible in the lifetime of an animal, thereby influencing its production of an

animal. It is generally held that shorter calving intervals favor a large yield for the lifetime of the cow. That frequent calving should give maximum lifetime yield seems in harmony with the known facts of the physiology of reproduction and lactation. The natural need of milk develops with birth of the young. The need increases with growth of the young so long as milk is the only food. As other food is taken, the need for milk decreases and finally disappears. In milch animals, where we have adequate information as to the amount of milk produced day by day, it is found that the rate of milk secretion parallels roughly the rising and declining needs of the young. That is, the rate of milk secretion is most rapid in the cow shortly after calving and slows up quite markedly and continuously thereafter. It would seem that frequent calving by giving more high points in the lifetime lactation curve should result in a greater total yield than less frequent calving. Another way of putting the matter is to relate the length of the calving interval to the average yield of milk per day over the calving interval. This relation may be derived in relative terms from the known characteristics of the lactation curve. The indication is that the highest lifetime yield should be obtained from calving intervals of less than a year rather than from calving intervals of more than a year.

4.6. Days to first service or waiting period

Waiting period (WP) or days to first service (DFS) is one of the important reproduction traits. WP or DFS is the initial phase of lactation during which no inseminations occur. The lower the WP or DFS shows, the higher the breeding efficiency in dairy animals. Reducing WP is tempting because of associated reductions in calving interval. Getting cows pregnant is perhaps one of the major challenges faced by the dairy farmers. Cows that do not become pregnant at a rational interval after calving will remain in the herd, reduced overall milk yield, and if they do become pregnant, they likely to develop post-parturient diseases in the subsequent lactation. Conversely, on the other hand, cows that become pregnant too early after calving would be dried off too early in lactation when they are still producing a reasonable amount of milk.

The voluntary waiting period (VWP) is a time during the early lactation in which cows are purposely not inseminated even though they show estrus signs, to allow for optimum uterine involution. The VWP is fairly inconsistent across dairy herds. Decision over the optimal VWP should be made according to individual situations and after careful analysis of probable gains and losses. The suggestion of extending the VWP is based on the reality that during the early lactation cows are recovering from a condition of negative energy balance. Therefore, extending the VWP may allow cows to recover from a metabolic state that is deleterious to reproductive efficiency and display estrus a few times prior to the first insemination, which has been correlated with improved fertility.

4.7. Daughter pregnancy rate

A genetic evaluation tool for reproduction exists in the form of daughter pregnancy rate (DPR). DPR is calculated from days open and is directly related to the proportion of females eligible to become pregnant in a 21-day period that actually become pregnant (i.e., the 21-day pregnancy rate).

DPR forecasts genetic improvement (or deterioration) in pregnancy rate for future daughters of a bull compared to a bull that is expected to produce no change. Better pregnancy rates decrease semen usage and can be an essential part of efforts to reduce service period. Workers also comment that genetics do not control fertility adequately to justify selection. Heritability of DPR is low—only about 4%—so producers should not expect dramatic improvement in fertility from selection. However, genetic control of fertility is real. DPR needs to be included with all the other traits of economic significance in dairy cattle breeding.

5. New breeding approaches to improve dairy animals

The selection of genetically superior sires is of utmost importance for any successful breed improvement program as semen of sires is disseminated in various herds under progeny testing program. The investigations on mode of genetic improvement around the world indicated that proper genetic evaluation and selection of bulls bring about more than 75% of the actual genetic improvement. The accuracy of estimating the breeding value of an animal is the major factor that affects the genetic progress from selection. The success of a breeding program depends on how early and how accurately young bulls can be evaluated at a minimum possible cost.

Animal breeding is the most important tool by which one can think about improving livestock sector in comparatively faster rate. Animal breeding is all about selecting best animals from population which are used as parent for the next generation. Milk yield is the single most important economic trait determining economic returns from the dairy animals. In animal breeding selection of animals is almost considered as selection of bulls since the progeny-producing ability of bull is many folds more than a cow and progeny testing is the most acceptable technique for the selection of bulls.

5.1. Part-lactation milk yield for genetic evaluation

The first important advancement was the use of part-lactation milk yield for genetic evaluation of cattle and buffalo bulls. The genetic and phenotypic correlation between 305-day and part-lactation monthly and cumulative monthly milk yields in cattle reported that the genetic correlation of monthly yields with 300-day yield was high up to the fifth month and thereafter the estimates declined. The phenotypic correlations among these traits were high and statistically highly significant. There is significant correlation between 100-day and 300-day milk yields, and selection on the basis of 100-day production was sufficiently accurate to select the animal for 300-day production in Gir cattle. In Sahiwal cattle selection on the basis of individual third month milk yield and cumulative 90-day milk yield was at least 89 and 79% as effective as on the basis of first lactation 305-day milk yield. Definitely, these findings will be very helpful in reducing duration for evaluating bulls as only 4–5 months milk records are sufficient enough to evaluate bulls. Hence, the application of part-lactation records of daughters will be helpful in ranking the sires at younger age resulting in reduced generation interval

and increased intensity of selection credited to the availability of more numbers of records on daughters even having part-lactation records.

5.2. Test-day milk yield for genetic evaluation

The second important advancement is the use of test-day milk yield for genetic evaluation of cattle and buffalo bulls. The use of test-day record is easier and advance than part-lactation record as in this case only one or two particular day (test day) record is required instead of taking all-day records up to a certain part of lactation. Genetic correlations between observed milk yield and predicted milk yield under various test-day sampling schemes (fortnightly, monthly, and bimonthly) were very high being greater than 0.95 for Karan Swiss cattle and to be nearly united in Karan Fries cattle. There are higher phenotypic correlations among test-day milk yields ranging from 0.55 to 0.93 in Murrah buffaloes. The genetic correlations among test-day milk yields and 305-day milk yield were close to unity and phenotypic correlations among test-day milk yields and 305-day milk yield were quite high and positive (0.60–0.99) in Murrah buffaloes. So this technique was also explored at research level and found that test-day records could also be used for fast progress in livestock improvement.

At the present time, test-day model is thus used instead of 305-day model for the genetic evaluation of dairy cattle. Test-day model is the statistical method that thinks about all genetic and environmental effects straight on a test-day basis. The test-day models have been recommended as the method of choice for the study of milk yield traits in order to maximize the use of all accessible information. This method becomes significant with smaller herd size and without well-established milk recording systems.

6. Conclusion and future perspectives

A variety of molecular markers for improving milk production and their association with disease and productive and reproductive traits have proved to be beneficial to the livestock breeders. They can also be used economically in breeding and management decisions. The application of diverse molecular markers in determining the vulnerability to economically significant diseases proves to be helpful to minimize loss of animals and their productivity. Advancement of technologies to evaluate polymorphisms provides an idea about the development in the field of genetics to improve cattle health and production. The genetic disease causes heavy losses because of poor animal performance; structural unsoundness reduces the production and reproductive potential of the animal. The massive spread of genetic defects like CVM and BLAD in recent years is caused by the extensive use of elite carrier sires. Artificial insemination hastens the spread of detrimental recessives worldwide. The new technologies of molecular genetics facilitate to find the cause at gene level. This makes it possible to identify heterozygous animals and to manage the genetic health of the cattle population. The use of molecular methods into animal research promises quick progress in animal potential. If no cases are found in routine screening even then, extensive screening programs for

identification of genetic disorders appear necessary to guarantee the utilization of bulls free from genetic disorders for artificial insemination programs.

Author details

Vijay Kumar

Address all correspondence to: jaisvet@gmail.com

Department of Animal Genetics and Breeding, U.P. Pt. Deen Dayal Upadhyaya Pashu Chikitsa Vigyan Vishwavidyalaya Evam Go Anusandhan Sansthan, Mathura, Uttar Pradesh, India

References

- [1] Lin C, Lin SC, Chang CP, Rosenfeld MG. Pit-1-dependent expression of the receptor for growth hormone releasing factor mediates pituitary cell growth. *Nature*. 1992;**360**:765–768. DOI: 10.1038/360765a0
- [2] Moody DE, Pomp D, Barendse W. Restriction fragment length polymorphism in amplification products of the bovine PIT1 gene and assignment of PIT1 to bovine chromosome 1. *Animal Genetics*. 1995;**26**:45–47. DOI: 10.1111/j.1365-2052.1995.tb02620.x
- [3] Moody DE, Pomp D, Barendse W, Womack JE. Assignment of the growth hormone receptor gene to bovine chromosome 20 using linkage analysis and somatic cell mapping. *Animal Genetics*. 1995;**26**:341–343. DOI: 10.1111/j.1365-2052.1995.tb02671.x
- [4] Stone RT, Kappes SM, Beattie CW. The bovine homolog of the obese gene maps to chromosome 4. *Mammalian Genome*. 1996;**7**:399–400. DOI: 10.1007/s003359900119
- [5] Fitzsimmons CJ, Schmutz SM, Bergen RD, McKinnon JJ. A potential association between the BM 1500 microsatellite and fat deposition in beef cattle. *Mammalian Genome*. 1998;**9**:432–434.
- [6] Konfortov BA, Licence VE, Miller JR. Re-sequencing of DNA from a diverse panel of cattle reveals a high level of polymorphism in both intron and exon. *Mammalian Genome*. 1999;**10**:1142–1145. DOI: 10.1007/s003359901180
- [7] Buchanan FC, Fitzsimmons CJ, Van Kessel AG, Thue TD, Winkelman-Sim DC, Schmutz SM. Association of a missense mutation in the bovine leptin gene with carcass fat content and leptin mRNA levels. *Genetics Selection Evolution*. 2002;**34**:105–116. DOI: 10.1051/gse:2001006
- [8] Lagonigro R, Wiener P, Pilla F, Woolliams JA, Williams JL. A new mutation in the coding region of the bovine leptin gene associated with feed intake. *Animal Genetics*. 2003;**34**:371–374. DOI: 10.1046/j.1365-2052.2003.01028.x
- [9] Wheeler TL, Cundiff LV, Koch RM. Effect of marbling degree on beef palatability in *Bos taurus* and *Bos indicus* cattle. *Journal of Animal Science*. 1994;**72**:3145–3151.

- [10] Horseman ND, Zhao W, Montecino-Rodriguez E, Tanaka M, Nakashima K, Engle SJ. Defective mammapoiesis, but normal hematopoiesis, in mice with a targeted disruption of the prolactin gene. *EMBO Journal*. 1997;**16**:6926–6935. DOI: 10.1093/emboj/16.23.6926
- [11] Le Provost E, Leroux C, Martin P, Gafe P, Dijane J. Prolactin gene expression in ovine and caprine mammary gland. *Neuroendocrinology*. 1994;**60**:305–313.
- [12] Agerholm JS, Andersen O, Almskou MB, Bendixen C, Arnbjerg J, Aamand G, Nielsen US, Panitz F, Petersen AH. Evaluation of the inheritance of complex vertebral malformation syndrome by breeding studies. *Acta Veterinaria Scandinavica*. 2004;**45**(3):133–137. DOI: 10.1186/1751-0147-45-133
- [13] Agerholm JS, Bendixen C, Andersen O, Ambjerg J. Complex vertebral malformation in Holstein calves. *Journal of Veterinary Diagnostic Investigation*. 2001;**13**:283–289. DOI: 10.1177/104063870101300401
- [14] Nielsen US, Aamand GP, Andersen O, Bendixen C, Nielsen VH, Agerholm JS. Effects of complex vertebral malformation on fertility traits in Holstein cattle. *Livestock Production Science*. 2003;**79**(2):233–238. DOI: 10.1016/S0301-6226(02)00170-7
- [15] Kehrli ME, Ackermann MR, Shuster DE, Maaten VD, Schmalstieg FC, Anderson DC, Hughes BJ. Bovine leukocyte adhesion deficiency. β_2 integrin deficiency in young Holstein cattle. *American Journal of Pathology*. 1990;**140**:1489–1492.
- [16] Nagahata H, Noda H, Takahashi K, Kurosawa T, Sonoda M. A suspected case of neutrophil dysfunction in a Holstein heifer. *Japanese Journal of Veterinary Science*. 1987;**49**(6):1165–1167.
- [17] Healy MH, Shanks RD. Performance of females heterozygous for deficiency of uridine monophosphate synthase. *Journal of Dairy Science*. 1987;**70**(5):945–951.
- [18] Gentry PA, Ross ML. Coagulation factor XI deficiency in Holstein cattle: expression and distribution of factor XI activity. *Canadian Journal of Veterinary Research*. 1994;**58**(4):242–247.
- [19] Fesus L, Anton I, Zsolnai A. Marker assisted selection in livestock. DUMPS, weaver-diseases and citrullinaemia in cattle population. *Allatt-es-Takarm*. 1999;**48**(2):193–203.

