Dramatic rise of the world human population combined with the severe nutritional deficiencies in many parts of the world has given impetus to improve efficiency of animal production. Improvements in efficiency arise from the development, spread and adoption of improved modern technologies in the field of breeding, feeding, management and healthcare of animals. There has been a substantial development of new technologies in the spectrum of biotechnologies, which offer new prospects in improving the efficiency of livestock production.

Milk is considered as the “nature’s perfect food”, because of its balanced protein, fat, carbohydrate and mineral content, which represents a fundamental dietary ingredient of many walks of life. Intensive cross-breeding strategies, nutritional management and application of quantitative genetics have resulted in a steady improvement in milk production, but failed to produce major changes in milk composition.

It has long been known that manufacturing properties of milk are influenced by relative composition of its protein [1], casein being one of the major milk proteins and a major source of amino acid, calcium and phosphorus. The proportion of protein components in milk exhibits individual variation because of environmental and genetic factors [2]. The genes that encode major milk proteins are thought of as “candidate genes” for the observed variation in protein[1]. Thus, studies on milk protein polymorphism would play a vital role in improving the quality of milk.

Buffalo contributes about 54 per cent of the total milk produced in India. Although the economic importance of buffaloes has always been known, very little work has been carried out to exploit the genetic potential of this animal. Buffalo milk significantly differs from that of cow milk with respect to many chemical compositions. Though extensive studies have been carried out on characterization of milk protein genes in cattle, similar studies in buffaloes are scarce. Well defined breeds of buffaloes with standard qualities are found mainly in India and Pakistan. There are 18 River buffaloes and 12 swamp buffaloes, which are further classified into five major groups designated as the Murrah, Gujarati, Uttar Pradesh, Nagpuri and Kundi. Most of the remaining buffaloes of the African continent belong to a nondescript group known as the Desi buffaloes.

The domestic water buffalo (Bubalis bubalis) belongs to the Bovidae family, sub-family Bovinae, genus bubalis and species arni or wild Indian buffalo. The animals are classified into two distinct classes as swamp and river buffalo. The water buffalo has many anatomical and physiological similarities with the other species in this family. River buffaloes have 50 chromosomes and swamp buffaloes have 48 chromosomes. While the two types of buffaloes can be mated to produce a fertile offspring having 49 pairs of chromosomes, buffaloes cannot be successfully mated with any other members in the Bovidae family[3].

The swamp buffaloes are found in the Indian subcontinent and throughout Southeast Asia and China. The name ‘swamp’ has probably arisen from the fact that they prefer to wallow in stagnant water pools and mud holes. These buffaloes produce relatively small quantities of milk, one to two kg per day and they are mainly used for meat and draught. These animals are very well adapted to hot and humid climates as well as marshy lands. With their large hooves they are able to wade through the swamps and reach a variety of fodder sources [4,3].

The Riverine breeds of the Indian subcontinent are mainly raised for milk production. Their milk yield is about 6 to 7 liters per day with an average content of fat, protein and lactose of 7.5, 4.2 and 5.0 per cent, respectively, which gives the buffalo milk a higher energy content than milk from dairy cattle [5; 6]. Twelve of the 18 major Riverine breeds of buffaloes are kept primarily for milk production. The main milk breeds of India are Murrah, Nili-Ravi, Surti, Mehsana, Nagpuri, and Jafarabadi. The river buffalo prefers, as its name reveals, to wallow in clear, running water [3].

Buffaloes are known to be good grazers, but they graze a wider range of plants than cattle [7; 8]. They utilize low-grade roughage more efficiently compared to cattle [9; 5]. The unique ability of the buffaloes to survive under the most difficult...
conditions of nutrition and management has given them a competitive edge over other milk producers in the areas. In addition, the buffalo has a long productive life. A normal healthy female buffalo could have as many as 9 to 10 lactations [10] in her life time.

**Limitations in buffalo milk production**

Buffalo is still largely an animal of the village and many of its reported limitations are caused more by its environment than by the animal itself. Moreover, much of the animal's genetic potential is obscured by environmental influences. For example, for many breeds and types the genetic variations in milk yield and growth cannot be accurately determined because these are overwhelmed by the effects of inadequate nutrition and management.

The buffalo has long been considered a poor breeder-slow to mature sexually, and slow to rebreed after calving. Accumulated experience now shows, however, that this is mainly a result of poor management and nutrition. Buffaloes are no sluggish breeders. Nevertheless, their gestation period is about a month longer than that of cows, buffalo estrus is difficult to detect, and many matings occur at night such that farmers are likely to encounter more problems in breeding buffaloes than cattle.

Although, the river buffalo is the main dairy animal in some countries, it is a primitive animal when compared to the developed dairy cattle breeds like Holstein-Friesian and Jersey. Many generations of selective breeding has produced cattle with almost predictable productive and reproductive traits. This has not been the case among the buffalo breeds as the majority of these animals are reared by land less and marginal farmers where they breed naturally [11].

In general the age of buffaloes at first calving is usually around 40 to 60 months [10]. However, there are indications that the productive traits can be improved. As an example, the Mediterranean breeds and the swamp buffaloes calved earlier than those of Indian subcontinent [5]. Average calving intervals for Indian and Pakistani buffaloes ranged from 15 to 18 months. The dry period has been reported to be 90 to 150 days for the Nili-Ravi breed of Pakistan while for the Murrah, it ranged from 60 to 200 days [12]. Average lactation length ranged from 252 to 270 days. As a result of these factors the productive traits can be improved. As an example, the productive traits can be improved. As an example, the productive traits can be improved.

In most of the buffalo milk-producing countries of Asia, it is observed that there are large seasonal variations in breeding and calving in buffaloes[10]. In India and Pakistan, 80 per cent of the buffaloes calved during June and December causing a decline in milk production in the summer months. However, others have suggested this summer decline in milk production could be due to heat stress and shortage of greens. Dark body, lesser density of sweat glands and thick epidermis makes it difficult for the buffaloes to thrive in extreme hot and dry conditions. Buffaloes have developed survival mechanisms to seek water for immersion in these conditions. When exposed to extreme hot or cold conditions, the buffaloes’ milk production and reproductive efficiency are strongly affected [12]. In addition to climatic influences, poor nutrition and management also affect breeding and production.

Many of the traits of interest in animal production are quantitative traits. Evaluation of genetic merit of animals is still essentially based on the application of the theory of quantitative genetics. The conceptual basis of this theory is the polygenic model, which assumes that quantitative traits result from the action (and interaction) of a large number of minor genes, each with small effect. The resulting effects are then predicted using powerful statistical methods (animal model), based on pedigree and performance recording of traits from the individual animal and its relatives.

The advances in molecular genetic technology in the past two decades, particularly Nucleic acid-based markers, has had a great impact on gene mapping, allowing identification of the underlying genes that control part of the variability of these multigenic traits. Broadly, two experimental strategies have been developed for this purpose: linkage studies and candidate gene approach.

Linkage studies rely on the knowledge of the genetic map and search for quantitative trait loci (QTL) by using pedigree materials and comparing segregation patterns of genetic markers (generally micro satellites) and the trait being analyzed. Markers that tend to co-segregate with the analyzed trait provide approximate chromosomal location of the underlying gene (or genes) involved in part of the trait variability determinism.

The second approach focuses on the study of the genetic polymorphism of a few genes (candidate genes) suspected, on the basis of the biological and physiological information of the trait, to be implicated for part of the trait variability. Hence, association analysis (QTL) is carried in order to test whether a particular genotype or haplotype (a series of alleles along a stretch of DNA) are stably associated with the analyzed trait, such as the rate of the synthesis of the protein or milk yield. Introduction of such additional molecular information in selection procedures of buffaloes would be definitely beneficial to assess the true genetic merit of buffaloes. That is, it allows selection to occur among individuals that do not exhibit the trait in question e.g. milk protein genotypes in males. This approach is already being employed with regard to bovine leukocyte adhesion deficiency and genes with major effects, such as the halothane locus in swine and alpha S1-casein in goat. Thus, studies on milk protein polymorphism in buffaloes would play a vital role in improving the quality of milk in India. With this background author studied casein gene polymorphism in buffaloes viz., alpha s1 casein genes [13], beta casein genes[14] and kappa casein genes [15] and observed monomorphic pattern of the three casein genes (a2, B, k) revealed by PCR-RFLP, SSCP technique and sequencing data analysis may be a buffalo specific character. There was significant difference in nucleotide sequence between milk protein genes of *Bubalus bubalis* and *Bos taurus* animals. Further study is required to associate these differences to variation in milk constituents in these two species.

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