I. INTRODUCTION

Milk meets the basic requirements of the body and is highly beneficial in the growth and development of bones. Cow milk is a highly nutritious food, which is rich in several nutrients like calcium, potassium, vitamins and protein. Considering the innumerable health benefits of cow’ milk, knowing about its different components will be highly helpful. Substantial increases of 3500 kg of milk, 130 kg of fat and 100 kg of protein per cow per lactation have resulted from improvements in genetics, nutrition, and management during the past 20 years (Tsuda et al., 2000).

India is the second largest milk producer in the world with a milk production of around 112 million tons, which is worth more than Rs. 1, 70,000 crores. Buffalo milk accounts for approximately 57 per cent of total milk production in India. This level has remained stable over the last few years. Despite the high growth rate in production, the per capita availability of milk in India (245 grams per day) is lower than the world average (285 grams per day). With rapid industrialization, economic growth and an economically potential 250 million strong domestic consumers of milk and milk products, there is a very strong potential for future growth of the industry. India is the seventh largest country in the world in which 70 % people earn their livelihood from agriculture and animal husbandry (Pundir and Ahlawat, 2010).

The full potential of the dairy cattle has to be realized to meet the requirements of the growing population. There are several hindrances in this direction, diseases affecting milk production being the main cause. Amongst these diseases, mastitis, a worldwide endemic disease of dairy cows, is an important cause of decreased efficiency in milk
production. Genetic improvement of milk production traits has been accompanied by an increased susceptibility to mastitis. Mastitis is a major concern within the dairy cattle industry, as it is associated with animal suffering and substantial economic losses. This disease, in addition to causing distress for the cow, is estimated to cost the producer approximately Rs. 1602.20 crores per annum (Singh and Singh, 1994). Mastitis is a highly complex disease, because it has numerous causative pathogens, a wide variety of physiological responses, and a multifactorial background in which several genes and many environmental factors are involved. Apart from the huge loss due to treatment costs, culling of the infected animals is necessitated in some cases.

Mastitis resistance is a complex trait, depending on a genetic component but also on physiological and environmental factors, including infection pressure. Breeding for increased resistance to mastitis is usually based on indirect selection. Genetic selection for mastitis resistance is especially important because of the unfavorable genetic correlation with milk production (Shook, 1989; Carlen, 2008; Veerkamp and Haas, 2005). Most genetic studies focused on milk Somatic Cell Count (SCC) and clinical mastitis as phenotypic measure to predict the bacterial status of udders. Accumulating results show moderate and low heritability for SCC and clinical mastitis. Genetic variability for mastitis resistance represents only a small proportion of the total variance but is not negligible and provides some interesting selection opportunity, and should be considered as an attractive complementary way to improve mastitis resistance in dairy cattle.
The presence of different alleles due to a distorted segregation at the genetic markers is indicative of the difference between selected and non-selected livestock. The advantage of using genetic markers in selection is that it enables us to select animals at much younger age before the actual expression of the traits of interest. Natural and artificial selection leads to a change in the genetic makeup of the cow. Genetic markers have also been used to measure the genomic response to selection in livestock. In some studies authors reported that in infected cows, the milk and serum concentration of Lactoferrin will change (Hirvonen et al., 1999; Barkema, 1998).

Lactoferrin is a component of the natural protection systems of human and animals. It is found in most exocrine secretions including tears, saliva and milk, and there are numerous reports of its antibacterial activity in vitro and in vivo (Nuijens et al., 1996; Nibbering et al., 2001; Sordillo and Streicher, 2002). Lactoferrin, an iron-binding glycoprotein, kills bacteria and modulates inflammatory and immune responses. In milk, Lactoferrin plays a key role in the defense mechanisms of the mammary gland of lactating animals.

Lactoferrin genotype BB was significantly associated with a decrease of the SCC in cow milk. Wojdak-Maksymiec et al. (2006) found two alleles of Lactoferrin, A and B, in Polish Black and White dairy cows, and observed association between SCC and Lactoferrin genotypes. The results showed that polymorphism existed in the promoter of bovine Lactoferrin gene, which suggested that this polymorphism could be associated with mastitis susceptibility.
The present study aims at understanding the molecular background to mastitis and, especially, to improve the evaluation of genotypes to clinical mastitis with study on bovine Lactoferrin gene. The assignment to animals of breeding values that facilitate accurate selection of superior individuals can contribute to genetic progress on mastitis resistance or decreased susceptibility and should, in turn, improve both the health status of the cow and the economic condition of the farmer.

With this background, the present investigation was undertaken with the following objectives:

1. PCR amplification of bovine Lactoferrin gene in cattle.

2. PCR-RFLP of bovine Lactoferrin gene.

3. Study the association of bovine Lactoferrin gene with mastitis incidence.