ABSTRACT

Milk is the balance diet as it contains all the necessary ingredients, i.e. fat, protein, carbohydrate and minerals that are needed for a complete diet. India is one of the leading milk producers of the world. World Health Organization (WHO) recommends at least a glass of milk a day for everybody from child to old person. The milk production of India has grown to 127.3 million tonnes in 2011-12 from a paltry 17 million tonnes in 1950-51. India is producing about 12% to 15% of total world milk production. From the total milk produced around 46% is used as a liquid milk, 50% is utilized for making dairy products like Ghee, Dahi, Paneer, etc. and 4% is used for making other products like milk powder, flavored milk, etc. In India, the milking animals include 41.4% are cattle, 56.6% are buffalo and 3% are other animals like goat, camel, etc.

Buffalo has been an integral part of livestock agriculture in Asia for over 5000 years producing draft power, milk, meat and hides. Buffalo is a more efficient milk producer than an indigenous cow in India. In cattle several attempts were being made to understand lactogenesis process, but still it requires in-depth study as knowledge gained is insufficient. In buffalo still not such initiative is taken up. In such situation India needs to take up such study as we are harboring the world largest buffalo population.

In present study, three non-pregnant, non-lactating buffalo were induced with standard estrogen-progesterone regime. Mammary gland tissue was isolated on 0, 7, 14 and 21 day of hormonal induction. A histological analysis was performed to observe the changes in the micro and macrostructure of mammary gland cells. It was observed that alveolar cell, volume of alveoli, diameter of alveoli and lobules were higher in 21, 14 and 7 day of hormonal induction compared to 0 day of hormonal induction.

RNA was isolated from the mammary gland tissue of 0th, 7th, 14th & 21st days of induction. cDNA was synthesized and used as template for isolation of differential EST’s using SSH and DDRT. About 161 EST’s were generated by differential display and suppression subtractive hybridization.
BLAST analysis using nucleotide database, EST division of nucleotide database, Genome contig division of cattle genome database, EST division of cattle genome database and Non-Redundant database of all these EST’s revealed that about 30% of EST’s was showing no significant similarity found with above mentioned database, whereas, the remaining EST’s showed identity with WD repeat domain (1 & 7), MUCIN (16 & 5B) gene, Butyrophilin Gene, α-Lactalbumin gene, β-Casein gene, SCD gene, Myosin VB gene, IK Cytokine gene, Chemokine receptor gene, Matrix GLA protein gene, H factor 1 Gene, Insulin induced gene, TRPS1 gene, CAPN1 gene, Ribosomal L-32 protein, Sugar ABC transporter protein, etc.

Real time quantification was performed using primers designed from novel EST’s showed expression of particular EST from the parental stage of hormonal induction, indicating some specific role of particular EST during lactogenesis.

Further, full length cDNA sequencing, transcriptomics study and protein expression study can reveal in-depth role of EST’s in induced lactation. Data generated by the above mentioned studies could be used for creating DUDHPATRI, which can give detailed information regarding the quality and quantity of milk production of a new born calf.