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SINGLE NUCLEOTIDE VARIATIONS IN *DNAJC30* GENE: A POTENTIAL MARKER FOR METABOLIC ADAPTATION IN TRANSITION DAIRY COWS

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ABSTRACT

Successful adaptation to metabolic changes associated with transition from non-lactating pregnant state to non-pregnant lactating state is very important in economic dairying. Though feeding and management plays an important role in adaptation to transition, animals kept on similar feeding and management exhibit difference in adaptation indicating an underlying genetic cause. In the present study, a comparison of the sequence of *DNAJC30* gene, which has been reported to influence metabolic adaptability, between Serum β hydroxy butyrate (BHBA) - high and low groups revealed four variations downstream to its exonic region. Whether these changes influence the metabolic adaptability of animals need to be ascertained in a large population.

Keywords: DNAJC30, metabolic adaptation, transition

INTRODUCTION

In dairy cattle, the time interval between three weeks before parturition until three weeks after parturition is called the transition period (Block, 2010). The transition from pregnancy to lactation is characterised by metabolic stress as there is reduction in dry matter intake in parallel with rapid increase in milk secretion. This imbalance between reduced intake and increased demand force animals into a state of negative energy balance, especially in high yielding dairy cows (Lean *et al.,* 2013). In order to compensate this negative energy balance, animal undergoes several metabolic adaptations. When animals fail to adapt, it suffers from metabolic disorders like fatty liver, ketosis and many others (Drakley *et al.,* 2001), leading to a reduction in milk yield causing economic loss to the farmers. It has been reported that there is a genetic element for metabolic adaptability. *DNAJC30,* a gene present on

chromosome 25 is reported to influence successful adaptation to transition. In the present study, the sequence of *DNAJC30* gene of metabolically robust and poor groups of animals were compared to discover variations between the two.

MATERIALS AND METHODS

The study included 30 age and parity matched apparently healthy pregnant crossbred dairy cows. Serum β hydroxy butyrate (BHBA) was estimated at fortnightly intervals from four weeks before the predicted day of parturition until four weeks after parturition in a semi-automatic analyser using commercially available kits from Randox Laboratories. Animals were grouped into two, based on their serum BHBA levels, as high BHBA (BHBA-H) and low BHBA (BHBA-L) groups by cluster analysis. DNA was isolated by standard phenol-chloroform method and *DNAJC30* was amplified using three sets of overlapping primers. Pooled samples of amplicons of representative animals of each group were sequenced by Sangers method at Agrigenome, Kochi. Sequences were aligned using MegAlign and analysed using Clustal-ω.

RESULTS AND DISCUSSION

The mean BHBA concentration of the animals estimated at fortnightly intervals from four weeks before the predicted day of parturition until four weeks after parturition were 0.599±0.038 mmol/L, 0.616±0.031 mmol/L, 0.645±0.027 mmol/L and 0.718±0.037 mmol/L, respectively. Animals were then grouped into two by cluster analysis into high and low BHBA groups. A high BHBA concentration is indicative of negative energy balance and consequent ketonemia. Significant difference in the BHBA concentration of age and parity matched animals kept under similar feeding and management conditions indicate their difference in the ability to adapt.

DNAJC30 is a gene present on chromosome 25 encoding the protein DNAJC30 which is composed of 226 amino acids. The gene is 2668 bp in length and is composed of a single exon. It is a member of DnaJ (hsp40) homolog, a subfamily C group of proteins. DnaJ is a member of the J-protein family, that regulates the activity of the hsp70 group of proteins. DnaJ (hsp40) binds to dnaK (hsp70) and stimulates its ATPase activity, generating the ADP-bound state of dnaK, which interacts stably with the polypeptide substrate (Walsh *et al.,* 2004).

A comparison of *DNAJC30* sequence of the metabolically robust BHBA-L group with the sequence of BHBA-H group showed that BHBA-L group animals had “G”, “T”, “G”, “G”

Fig. 1. Clustal ω (MSA) for comparison of DNAJC30 gene; A: BHBA-H, B: BHBA-L

respectively, at positions 1881, 1892, 2043 and 2169 of the gene as against "A", "C", "A", "A" respectively, at these locations in BHBA-H group (Fig. 1). The nucleotides at positions 1881 and 1892 occur at the 3' un-translated region of the mature mRNA.

Ha *et al.* (2015) reported the association of certain single nucleotide polymorphisms in *DNAJC30* with BHBA concentration during transition period. The extent to which the variations observed in *DNAJC30* between the two sets of animals in this study contributed to adaptability can be established only through a population study involving a larger number of animals.

SUMMARY

Healthy transition from non-lactating pregnant state to non-pregnant lactating state is important in the profitability of dairying. Proper feeding and management are important in ensuring metabolic adaptation and healthy transition, but it is also found to have an associated genetic element. *DNAJC30* is reported to influence metabolic adaptation and so the variations in the sequence of the gene in metabolically robust and challenged groups were analysed. Though there were changes in four nucleotide positions, the effect of these changes in metabolic adaptability need to be determined in a large population.

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