ISSN: 2226-7522(Print) and 2305-3327 (Online)
Science, Technology and Arts Research Journal
July-Sep 2013, 2(3): 79-84
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Original Research

Identification of *Cis*-regulatory Elements of Butyrophilin Gene of the Mammary Gland

Demie Aschalew L[1*], Zegeye Abiy [2] and Qayyum Khan A[3]

[1]Department of Biology, Faculty of Natural and Computational Sciences, Wollega University, Post Box No: 395, Nekemte, Ethiopia

[2] Biotechnology Program, School of Postgraduate Studies, Addis Ababa University, Addis Ababa, Ethiopia

[3]Department of Biology , Faculty of Natural Sciences, Arba Minch University, Arba Minch, Ethiopia

Abstract

Butyrophilin subfamily 1 member A1 is a highly expressed gene in mammary gland of all mammals during lactation. It is found to be the major integral protein in the milk fat globule membrane. Its interactions with other membrane elements and soluble proteins of the mammary epithelial cells regulate the secretion of milk fat. In order to reveal any shared *cis*-acting elements, the human butyrophilin subfamily 1member A1 5'-flanking genomic sequence was analyzed and compared with four mammals comprising of a rodent and three primates, *viz.*, *Mus musculus*, and *Pan troglodytes*, *Pongo obelli*, and *Macaca mulata*, and three other mammary specific human milk genes using publicly available bioinformatics tools. Prior to a multiple sequence analysis, low complexity DNA sequences were masked using CENSOR. The multiple sequence analysis revealed nine highly conserved regions of similarities in the 5'- flanking region of butyrophilin genes across species. Consensus putative transcription factor binding sites were identified using MatInspector and compared with SiteGA results. They were subsequently examined for the expression in the mammary gland as well as for their occurrence in the previously identified region of homology. Finally, CCCTC-binding factor (CTCF) and nuclear receptor subfamily 2 - factor (NR2F) were identified at a similar distance from the transcription start site in the 5'- flanking region of butyrophilin gene across the species. However, the exact interaction of these transcription factors with the butyrophilin gene is not known, which needs further investigation.

Article Information

Article History:

Received : 17-07-2013

Revised : 27-09-2013

Accepted : 29-09-2013

Keywords:

Milk fat globule

Butyrophilin gene

Transcription factor

Binding sites

***Corresponding Author:**

Demie Aschalew L

E-mail:

aschusmart2006@gmail.com