

## **IN-SILICO COMPARATIVE ANALYSIS OF THE PROMOTER REGIONS OF OVINE AND BOVINE LEPTIN (*LEP*) GENE**

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**Abstract:** The promoter region of the *LEP* gene approximately 2500 bp was screened for the CCAAT/enhancer-binding protein (C/EBP) motifs using the online software 'TFSEARCH' (<http://www.cbrc.jp/research/db/TFSEARCH.html>). The promoter region of Ovine *LEP* gene revealed nine binding sites for the C-EBP of which two were for C/EBP $\alpha$ . The binding sites for ovine were identical to that of bovine as *LEP* is highly homologous in these species. Four elements in the proximal 109 bp contribute to leptin promoter activity: the TATA box at -30, a C/EBP motif at -53, LP1 region at -87, and a Sp1 motif at -97. The analysis revealed that site of the leptin promoter is conserved in evolution, binds Sp1 present in adipocyte nuclear extracts, and contributes to promoter activity.

**Keywords:** Sheep, Leptin gene promoter region, *in-silico* analysis.

### **Introduction**

*In silico* is an expression used to mean "performed on computer or *via* computer simulation." The term "*in silico*" characterizes biological experiments carried out entirely in a computer. The leptin (*LEP*) gene could be a potential candidate gene controlling some proportion of adipose and lean accretion in sheep. The present study was designed to compare the genomic organization and promoter activity of the ovine *LEP* gene to that of the bovine. The binding of C/EBP (especially C/EBP $\alpha$ ) was reported to enhance the leptin receptor mRNA expression. The C/EBP $\alpha$  is a basic region/leucine zipper transcription factor important for the transcription of most adipocyte genes and of other genes involved in energy metabolism.

### **Materials and Methods**

The complete sequence of the ovine *LEP* genes was obtained from the online database, the National Centre for Biotechnological Information (NCBI) ([www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)) which provides access to biomedical and genomic information. The gene accession number for the *LEP* gene is NC\_019461 and GeneID 443534. The sequence was obtained in FASTA format.

Sequence data were analysed using the SeqMan program of LASERGENE software (DNASTAR Inc., USA). The *LEP* gene sequence obtained from NCBI were used as

reference sequences for analysis. The promoter region was screened for transcription factors using the free online software 'TF search' (<http://www.cbrc.jp/research/db/TFSEARCH.html>) (Heinemeyer *et al.*, 1998).

### **Results and Discussion**

The expression of *LEP* gene is controlled by cis- and trans-acting elements and factors. Analysis on approximately 2500 bp of the promoter region of the *LEP* gene screened for the CCAAT/enhancer-binding protein (C/EBP) motifs since binding of C/EBP (especially C/EBP $\alpha$ ) was reported to enhance the leptin receptor mRNA expression. The promoter region of Ovine *LEP* gene revealed nine binding sites for the C-EBP of which two were for C/EBP $\alpha$ . As bovine *LEP* is highly homologous to the ovine *LEP* gene, the binding sites were identical. The results of this *in-silico* analysis are shown in Fig. 1. Four elements in the proximal 109 bp contribute to leptin promoter activity: the TATA box at -30, a C/EBP motif at -53, LP1 region at -87, and an Sp1 motif at -97. The C/EBP $\alpha$  is a basic region/leucine zipper transcription factor important for the transcription of most adipocyte genes and of other genes involved in energy metabolism (Fukuda and Iritani, 1999; Liefers *et al.*, 2005). The site of the leptin promoter is conserved in evolution, binds Sp1 present in adipocyte nuclear extracts, and contributes to promoter activity. The regulation of leptin promoter by Sp1 and C/EBP in bovines was predicted by Mullis *et al.*, (2005) and was confirmed *via* cotransfection with C/EBP caused that resulted 24-fold activation of leptin reporter expression, as compared to cotransfection with control plasmid by Taniguchi *et al.* (2002). The leptin gene expression has been known to respond to hormones and metabolic state. The *ob/ob* mice, which have a nonsense mutation, exhibit a 20-fold increased leptin RNA level, suggesting existence of an intact mechanism to sense adiposity and to transcribe the leptin gene.

### **Conclusion**

The transcription factor binding motifs in the leptin promoter, such as the putative C/EBP site, seem to play a role in mediating gene regulations. The active binding sites predicted need to be assessed by promoter assay

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Figure 1. In-silico analysis of the Ovine Leptin Promoter The TATA box (highlighted green), the exons (highlighted grey) and start codon (red and bold) are shown. Nine C-EBP binding sites were predicted in the Ovine Leptin promoter of which three are C-EBP (highlighted blue), two are C-EBP $\alpha$  (underlined red) and four are C-EBP $\beta$  (highlighted yellow) sites. The SP1 sites are also shown (bold underlined).

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