Cloning, expression analysis and sequence prediction of the CCAAT/enhancer-binding protein alpha gene of Qinchuan cattle

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ABSTRACT. CCAAT/enhancer-binding protein alpha (C/EBPα) is an essential transcription factor, regulating the differentiation of adipocytes. We cloned the complete open reading frame of C/EBPα gene of Qinchuan cattle and analyzed its protein structures and expression profile in 15 tissues via DNA cloning, sequencing and RT-PCR. Analysis of the putative protein sequences revealed that C/EBPα consists of alpha helices, random coils and a few extended strands. A significant transmembrane structure was observed in amino acid region 233 to 252. A basic leucine zipper domain was also found in amino acid region 277 to 340, which is characteristic of C/EBPs. Homologous comparison with various species indicated that the C/EBPα gene of Qinchuan cattle shares 97, 95, 94, 94, and 93% similarity in amino acid sequences with *Sus scrofa*, *Homo sapiens*, *Rattus norvegicu*s, *Oryctolagus cuniculus*, and *Mus musculus*, respectively, implying strong sequence conservation of C/EBPα during evolution. RT-PCR revealed that the mRNA expression level of bovine C/EBPα gene in subcutaneous fat is much higher than that

in the other 14 tissues, and the relative quantity in fat tissue increases with cattle age.

Key words: C/EBPα gene; Qinchuan cattle; Expression profile; Cloning; Protein structure prediction