



Molecular cloning and sequence analysis of follicle-stimulating hormone beta polypeptide precursor cDNA from the bovine pituitary gland

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ABSTRACT. Follicle-stimulating hormone (FSH) plays an essential role in mammalian spermatogenesis and follicular development. In a previous study, we demonstrated that some bulls carry numerous linked mutations in the FSH beta-subunit (*FSHB*) gene, and that these bulls have poor-quality semen, low fertility, and slightly lower serum FSH concentration compared to those without such mutations. Here, we identified the different *FSHB* mRNA transcripts in such individuals and analyzed the evolutionary pattern of the *FSHB* open reading frame (ORF) in different species. Two different lengths of *FSHB* mRNA transcripts corresponding to two different polyadenylation sites in the 3'-UTR were detected in wild-type bull pituitary glands, and four different mRNA transcripts resulting from the different polyadenylation sites and linked mutations were identified in mutation-bearing bull pituitaries. All transcripts had almost the same putative *FSHB* precursor molecule. When the ORF

sequences of wild-type and mutation-bearing genes were compared with those of other tetrapod species, the leopard frog had the lowest level of homology (57.8 and 58.1%) and the buffalo had the highest level (95.9 and 96.7%), respectively. These results indicated that the bovine *FSHB* gene transcribes at least two classes of mRNA in the wild-type and four classes of mRNA in the mutation-bearing individuals, which provides a new insight into the bovine *FSHB* evolutionary pattern. In addition, these findings lay a foundation for further study of gene expression regulation and the effects of mutations on male fertility traits in cattle.

Key words: Bovine; FSHB; RACE; mRNA transcripts