



Sequence characterization and comparative analysis of the gastrotropin gene in buffalo (*Bubalus bubalis*)

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ABSTRACT. In this study, we compared the complete sequence of the *FABP6* gene from an animal representing the Murrah breed of the river buffalo (*Bubalus bubalis*) with the gene sequence from different mammals. The buffalo *FABP6* gene is 6105 bp in length and is organized into four exons (67, 176, 90, and 54 bp), three introns (1167, 1737, and 2649 bp), a 5'UTR (93 bp), and a 3'UTR (72 bp). A total of 22 repetitive elements were identified at the intronic level, and four of these (L1MC, L1M5, MIRb, and Charlie4z) were identified as being exclusive to buffalo. Comparative analysis between the *FABP6* gene coding sequence and the amino acid sequence with its homologues from other mammalian species showed a percentage of identity varying from 79 to 98% at the DNA coding level and 70 to 96% at the amino acid level. In addition, the alignment of the gene sequence between the Murrah and the Mediterranean breeds revealed 20 potential single nucleotide polymorphisms, which could be candidates for validation in commercial buffalo populations.

Key words: BAC library; FABP6; Murrah; Next generation sequencing