



Molecular characterization of interferon regulatory factor 1 in *Bubalus bubalis*

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ABSTRACT. Interferon regulatory factor 1 (IRF1) is functionally diverse in the regulation of immune response and is considered to be an important candidate gene for studying disease susceptibility in mammals. In this paper, we characterized the whole sequence of the IRF1 gene in river buffalo (*Bubalus bubalis*) and compared genomic and the amino acid sequences between different species. The buffalo IRF1 gene was 7099 bp long and organized into 10 exons and nine introns. Its molecular structure showed exactly the same number of exons (10) and introns (nine) in bovids, mice, horses, humans, and chickens. However, rats did not have exon 5, but had the largest exon 4, which suggests that exon 5 was incorporated into exon 4. The coding and the amino acid sequences of the gene showed that identity varied from 73 to 99% at the coding sequence level and from 61 to 100% at the amino acid level when compared with other mammals and chickens. Comparative analysis of the gene sequence between two different buffalo breeds, Murrah and Mediterranean, revealed six potential SNPs that are primarily located in the 5' and 3'UTRs.

Key words: BAC library; Interferon regulatory factor 1; Murrah; Pyrosequencing; River buffalo