Comparative analysis of the river buffalo somatostatin gene

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ABSTRACT. The somatostatin protein plays a crucial role in the regulation of multiple biological functions, such as growth, fat deposition, and nutrient absorption in vertebrates. Polymorphisms in the somatostatin gene have been associated with growth traits in livestock species, including cattle and goat. In this study, we conducted complete molecular characterization of the somatostatin gene in *Bubalus bubalis* (Murrah breed) by sequencing a Murrah BAC clone spanning 72,489 base pairs (bp) in length. The buffalo somatostatin gene contains 1481 bp organized into a 5'-untranslated region (135 bp), exon 1 (139 bp), intron 1 (839 bp), exon 2 (212 bp), and 3'UTR (156 bp). Comparative analysis between the buffalo somatostatin DNA coding sequence and the amino acid sequence with other bovids (cattle, goat, and sheep), horse, pig, human, rodents (mouse and rat), and chicken. Identity varied from 83-99% on the DNA sequence level and 88-100% on the protein level. In addition, a comparison of gene sequences between Murrah and Mediterranean breeds revealed 6 potential single-nucleotide polymorphisms (1 in exon 1 and 5 in intron 1), which were validated in different buffalo populations. This comparative analysis provides basic information for future studies of different buffalo herds using the

position candidate gene approach, quantitative trait loci analysis, and polymorphisms associated with growth traits.

Key words: 3-D screening; BAC library; *Bubalus bubalis*; Somatostatin gene; Pyrosequencing