Sequence analysis of the *S1PR1* gene in river buffalo

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ABSTRACT. Recent developments in methodologies for genomic analyses have enabled a significant advance in understanding of the river buffalo genome. The *S1PR1* gene has been mapped to buffalo chromosome 6 and bovine chromosome 3; this gene is of interest as it is a candidate for marbling in meat, an important economic trait. Here, we performed next generation sequencing in a buffalo BAC DNA clone and obtained a 54.5-kb sequence encompassing the entire buffalo *S1PR1* gene as well as the 27 kb upstream region and the 22 kb downstream region. The gene had a total length of 4716 bp, including three exons and two introns; exons 1 and 2 were classified as non-protein-coding. In comparison with homologues from other species, the structural organization of buffalo *S1PR1* was closest to that of the goat and in both species exon 2 of the gene was non-protein-coding. One hundred and nine repetitive elements were found within the buffalo gene and its boundary regions, with 50 SINE repeats being the most abundant. Alignment of *S1PR1* sequences from the Murrah and Mediterranean breeds revealed two nucleotide substitutions (g.1176C>G

and g.2740T>C), which represent potential SNPs that could be used in further studies of buffalo genetic structure.

Key words: BAC library; *Bubalus bubalis*; Murrah; Pyrosequencing; Shingosine-1-phosphate receptor 1

