



Polymorphism in the *A2M* gene associated with high-quality milk in Murrah buffaloes (*Bubalus bubalis*)

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ABSTRACT. The study of genes associated with host defense mechanisms, such as the *A2M* gene, plays a critical role in preventing diseases that reduce milk yield and its constituents. The aim of this study was to identify polymorphisms in the *A2M* gene in Murrah buffaloes (*Bubalus bubalis*), and investigate their associations with milk yield, fat and protein production, fat and protein percentages, and somatic cell count. Hair follicle samples of 136 animals were collected for DNA extraction, and polymorphisms were identified by polymerase chain reactions and sequencing. Statistical analyses were performed to ascertain the allelic and

genotypic frequencies, the Hardy-Weinberg equilibrium, and association analysis was conducted between the polymorphisms and the traits studied. Comparative analysis between buffalo and bovine sequences revealed seven nucleotide substitutions. Alignments among the buffalo sequences identified three single nucleotide polymorphisms (SNPs), including one in exon 29, g.241A>G, which was used in subsequent statistical analyses. A Hardy-Weinberg test indicated that this SNP was in equilibrium in this population, and was significantly associated ($P < 0.05$) with fat production and fat and protein percentages. Therefore, this SNP can be used as a molecular marker for these traits.

Key words: Allele; *Bubalus bubalis*; Protein production; Somatic cell count