

ABSTRACT

**Expression of the *Tas1r3* and *Pept1* genes in the digestive tract of wagyu cattle**

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Animals have precise recognition systems for amino acids and peptides that regulate their feeding behavior as well as metabolic responses. Because of their particular gastrointestinal structure, ruminants are expected to have unique mechanisms of amino acid regulation in the digestive tract. To better understand these mechanisms in the ruminant digestive tract, the expression of *Tas1r3* and *Pept1* was studied along the gastrointestinal tract of Japanese Black cattle through quantitative RT-PCR and immunohistochemistry. *Tas1r3* mRNA was detected ubiquitously along the gastrointestinal tract, and the most predominant expression was observed in the reticulum. In addition, the presence of *Tas1r3* receptor was confirmed in the rumen through immunohistochemistry. The expression level of *Pept1* mRNA was higher in the forestomach (rumen, reticulum, and omasum) and small intestine (duodenum) than that in the tongue, and predominant expression was observed in the rumen. By contrast, a negligible amount of *Pept1* mRNA was detected in the abomasum and large intestine. Further studies on the roles of *Tas1r3* and *Pept1* in the digestive tract, in particular, in the four components of the stomach, will help us to understand the mechanisms of amino acids regulation in ruminants and provide the basis for formulating cattle diets to improve the health and productivity of cattle.