



Porcine *MAP3K5* analysis: molecular cloning, characterization, tissue expression pattern, and copy number variations associated with residual feed intake

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ABSTRACT. Mitogen-activated protein kinase kinase kinase 5 (MAP3K5) is essential for apoptosis, proliferation, differentiation, and immune responses, and is a candidate marker for residual feed intake (RFI) in pig. We cloned the full-length cDNA sequence of porcine *MAP3K5* by rapid-amplification of cDNA ends. The 5451-bp gene contains a 5'-untranslated region (UTR) (718 bp), a coding region (3738 bp), and a 3'-UTR (995 bp), and encodes a peptide of 1245 amino

acids, which shares 97, 99, 97, 93, 91, and 84% sequence identity with cattle, sheep, human, mouse, chicken, and zebrafish *MAP3K5*, respectively. The deduced *MAP3K5* protein sequence contains two conserved domains: a DUF4071 domain and a protein kinase domain. Phylogenetic analysis showed that porcine *MAP3K5* forms a separate branch to vicugna and camel *MAP3K5*. Tissue expression analysis using real-time quantitative polymerase chain reaction (qRT-PCR) revealed that *MAP3K5* was expressed in the heart, liver, spleen, lung, kidney, muscle, fat, pancrea, ileum, and stomach tissues. Copy number variation was detected for porcine *MAP3K5* and validated by qRT-PCR. Furthermore, a significant increase in average copy number was detected in the low RFI group when compared to the high RFI group in a Duroc pig population. These results provide useful information regarding the influence of *MAP3K5* on RFI in pigs.

Key words: Copy number variation; *MAP3K5*; Porcine; RACE; mRNA expression: Residual feed intake