

Localization, Expression Change in PRRSV Infection and Association Analysis of the Porcine TAP1 Gene

Nunu Sun^{1, 2, *}, Dewu Liu^{1, *}, Hongbo Chen³, Xiangdong Liu², Fanming Meng¹, Xianwei Zhang¹, Huiyong Chen⁴, Shengsong Xie², Xinyun Li², Zhenfang Wu^{1 ?}

1. Guangdong Provincial Key Lab of Agro-Animal Genomics and Molecular Breeding, College of Animal Science, South China Agricultural University, Guangzhou 510642, P. R. China; 2. Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, Huazhong Agricultural University, Wuhan 430070, P. R. China 3. School of Animal Science and Nutritional Engineering, Wuhan Polytechnic University, Wuhan 430023, P. R. China 4. Molecular Biology Research Center, College of Biological Science and Technology, Central South University, Changsha 410078, P. R. China

Abstract :

The transporter associated with antigen processing (TAP) translocates antigenic peptides from the cytosol into the lumen of the endoplasmic reticulum and plays a critical role in the major histocompatibility complex (MHC) class I molecule-mediated antigenic presentation pathway. In this study, the porcine *TAP1* gene was mapped to the pig chromosome 7 (SSC7) and was closely linked to the marker SSC2B02 (retention fraction=43%, LOD=15.18). Subcellular localization of TAP1 by transient transfection of PK15 cells indicated that the TAP1 protein might be located in the endoplasmic reticulum (ER) in pig kidney epithelial cells (PK-15). Gene expression analysis by semi-quantitative RT-PCR revealed that *TAP1* was selectively expressed in some immune and immune-related tissues. Quantitative real-time PCR (qRT-PCR) analysis revealed that this gene was up-regulated after treatments that mimic viral and bacterial infection (polyriboinosinic-polyribocytidylic acid (poly(I:C)) and lipopolysaccharide (LPS), respectively). In addition, elevated *TAP1* expression was detected after porcine reproductive and respiratory syndrome virus (PRRSV) infection in porcine white blood cells (WBCs). One single nucleotide polymorphism (SNP) in exon 3 of *TAP1* was detected in a Landrace pig population by *Bsp143I* restriction enzyme digestion. Different genotypes of this SNP had significant associations ($P < 0.05$) with the red blood cell distribution width (RDW) of 1-day-old (1 d) pigs ($P = 0.0168$), the PRRSV antibody level (PRRSV Ab) ($P = 0.0445$) and the absolute lymphocyte count (LYM#) ($P = 0.024$) of 17 d pigs. Our results showed that the *TAP1* gene might have important roles in swine immune responses, and these results provide useful information for further functional studies.

Key Word :

Pig, TAP1, Localization, Expression, PRRSV, Association analyses

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