



Molecular characterization and tissue expression profile analysis of the porcine *JAZF1* gene

H. Yang^{1,2}, J. He¹, X.L. Xu², J. Jiang¹, C.Q. He¹ and H.M. Ma¹

¹College of Animal Science and Technology of Hunan Agricultural University, Changsha, China

²College of Life Sciences and Resource Environment of Yichun University, Yichun, China

Corresponding author: H.M. Ma
E-mail: mahaiming2000@163.com

Genet. Mol. Res. 14 (1): 542-551 (2015)
Received January 15, 2014
Accepted August 6, 2014
Published January 26, 2015
DOI <http://dx.doi.org/10.4238/2015.January.26.9>

ABSTRACT. A recent study indicated that the *JAZF1* gene was related to lipid metabolism by regulating the level of gene expression in humans and mice. In order to investigate whether *JAZF1* gene expression was associated with fat deposition in pig, we cloned the full-coding region of the *JAZF1* gene (GenBank accession No. KF307636) from porcine longissimus dorsi. Results showed that the open reading frame of *JAZF1* covered 732 bp and encoded 243 amino acids. Multiple alignment of isoform sequences revealed that the deduced amino acid sequence of JAZF1 had a high degree of sequence similarity to other vertebrates, indicating that it was highly conserved during evolution. Bioinformatic analysis indicated that pig JAZF1 contained 23 phosphorylation sites and 19 glycosyl sites. JAZF1 was predicted to have 3 ZnF-C₂H₂ and 2 low-complexity domains. The *JAZF1* mRNA expression pattern indicated that *JAZF1* mRNA expression level in the liver was significantly different in 2 divergent breeds ($P < 0.05$). This article perhaps provided an

important experimental basis for further research on the mechanisms of lipid metabolism and fat deposition in pigs.

Key words: Shaziling pig; *JAZF1* gene; Tissue expression