



Molecular cloning, characterization and expression analysis of *WAG-1* in the pistillody line of common wheat

Q.H. Wang, Z.J. Yang, S.H. Wei, Z.Y. Jiang, Y.F. Yang, Z.S. Hu,
Q.X. Sun and Z.S. Peng

The Ministry of Education Key Laboratory of Southwest China Wildlife
Resources Conservation, College of Life Science,
China West Normal University, Nanchong City, Sichuan, China

Corresponding author: Z.S. Peng
E-mail: pzs8833@163.com

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ABSTRACT. Wheat *WAG-1* is a C-class MADS-box gene, which is orthologous to *AGAMOUS* in *Arabidopsis*. In this study, we report the cloning, characterization, and expression patterns of *WAG-1* in the pistillody mutant HTS-1 and its sib-line CSTP. The cDNA of *WAG-1* was found to be 765 bp in length, which was equal to the length of its open reading frame, encoding 254 amino acids. The location of *WAG-1* revealed that it has three homologous genes from the short arm of chromosome 1A, 1B, and 1D. Their genomic sequences were determined to be 5864, 6454, and 6447 bp long, respectively, and possessed seven exons and six introns. Young spikes from HTS-1 contained higher levels of *WAG-1* transcript than did those from CSTP, and the transcript levels in the young spikes (7-10 mm in length) of HTS-1 increased 3.3-fold relative to those of the CSTP line. The transcript level in the pistil and pistil-like stamens of HTS-1 was over 2-fold higher than that in the

stamens of CSTP, and expression in the pistil-like stamens of HTS-1 was slightly higher than that in its pistils. These data provide a basis for future research into the function of *WAG-1*, and offer further insight into the molecular mechanism of the pistillody mutation in common wheat.

Key words: *WAG-1*; Cloning; Pistillody line; Expression pattern; Wheat