Wei Wei , Yang Hu , Yong-Tao Han , Kai Zhang , Feng-Li Zhao , Jia-Yue Feng The WRKY transcription factors in the diploid woodland strawberry Fragaria vesca: Identification and expression analysis under biotic and abiotic stresses **Plant Physiology and Biochemistry** 105 (2016) 129e144

Doi：10.1016/j.plaphy.2016.04.014

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WRKY proteins comprise a large family of transcription factors that play important roles in response to biotic and abiotic stresses and in plant growth and development. To date, little is known about the WRKY gene family in strawberry. In this study, we identified 62 WRKY genes (FvWRKYs) in the wild diploid woodland strawberry (Fragaria vesca, 2n ¼ 2x ¼ 14) accession Heilongjiang-3. According to the phylo-genetic analysis and structural features, these identified strawberry FvWRKY genes were classified into three main groups. In addition, eight FvWRKY-GFP fusion proteins showed distinct subcellular localizations in Arabidopsis mesophyll protoplasts. Furthermore, we examined the expression of the 62 FvWRKYgenes in ‘Heilongjiang-3’ under various conditions, including biotic stress (Podosphaera aphanis), abiotic stresses (drought, salt, cold, and heat), and hormone treatments (abscisic acid, ethephon, methyl jasmonate, and salicylic acid). The expression levels of 33 FvWRKY genes were upregulated, while 12 FvWRKY genes were downregulated during powdery mildew infection. FvWRKY genes responded to drought and salt treatment to a greater extent than to temperature stress. Expression profiles derived

from quantitative real-time PCR suggested that 11 FvWRKY genes responded dramatically to various stimuli at the transcriptional level, indicating versatile roles in responses to biotic and abiotic stresses. Interaction networks revealed that the crucial pathways controlled by WRKY proteins may be involved in the differential response to biotic stress. Taken together, the present work may provide the basis for

future studies of the genetic modification of WRKY genes for pathogen resistance and stress tolerance in strawberry.