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Isolation and Characterization of *MdMADS8* and *MdMADS9*, a Member of the *AGAMOUS* Subfamily Gene, in the Apple

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Two MADS-box genes, *MdMADS8* and *MdMADS9*, were isolated in the mature flowers of apple (*Malus x domestica* Borkh.) variety Fuji. The deduced amino acid sequences of cloned genes were 242 aa and showed 88.4% identity to each other. Deduced amino acid sequences of the *MdMADS8* was identical with the previously isolated MADS box gene (GenBank accession number AJ251117). *MdMADS9* is found to be a novel gene (GenBank AF401637). The *MdMADS8* and *MdMADS9* shares a high degree of amino acid sequence identity with the *AGAMOUS* subfamily genes. Quantative analysis of their RNA expression levels showed that the expression levels of the *MdMADS8* transcripts were much higher than those of the *MdMADS9* transcripts in the flower and fruit development. RNA *in situ* hybridization revealed that the

MdMADS8 transcript was detected at all stages of the flower development and fruit development. The *MdMADS8* mRNA is highly detected in the carpel primordia and ovules in floral meristem and post-anthesis flower. To understand the role of *MdMADS8* gene in the flower and fruits development, we produced transgenic tomato which was sense and antisense RNA expression of the *MdMADS8* controlled by the CaMV 35S promoter. The ectopic (over-expression) expression of the *MdMADS8* showed a abnormal development of seeds. The antisense RNA expression of the *MdMADS8* showed the inhibition of fruit development and the homeotic change eq. conversion of fruits to sepal. These results suggest that *MdMADS8* play an important role seed and fruit development.

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