



Identification of differentially expressed genes involved in early bolting of *Angelica sinensis* (Apiaceae)

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ABSTRACT. *Angelica sinensis* is a highly valued medicinal herb, known as female ginseng that is widely cultivated in China. Although *A. sinensis* is in great demand due to its multiple medicinal and food applications, its early bolting rate (almost 40%) seriously affects crop quality. To better understand its flowering mechanism, cDNA-amplified RFLP analysis was employed to look for gene expression differences between flower bud and shoot apical meristem tissues. Sixty-four primer sets were used, with each primer set amplified to 60 transcript-derived fragments. Some transcript-derived fragments were expressed only in the flower bud. After cloning, sequencing and a homology search, 46 distinct sequences were obtained; 26 of these were found to have homologous sequences in databases. These included transcaffeoyl-CoA 3-O-methyltransferase, 1-deoxy-D-xylulose 5-phosphate reductoisomerase, 15-cis-zeta-carotene isomerase, isoamylase, and calmodulin-binding protein. These genes are closely related to pollen germination and pollen tube growth, terpenoid backbone biosynthesis, and other metabolic pathways. Confirmation of differential expression

of 10 sequences was obtained by semi-quantitative RT-PCR, showing higher expression levels in flower buds.

Key words: cDNA-AFLP; Early bolting; *Angelica sinensis* Diels; TDFs; sqRT-PCR; Female ginseng