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Functional characterization of the *Ginkgo biloba* chalcone synthase gene promoter in transgenic tobacco

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ABSTRACT. The regulative sequence (2273 bp) of the chalcone synthase gene promoter of *biloba* was cloned by genomic walking. A 2273-bp promoter 5' upstream translation start site of *GbCHS* was cloned and designated as *GbCHSP*. pBI121+*CHSP:GUS* and pBI121-*35S:GUS* were constructed and transformed into tobacco by LBA4404. We found that *GbCHSP* could drive transient expression of GUS in tobacco and differentially expressed in root, stem and leaf tissues of this plant. GUS activity regulated by the *CHSP* promoter were located in tissues (apical meristems) at the growing points of roots and stems. pBI121+*CHSP:GUS* could be induced by wounding, copper, UV-B, abscisic acid, and ethephon treatments of transgenic seedlings. This activity was weakly

inhibited by gibberellin. Deletion analysis of the *CHSP* promoter in transgenic tobacco showed that *CHSP1* complete promoter conferred a GUS expression and activity similar to that of 35 S(CaMV). GUS activity dropped dramatically when there were *CHSP4*, *CHSP5* constructs and was almost totally absent when the *CHSP6* construct was present. We conclude that the upstream sequence -1548 to -306 of *GbCHSP* is the main region for transcriptional regulation of the *CHS* gene and that it is activated by hormone and stress factors in *G. biloba*. These results will help us to understand the transcriptional regulatory mechanisms involved in *GbCHS* expression and flavonoid accumulation in *G. biloba*.

Key words: *Ginkgo biloba*; *CHSP*; Transgenic tobacco; Functional analysis

