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Homology-based analysis of the *GRAS* gene family in tobacco

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ABSTRACT. Members of the *GRAS* gene family are important transcriptional regulators. In this study, 21 *GRAS* genes were identified from tobacco, and were classified into eight subgroups according to the classification of *Arabidopsis thaliana*. Here, we provide a preliminary overview of this gene family in tobacco, describing the gene structure, gene expression, protein motif organization, phylogenetic analysis, and comparative analysis in tobacco, *Arabidopsis*, and rice. Using the sequences of 21 *GRAS* genes in *Arabidopsis* to search against the American tobacco genome database, 21 homologous *GRAS* genes in tobacco were identified. Sequence analysis indicates that these GRAS proteins have five conserved domains, which is consistent with their counterparts in other plants. Phylogenetic analyses divided the *GRAS* gene family into eight subgroups, each of which has distinct conserved domains and biological functions. Furthermore, the expression pattern of these 21 *GRAS* genes reveals that most are expressed in all six

tissues studied; however, some have tissue specificity. Taken together, this comprehensive analysis will provide a rich resource to assist in the study of GRAS protein functions in tobacco.

Key words: *GRAS* gene family; Gene structure; Protein motif analysis; Phylogenetic analysis; Gene expression pattern analysis; Tobacco

