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An R2R3-type MYB transcription factor, GmMYB29, regulates isoflavone biosynthesis in soybean

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Isoflavones comprise a group of secondary metabolites produced almost exclusively by plants in the legume family, including soybean [*Glycine max* (L.) Merr.]. They play vital roles in plant defense and have many beneficial effects on human health. Isoflavone content is a complex quantitative trait controlled by multiple genes, and the genetic mechanisms underlying isoflavone biosynthesis remain largely unknown. Via a genome-wide association study (GWAS) we identified 28 single nucleotide polymorphisms (SNPs) that are significantly associated with isoflavone concentrations in soybean. One of these 28 SNPs was located in the 5'-untranslated region (5'-UTR) of an R2R3-type MYB transcription factor, GmMYB29, and this gene was thus selected as a candidate gene for further analyses. A subcellular localization study confirmed that GmMYB29 was located in the nucleus. Transient reporter gene assays demonstrated that GmMYB29 activated the IFS2 (isoflavone synthase 2) and CHS8 (chalcone synthase 8) gene promoters. Overexpression and RNAi-mediated silencing of GmMYB29 in soybean hairy roots resulted in increased and decreased isoflavone content, respectively. Moreover, a candidate-gene association analysis revealed that 11 natural GmMYB29 polymorphisms were significantly associated with isoflavone contents, and regulation of GmMYB29 expression could partially contribute to the observed phenotypic variation. Taken together, these results provide important genetic insights into the molecular mechanisms underlying isoflavone biosynthesis in soybean.