

GENETIC BASIS OF ISOFLAVONE ACCUMULATION DURING SOYBEAN SEED DEVELOPMENT: SPECIAL FOCUS ON WATER-DEFICIT CONDITIONS

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ABSTRACT

Soybean (*Glycine max* [L] Merr.) seed isoflavones have long been considered a desirable trait to target in selection programs for their contribution to human health and plant defense systems. The plant synthesizes isoflavones in response to several biotic and abiotic stresses and, as a consequence, they are known to be tremendously influenced by environmental conditions. Attempts to modify seed isoflavone contents have not always produced the expected results because their genetic basis is polygenic and complex. Without any doubt, the tremendous variability that isoflavones display over locations and years has hindered the genetic basis underlying their synthesis and accumulation in seeds. Our findings suggest that isoflavone seed concentration is controlled by a complex network of multiple minor-effect loci interconnected by a dense epistatic map of interactions. We hypothesize that the magnitude and significance of the main and epistatic effects of the nodes in the network will vary depending on the genetic background and environmental conditions. In an attempt to unravel the genetic architecture underlying the traits studied, we searched on a genome-wide scale for genomic regions homologous to the most important identified isoflavone biosynthetic genes. Overall, we advanced the knowledge of the genetics underlying isoflavone synthesis. We also focus on knowing the mechanisms regulating isoflavone accumulation under drought conditions. It will be of vital importance for development of soybean varieties with increasing isoflavone seed content under low soil moisture levels.