Public Abstract
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Title:Genetic basis of isoflavone accumulation during soybean seed development: special focus on water-deficit conditions

Soybean is an important component of many foods and animal feeds. Compounds called isoflavones, a nutritional component of soybean seeds, have long been the focus of soybean breeding efforts due to their known roles in both human health and plant fitness. A continuing endeavor is being made to assess the properties derived from their consumption by humans, and is reflected in the numerous articles about the topic published every year. Unfortunately, efforts to either enhance or reduce the levels of isoflavones have been hampered by the extremely complex nature of the trait and the high level of environmental induced variability. In an attempt to better understand the underlying genetics of isoflavone accumulation, we performed a large scale analysis to identify genomic regions associated with isoflavone accumulation. We identified a number of such regions, which form a complex network controlling seed isoflavone levels. We also noted a strong interaction between these regions, a condition referred to as epistasis. The recent release of the whole genome sequence for soybean allowed the identification of putative candidate genes for a number of these genomic regions. Isoflavone seed content is known to be tremendously influenced by environmental conditions being temperature and water regime the two main factors, also likely associated with global climate change. Temperature is by far the most well studied factor affecting seed isoflavone accumulation but not much is known about accumulation under drought conditions other than it is significantly elevated by irrigation. Drought is an increasing problem in many regions of the world, thus knowing the factors affecting and the mechanisms regulating the seed isoflavone accumulation will be of vital importance for development of soybean varieties with increasing isoflavone seed content under low soil moisture levels. 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. As a consequence, attempts to modify seed isoflavone contents have not always produced the expected results because their genetic basis is polygenic and complex. Overall, we advanced the knowledge of the genetics underlying isoflavone synthesis. This work paves the way for future genetic studies to develop more efficient and effective breeding methods for fine control of soybean seed isoflavone levels.