Integrated physical mapping of the soybean genome: A tool for rapid identification of economically important genes.

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Investment in crop genomic science is justified by the existence of genus, species and cultivar specific genes with no known function. A subgroup, within this group of genes, is expected to be genes of agronomic and economic importance such as disease resistance genes, major yield determinates and genes that produce specific chemicals and components. Identification of members of the economically important gene subgroup has been painstakingly slow by conventional genetics and preliminary genomics. A microsattelite marker map, with about 600 mapped markers, is available in soybean. This anchored genetic map has been integrated with RFLP, RAPD, and AFLP marker maps (Shoemaker and Specht 1995; Mansur et al. 1996; Keim et al., 1996; Chang et al., 1997 Cregan et al., 1999). About 300 QTL conditioning traits of agronomic importance have been identified by about 15 groups over the last 10 years (Imsande et al., 1998; Soybase http://probe.nalusda.gov:8300). However, it is not feasible to fine-map and isolate large numbers of soybean genes by this technology.