P-10

Integration of sudden death syndrome resistance loci in the soybean genome

Hao-Xun Chang, Department of Plant, Soil, and Microbial Sciences, Michigan State University, Michigan, USA

Soybean sudden death syndrome (SDS) is a soil-borne disease that causes annual yield losses up to $669 million dollars. Two decades of effort in mapping SDS resistance has pointed to a quantitative interaction between soybean and the casual pathogen *Fusarium virguliforme* in the United States. Inconsistencies in screening methodologies and naming systems for quantitative trait loci (QTL) have resulted in confusion about the validity of QTL for SDS resistance. More than 50 QTL are reported in the literature, and with the recent addition of single nucleotide polymorphisms (SNPs), reproducibility has become questionable especially because SDS occurrence is highly variable and depends on environment. Accordingly, this study aims to integrate and compile mapping results for SDS. A schematic ideogram was generated for direct visualization of resistance QTLs, with eight regions being identified with at least three published citations. We propose that these regions be named as meta-Rfv (Resistance to *F. virguliforme*). Two regions of particular interests are the meta-Rfv18-01, which received the most literature support and co-localized with a soybean cyst nematode (SCN) resistance locus (*Rhg1*), and the meta-Rfv06-01, a region identified using a phytotoxic culture filtrate stem cutting assay and as SDS field evaluations. Future studies on these two regions may clarify the synergistic effects between SDS and SCN, and the genetics of soybean foliar resistance to SDS phytotoxins. In summary, meta-analysis simplifies the current status of SDS resistance mapping, and will be useful for future research and breeding programs.