Development of Transposon and Fast Neutron Mutants of Soybean for Functional Genomic Studies

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Soybean is a major plant source of protein and oil, can fix atmospheric nitrogen and produces important secondary metabolites beneficial for human health. The recently published whole-genome soybean sequence (Schmutz et al., 2010) identified 46,430 protein coding genes. A major future challenge will be assigning function to each of these genes, or at least identifying critical genes necessary for agronomic improvement. We are developing a collection of deletion, insertion and gene activation soybean mutants through transposon-based (mPing, Ac/Ds, Tnt1) and fast neutron mutagenesis. Our goal is to develop efficient resources for investigation of soybean gene function through forward and reverse genetics. Unlike transposon-tagged mutants, deletion mutants (e.g., induced by fast neutron irradiation) are not widely utilized because mutated genes are often difficult to identify. We are currently evaluating the utility of whole-genome, array-based oligonucleotide comparative genome hybridization (aCGH) to identify deleted genes in soybean. Using aCGH, we were able to confirm published deletion of FAD2-1A in M23, an X-ray mutant used for breeding for increased oleic acid content in soybean (Alt et al., 2005; Anai et al., 2008). Moreover, we were able to detect deletions ranging from one gene model to >2.5 Mb in our Fast Neutron mutant population.

Poster Number: