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Development of an mPing-based activation tagging system for soybean

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Development of a powerful mutagenesis system in soybean will facilitate identification of the genes responsible for agronomically important traits. An efficient mutagenesis system requires high germinal mutation rates, the ability to produce overexpression phenotypes (activation tagging), and the ability to readily identify the location of the mutations. We previously used the *mPing* transposable element from rice to create a mutagenized soybean population. This strategy showed that *mPing* induces mutations and preferentially inserts into gene-rich regions. While these original *mPing* mutagenesis lines were successful at generating some germinal insertions, they relied on the native *mPing* element, which generally produces recessive knockout phenotypes. In addition, the transposition rate in these populations was limited because they relied on the native transposase proteins from rice. In order to improve the system, we have developed a second-generation mutagenesis tool that incorporates an *mPing*-based activation tag. This activation tag carries the enhancer region from the *Fig Mosaic Virus*, allowing for upregulation of nearby genes. Thus, this population should be more efficient at altering gene expression, resulting in more dominant phenotypes than can be produced by knockout mutagenesis strategies. In addition, these lines contain hyperactive versions of *mPing* and modified *Pong* transposase proteins designed to induce higher rates of transposition. Evaluation of the transposition in these lines has shown that transposition is occurring. The lines showing the highest rates of germinal transposition are being developed into new mutagenic populations. A grow out of these plants will be included in the 2018 Mutant Finder Workshop to allow for identification of mutant phenotypes.