

Abstract

Identification of novel transposition insertion sites of the soybean transposon *Tgm9*

The US is the world leader in the production of soybeans, an important source of protein and oil for humans and animals. To increase soybean yield, it is important to identify and study genes that code for agronomically important traits, such as size and bacterial resistance. Currently, there is no library or collection of mutants available for the study of gene function in soybeans. Therefore, mutants in these genes must be found or made. Transposons are segments of DNA that can move within an organism's genome. When transposons move to a new location, they can cause mutations in genes and gene regulatory DNA. Studying these mutants can provide insight into the role or function of these genes. In our experiment, we tracked the movement of the DNA transposon *Tgm9* in the soybean genome. In the parent plants, with green stems and white flowers, *Tgm9* is inserted into a gene responsible for purple pigment. Movement of the transposon can be visualized by the presence of purple pigment in both stems and flowers. We wanted to identify plants where *Tgm9* may cause mutations to genes. To identify transposon insertion sites, a genome walking approach was taken. For this approach, genomic soybean DNA was first digested with restriction enzymes. Then adaptors were ligated to the digested DNA and regions containing the transposon were amplified with two rounds of PCR and sequenced. We identified *Tgm9* insertion sites in three independent soybean plants.