

Tool helps identify gene function in soybeans

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In the race for bioengineered crops, sequencing the genome could be considered the first leg in a multi-leg relay. Once the sequence is complete, the baton is passed forward to researchers to identify genes' functions. A draft sequence of the soybean genome is now available, and the complete genome will be available soon. Taking the next step in a new study, University of Missouri Interdisciplinary Plant Group researchers have demonstrated the applicability of a genomic tool for identifying gene function in soybeans. Understanding gene function in soybeans will ultimately benefit crop performance.

The new genomic tool uses transposons, which are fragments of DNA that can "hop around" the genome. When these fragments move, they often land within an existing gene sequence, causing a mutation, or disruption, in that gene's function. By "tagging" transposons, scientists have found that they can screen plants for visible mutations in important agronomic traits, such as seed composition or root growth.

By "tracing" a tagged transposon, scientists can easily identify the exact gene where any single mutation occurs. This technique has been successfully used in a number of plants, including maize and the model plant *Arabidopsis thaliana*. In the study, IPG scientists demonstrated the feasibility of this technique in the soybean.

"Studying gene function in soybeans presents special challenges because the plant is tetraploid, meaning it has extra copies of most genes," said IPG member Gary Stacey, lead author of the report and an investigator in the MU Christopher S. Bond Life Sciences Center. "Nevertheless, we

were able to create a number of plant variants containing different mutations and to identify a specific gene associated with a particular mutation, specifically male sterility."

Several of the scientists involved in the study were part of a team that was recently awarded a three-year, \$2.5 million grant from the National Science Foundation to test the feasibility of additional functional genomic techniques in soybean.

"Our goal is to create a repository that will be a resource for the soybean community to study gene function and that, in the long run, will aid in translating genomics data into information that will ultimately benefit crop performance," Stacey said.

Source: University of Missouri-Columbia

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