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Transmission of on-target and off-target mutations in a series of CRISPR/Cas9-induced soybean plants

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Identification and characterization of the genes and DNA sequence polymorphisms that underlie specific trait variants remains a challenge in soybean due to limitations in mutant resources and transformation capacities. We recently developed and screened a soybean fast neutron mutant population to identify mutants with alterations to plant morphology, architecture and seed composition. A combination of genome structural analysis and genetic mapping led to the cloning of two genes, one underlying an altered trichrome development phenotype and another underlying a high-sucrose/low-oil seed composition phenotype. Furthermore, candidate genes have been identified for short petiole and branch angle mutants. However, for most map-based cloning projects, we have difficulty validating the candidate genes that reside within a mapped interval. We have recently initiated experiments using targeted mutagenesis approaches with CRISPR/Cas9 to validate the candidate genes for specific traits. The challenges and opportunities for using this approach in soybean will be highlighted in this talk.