Public Abstract

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Graduation Term:FS 2016

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Degree:MS

Title:APPLICATION OF CRISPR/CAS9-MEDIATED GENOME EDITING FOR STUDYING SOYBEAN RESISTANCE TO SOYBEAN CYST NEMATODE

Soybean cyst nematode (SCN) Heterodera glycines has become one of the most economically important pathogens of soybean in the world. The main strategy of SCN management is planting resistant soybean cultivars. The main sources of resistance include plant introductions (PI) PI 88788 and PI 548402 (Peking) from the USDA germplasm collection. Rhg1 and Rhg4 represent two major SCN resistance QTLs in these soybean PIs. Peking-type resistance requires both Rhg1 and Rhg4 for resistance, while PI 88788-type resistance only requires Rhg1. In Peking-type resistance, at the Rhg4 locus on chromosome 8, a gene encoding an enzyme called serine hydroxymethyltransferase (GmSHMT08) has been confirmed to play a role in resistance to SCN. Additional copies of SHMT on different chromosomes have been identified, including a closely related SHMT gene on chromosome 5 (GmSHMT05), but the function of this gene in soybean remains to be determined. Although reverse genetic methods such as RNAi (RNA interference), TILLING (Targeting Induced Local Lesions in Genomes), and VIGS (Virus-Induced Gene Silencing) have been used effectively to study SCN resistance in soybean, limitations such as off-targeting, incomplete silencing, and background mutations can potentially complicate the analysis. In recent years, the novel genome editing CRISPR (clustered regularly interspaced short palindromic repeat)/Cas (CRISPR-associated) system has shown great promise for precise genome editing to generate knock-outs. In this study, type II CRISPR/Cas9 methods were evaluated as an approach to identify soybean genes with a role in SCN resistance by targeting GmSHMT08, as well as further characterize its function and that of GmSHMT05 in basal resistance and root development.