CRISPR-based genome editing to modify flowering time and nutritional traits in rice

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We are exploring strategies to optimize and deploy CRISPR/Cas9-based genome editing to rapidly validate genes underlying important QTLs and modify traits for rice improvement. The Crop Genome Editing Lab at Texas A&M is using *Agrobacterium*-mediated transformation of the southern U.S. rice variety Presidio for CRISPR/Cas9-based multiplexed editing. Three projects are highlighted: understanding interactions between genes controlling flowering time in rice, increasing the levels of resistant starch, and increasing lysine content in rice grains. Our team has pursued two editing projects to modify flowering time in rice: knocking out Hd3a and RFT1, and targeting six flowering time repressor genes, to develop gene edited progeny with different combinations of flowering time gene knockouts. Multiple mutations were observed and subsequent generations are being analyzed to better understand the roles of these genes in affecting heading date in a tropical japonica background. Resistant starch is not easily digestible and cereals with high resistant starch levels may be beneficial for human health. A second project employed multiplex editing of four starch branching enzyme (SBE) genes to increase levels of resistant starch in rice grains and better understand the relationship between high amylose and resistant starch content. Knockout mutations were identified across all four SBE targets in different combinations, leading to a 15% increase in resistant starch in several edited lines. Lastly, genes downstream of lysine in the lysine biosynthesis pathway were targeted for knockout to increase lysine content in rice grains, with transgenic lines currently undergoing characterization.

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