CRISPR/Cas Genome Editing for Rice Functional Genomics and Trait Improvement

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During the past decade, the bacterial cluster regularly interspaced short palindromic repeats(CRISPR)/CRISPR-associated (Cas) system has emerged as the most powerful and popular technology for genome engineering due to its simplicity, versatility and broad applicability. To facilitate functional genomic analysis and crop improvement, we have adapted and improved various CRISPR/Cas9 toolkits (e.g., multiplex editing, base editing and prime editing) for efficient and precise genome editing in rice plants. Particularly, the polycistronic tRNA-gRNA (PTG) strategy was developed for efficient multiplex genome editing based on the endogenous tRNA processing system. In addition, base editors and prime editors have been successfully used to allow accurate nucleotide substitutions, allele replacement and epitope tagging of endogenous proteins in rice. Targeted mutation of single rice genes and generation of a rice receptor kinase mutant library have enabled functional discovery of protein kinases and disease resistance genes. By precisely editing a rice resistance gene or fine-turning specific gene promoters and kinase activities, the CRISPR/Cas technology has been shown to hold great promise to improve commercial rice cultivars for high yield, disease resistance and other agronomically important traits.