BOOSTING BASIC AND TRANSLATIONAL SCIENCE IN PLANTS WITH GENOME EDITING TOOLS

Yiping Qi, Department of Plant Science and Landscape Architecture, University of Maryland, College Park, MD 20742

Genome editing promises giant leaps forward in advancing biotechnology, agriculture, and basic research. The process relies on the use of sequence specific nucleases (SSNs) to make DNA double stranded breaks at user defined genomic loci, which are subsequently repaired by two main DNA repair pathways: non-homologous end joining (NHEJ) and homology directed repair (HDR). NHEJ can result in frameshift mutations that often create genetic knockouts. These knockout lines are useful for functional and reverse genetic studies but also have applications in agriculture. HDR has a variety of applications as it can be used for gene replacement, gene stacking, and for creating various fusion proteins. In recent years, Zinc Finger Nuclease (ZFN), transcription activator-like effector nucleases (TALEN) and clustered regularly interspaced palindromic repeats (CRISPR) and CRISPR associated protein 9 (Cas9) or CRISPR from Prevotella and Francisella 1 (Cpf1) have emerged one after the other as preferred SSNs. Here, I present our research work on these SSNs, particularly CRISPR systems, in plants. Looking ahead, there are enormous opportunities onimproving and applyingthese genome editing tools to advance plant science including plant pathology.