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Genome editing for crop improvement in ChinaXun Wei¹, Yiqiang Ge¹, Huijun Guo², Hongguan Zhao¹ and Luxiang Liu²¹China Rural Technology Development Center, China²Chinese Academy of Agricultural Sciences, China

Rapid development of genome editing technologies has provided an additional option for reverse genetics and gene functional understanding, which include Zinc-finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs) and clustered regularly interspaced short palindromic repeats/CRISPR-associated protein 9 (CRISPR/Cas9) system. These techniques have been applied in wheat (three *TaMLO* homologs), rice (*OsBADH2*, *OsPDS*, *Os02g23823* and *OsMPK2* genes), maize (*ZmPSY1*), soybean (*GmFT2a*) and other crops in China. The optimized RNA-guided endonuclease system based on CRISPR/Cas9 increased mutation frequency in T₀ transgenic plants up to 91.2% and could generate and spread desired mutations rapidly. The induced mutation by genome editing was heritable and resulted in phenotypic variation in subsequent hybridization and backcrossing. It has been used to generate mutations with target improved agronomic traits, such as powdery mildew resistance (strong resistance to tested virulent *Bgt* races) in wheat, smaller leaf angle (more than 50%) in maize, later flowering time (both long-day and short-day conditions) in soybean. This technology has showed great commercial potentialities because of transgene-clean progeny. A five-step guiding principle for genome edited crops has been recommended by scientists.

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