



Novelties in Gene Targeting in Plants

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Message from the Guest Editors

Dear Colleagues,

Genome targeting (GT) has become the cutting-edge technology for genome reconstruction. Initially, it was based on homologous recombination (HR) that is able to precisely introduce desired modifications within a target locus. However, higher plants predominantly use non-homologous end joining (NHEJ), an error-prone DNA repair mechanism that tends to cause mutations which are not predictable on the sequence level. It was shown some time ago that site-specific nucleases are able to induce double-strand breaks at particular loci and stimulate both NHEJ and HR. Site-specific nucleases based on the CRISPR/Cas system are the most important development in recent biotechnology for genome engineering due to their ease in application. Despite all the advantages of CRISPR-Cas, there are also some limitations, in particular, a limited range of mutations, mainly genetic knockouts, low efficiency of delivery of vectors or RNP complexes to plant cells, and so on. However, many of these limitations we previously overcome successfully. This issue highlights recent progress in GT technologies in plants.





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Message from the Editor-in-Chief

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