https://doi.org/10.17816/ecogen567885

The strong base for using base editing in plants

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The most common application of CRISPR-Cas9 genome editing system is a gene knockout via indel mutations introducing. It is obvious, because this approach has minimum critical conditions in guide RNA design: available PAM sequence and conservative 19–25 nucleotides within all alleles of a target gene. Precise nucleotide changing with base editing systems has more limitations: target nucleotide should locate in editing window of adenine- or cytidine-deaminase, besides this, all undesired adenines or cytosines in editing window will be likely changed. However, there is a more fundamental issue — it is very difficult to find a single aminoacid substitution, which changes protein features in a desirable side. One of the good examples of base editing target will be considered in this work.

Nicotiana tabacum L. is a plant from *Solanaceae* family, the same as potato, tomato and pepper. All these plants are strongly affected by potato virus Y (PVY). It is known, that PVY recruits host translation initiation factor eIF4E by the viral protein VPg in order to start synthesis its proteins. If eIF4E can't interact with VPg, plant will be resistant.

In our work, we established an aminoacid substitution in tobacco eIF4E factor, which disrupted interaction with PVY VPg in yeast two-hybrid conditions, but didn't influence the factor functionality. Then we designed two genetic constructions with different sgRNAs for introducing this mutation in tobacco plants using cytidine-deaminase system. These constructions were used to plant transformation and development of edited tobacco plants.

This work is supported by State Task No. 0431-2022-0004.

Keywords: CRISPR-Cas9; base editing; *Nicotiana tabacum*.

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