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## 近期发表论文

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### Genome-wide analyses of PAM-relaxed Cas9 genome editors reveal substantial off-target effects by ABE8e in rice

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#### Abstract

PAM-relaxed Cas9 nucleases, cytosine base editors and adenine base editors are promising tools for precise genome editing in plants. However, their genome-wide off-target effects are largely unexplored. Here, we conduct whole-genome sequencing (WGS) analyses of transgenic plants edited by xCas9, Cas9-NGv1, Cas9-NG, SpRY, nCas9-NG-PmCDA1, nSpRY-PmCDA1 and nSpRY-ABE8e in rice. Our results reveal that Cas9 nuclease and base editors, when coupled with the same guide RNA (gRNA), prefer distinct gRNA-dependent off-target sites. De novo generated gRNAs by SpRY editors lead to additional, but insubstantial, off-target mutations. Strikingly, ABE8e results in ~500 genome-wide A-to-G off-target mutations at TA motif sites per transgenic plant. ABE8e's preference for the TA motif is also observed at the target sites. Finally, we investigate the timeline and mechanism of somaclonal variation due to tissue culture, which chiefly contributes to the background mutations. This study provides a comprehensive understanding on the scale and mechanisms of off-target and background mutations occurring during PAM-relaxed genome editing in plants.

**Key words:** AM-relaxed Cas9 nucleases, cytosine base editor, adenine base editor, off-target effect, whole-genome sequencing, genome editing, rice

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