

Robust CRISPR/Mb2Cas12a genome editing tools in cotton plants

Fengjiao Hui¹, Xu Tang², Bo Li³, Muna Alariqi¹, Zhongping Xu¹, Qingying Meng¹, Yongxue Hu¹, Guanying Wang¹, Yong Zhang², Xianlong Zhang¹, Shuangxia Jin¹

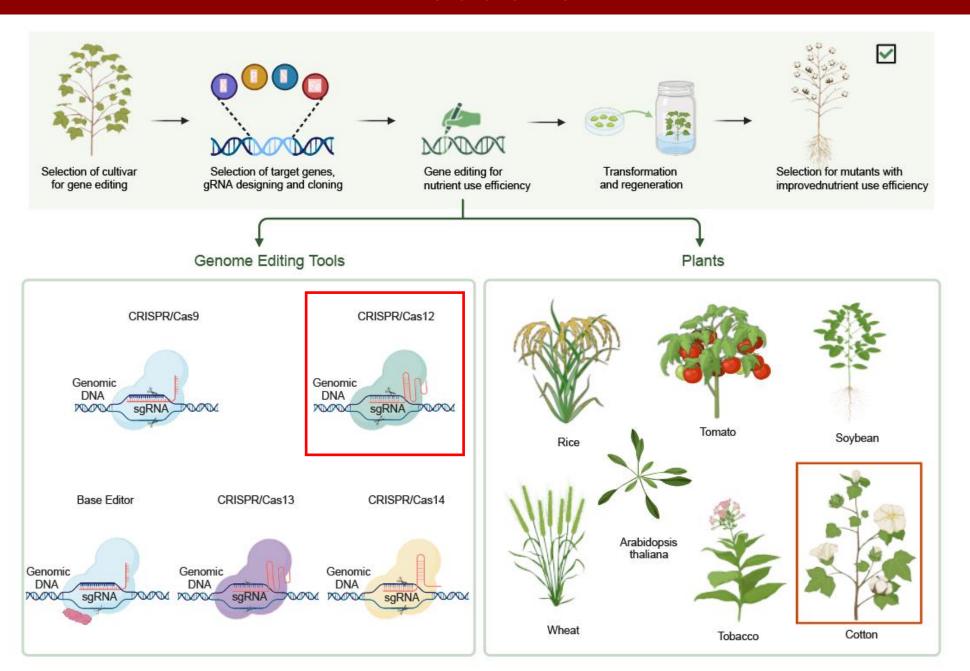
¹National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan, China ²School of Life Sciences, Southwest University, Chongqing, China ³Institute of Nuclear and Biological Technology, Xinjiang Academy of Agricultural Sciences, Urumqi, China



Fengjiao Hui, Xu Tang, Bo Li, Muna Alariqi, Zhongping Xu, Qingying Meng, Yongxue Hu, Guanying Wang, Yong Zhang, Xianlong Zhang, and Shuangxia Jin. 2024. Robust CRISPR/Mb2Cas12a genome editing tools in cotton plants. iMeta 3: e209. https://doi.org/10.1002/imt2.209

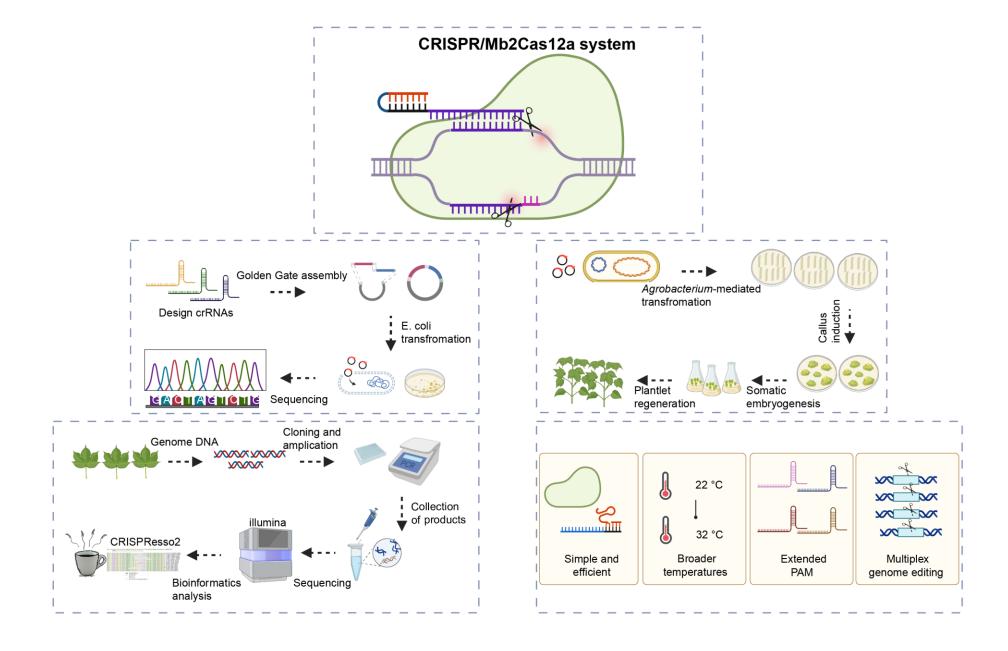


Introduction





Graphical Abstract





Results: Enable highly effective targeted mutations

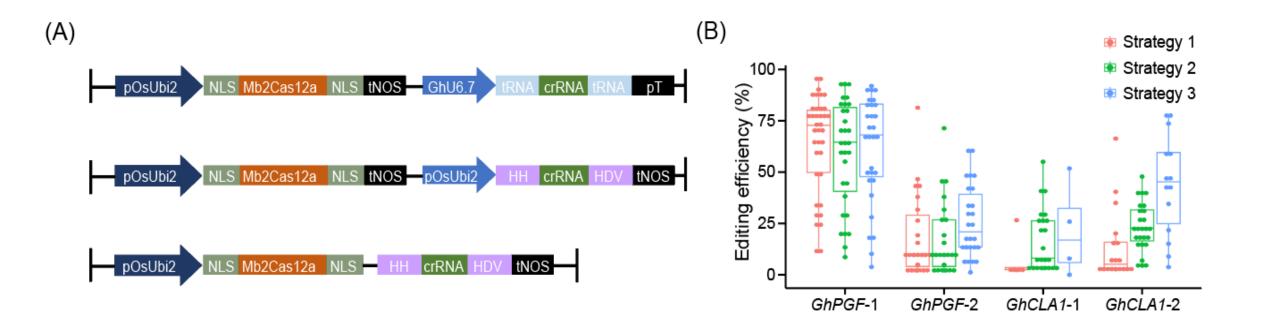
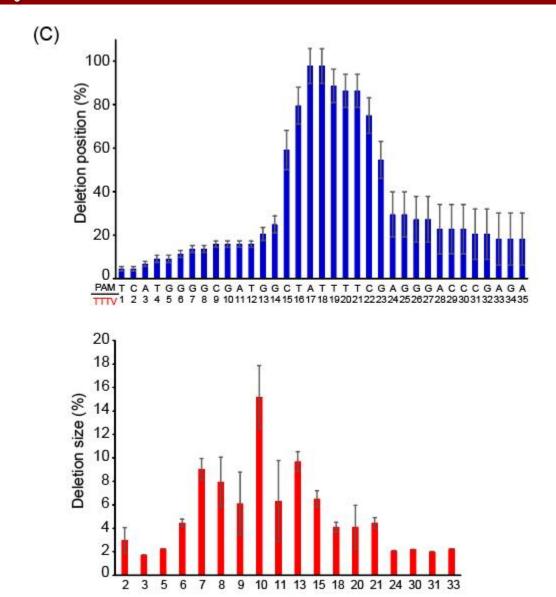
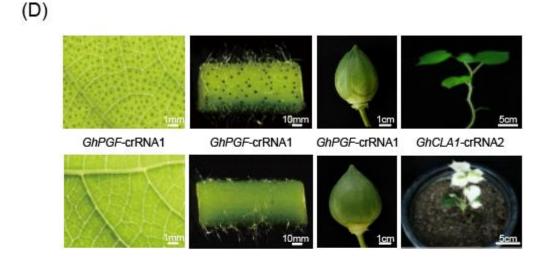


Figure 1. (A) A schematic illustration of the T-DNA region of the CRISPR/Mb2Cas12a binary vector for single site targeted editing. (B) Editing efficiency (%) at target sites of *GhPGF* and *GhCLA1* with different vectors.



Results





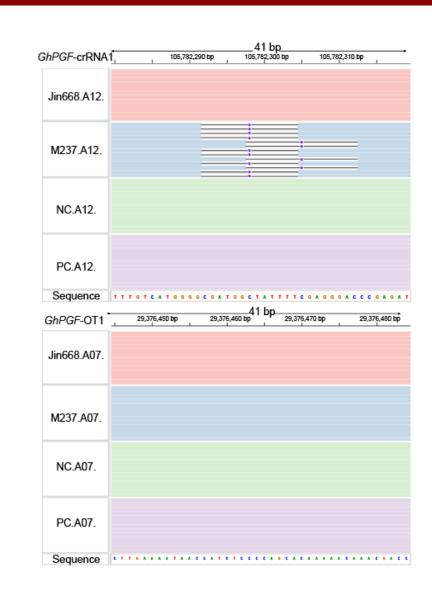
- ☐ The main editing window of Mb2Cas12a ranged from 13 to 26 nt downstream of the PAM sites;
- ☐ The deletion sizes mainly ranging from 7 to 18 bp;
- ☐ The density of gossypol glands in both the leaf and stem tissues was significant decreased;
- □ Plants carrying the *GhCLA1*-crRNA2 component exhibited a partially bleached phenotype on their leaves.

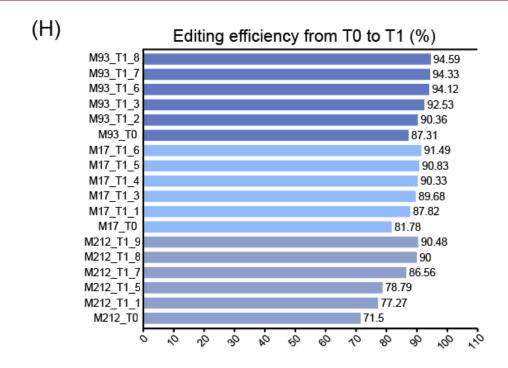
Figure 1. (C) Frequency of DNA deletion position and size at the target site of *GhPGF*-crRNA1 induced by Mb2Cas12a. (D) Phenotype of the T0 cotton plants with the target mutations in *GhPGF* and *GhCLA1*.



(E)

Results: Target specificity and genetic stability





- No off-target mutation was detected at any predicted off-target sites;
- ☐ The genotypes at the edited loci in cotton plants were faithfully inherited from the T0 to the T1 progeny

Figure 1. (E) Evaluation of potential off-target editing through whole genome sequencing technology. (H) Determination of the target mutation efficiency at the *GhPGF*-crRNA1 target site in T1 lines using NGS.



Results

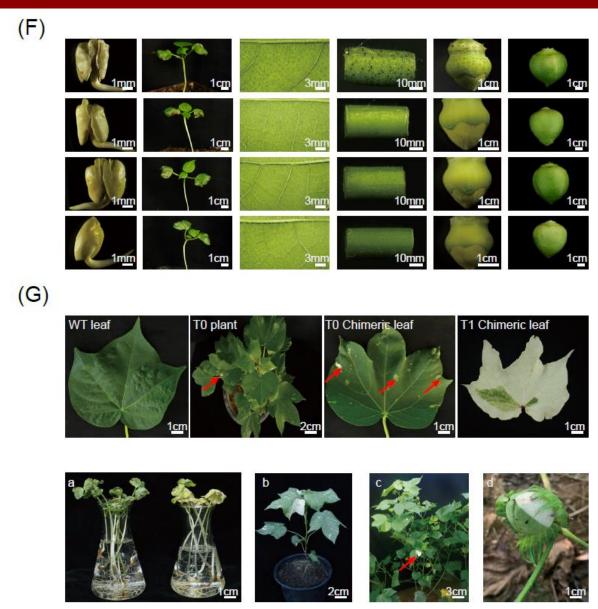


Figure 1. (F) Phenotypic characterization of T1 lines at the *GhPGF*-crRNA1 site. (G) T1 cotton plants with mutations in *GhCLA1*-crRNA2 site showed leaf bleaching in different environments.



Results: Exhibit wide temperature adaptability

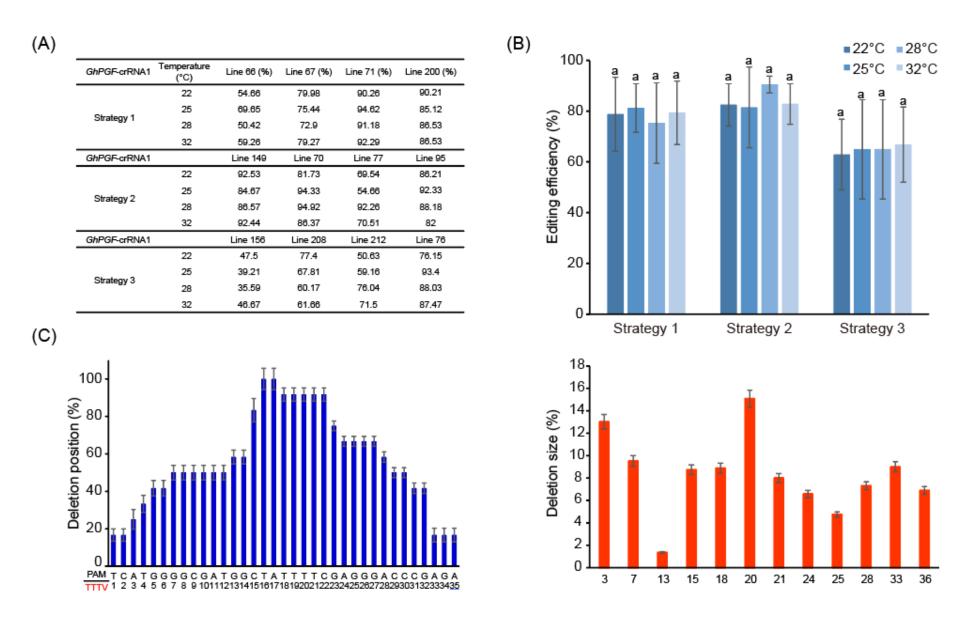
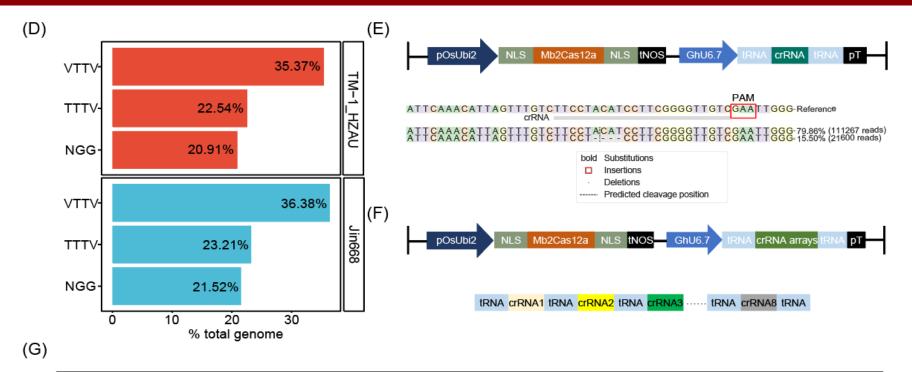


Figure 2. Wide temperature tolerance and multiplex genome editing by Mb2Cas12a in cotton.



Results: Expands the scope of cotton genome editing



Strategy	Target	Gene	crRNA	No. of transgenic events identified	Editing efficiency	No. of events with edited
Strategy 1 with TTTV	crRNA1	GhPGF	TCATGGGGCGATGGCTATTTTCG	79	1.8-39.7%	29 (42.03%)
	crRNA2	GhPGF	TCTTCCTACATCCTTCGGGGTTG	79	4.93-5.47%	2 (2.53%)
	crRNA3	GhCLA1	TCTGCCAACTGCCAATCTCGACG	79	7.46%	1 (1.45%)
	crRNA4	GhTAC1	CTGGAACAAGTGGCACTGGTTGA	79	1.82-17.93%	6 (8.70%)
	crRNA5	GhTAC1	ATGGGACGTGAATCCTCGCCAAC	79	4.08-26.43%	33 (47.83%)
	crRNA6	GhMYB25	GCAAATGAGCCGCAATAGCCGAC	79	1.06-19.92%	28 (40.58%)
	crRNA7	GhMYB25	GTAGCATGAGCCAAACCAACATC	79	10.02-71.47%	59 (85.51%)
	crRNA8	GhFAD	ACTTTCTCCCACAACCCTTTTCC	79	17.12-58.62%	60 (86.96%)



Summary

- CRISPR/Mb2Cas12 significantly enhances the capability and accuracy in cotton genome editing;
- Mb2Cas12a exhibits wide temperature adaptability;
- ☐ Mb2Cas12a greatly expands the scope of cotton genome editing;
- ☐ We have established an efficient multiplex genome editing system based on Mb2Cas12a.

Fengjiao Hui, Xu Tang, Bo Li, Muna Alariqi, Zhongping Xu, Qingying Meng, Yongxue Hu, Guanying Wang, Yong Zhang, Xianlong Zhang, and Shuangxia Jin. 2024. Robust CRISPR/Mb2Cas12a genome editing tools in cotton plants. iMeta 3: e209. https://doi.org/10.1002/imt2.209



Integrated meta-omics to change the understanding of the biology and environment

WILEY











"iMeta" is an open-access Wiley partner journal launched by iMeta Science Society consist of scientists in bioinformatics and metagenomics world-wide. iMeta aims to promote microbiome, and bioinformatics research by publishing research, methods/protocols, and reviews. The goal is to publish high-quality papers (top 10%, IF>20) targeting a broad audience. Unique features include video submission, reproducible analysis, figure polishing, bilingual, and promotion by social media with 500,000 followers. Since 2022 have been published 160 papers and cited > 2300 times. Index by ESCI, Google Scholar, DOAJ and Scopus.

Society: http://www.imeta.science

Publisher: https://wileyonlinelibrary.com/journal/imeta

Submission: https://wiley.atyponrex.com/journal/IMT2



office@imeta.science



iMetaScience





iMetaScience