

CORRESPONDENCE

Open Access

# Response to “Reproducibility of CRISPR-Cas9 methods for generation of conditional mouse alleles: a multi-center evaluation”



Hui Yang<sup>1\*</sup>, Haoyi Wang<sup>2\*</sup> and Rudolf Jaenisch<sup>3,4\*</sup>

This comment refers to the article available at <https://doi.org/10.1186/s13059-019-1776-2>.

\* Correspondence: [huiyang@ion.ac.cn](mailto:huiyang@ion.ac.cn); [wanghaoyi@ioz.ac.cn](mailto:wanghaoyi@ioz.ac.cn); [jaenisch@wi.mit.edu](mailto:jaenisch@wi.mit.edu)

<sup>1</sup>Institute of Neuroscience, State Key Laboratory of Neuroscience, Key Laboratory of Primate Neurobiology, CAS Center for Excellence in Brain Science and Intelligence Technology, Shanghai Research Center for Brain Science and Brain-Inspired Intelligence, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai 200031, China

<sup>2</sup>State Key Laboratory of Stem Cell and Reproductive Biology, Institute of Zoology, The Chinese Academy of Sciences, Beijing, China

<sup>3</sup>Whitehead Institute for Biomedical Research, Cambridge, MA, USA

Full list of author information is available at the end of the article

Gurumurthy et al. [1] recently reported that a method developed by Yang et al. to generate floxed allele (designated as “two donor method” by Gurumurthy et al.) [2] had poor reproducibility. They claimed that three centers could not reproduce our results on generating conditional alleles of the *Mecp2* locus and that the “two-donor method” had very low success rate on other loci.

Here, we provide our responses to these claims:

1. Our results on *Mecp2* locus published by Yang et al. have been reproduced by independent experiments in the Jaenisch (8–10% correct alleles), Yang (8% correct alleles) and Hatada’s groups (2–6% correct alleles) [3], respectively. In addition, multiple peer-reviewed publications [3–7] have successfully used this method to create conditional knockout (CKO) mice (9 out of 11 loci succeeded, 2.5% to 18% efficiency). We noticed that the efficiency of generating CKO mice by CRISPR/Cas9 could vary, which might due to different platform features or experiment conditions.
2. The conditions used by Gurumurthy et al. [1] do not correspond to the conditions used in our paper. The concentrations of CRISPR reagents used in the Gurumurthy et al.’s study [1] on the *Mecp2* locus (10 ng/μl for Cas9 mRNA, 10 ng/μl for sgRNA, and 10 ng/μl for oligos) were much lower (10-fold lower RNA and 20-fold lower oligo donor concentration) than those used in the Yang et al.’s experiments (Cas9 100 ng/μl, sgRNA 50 ng/μl and 100 ng/μl for each oligo) [2] and Yang et al.’s previous [8] and following publications [9–12]. It is well known that the concentrations of CRISPR reagents are well correlated with the genome editing efficiency.
3. We utilized piezo-driven zygote injection method in our original paper, which allows for injecting CRISPR components at much higher concentration. The difference between this method and pronuclear injection method used by Gurumurthy et al. might also contribute to the difference of successful rates.



© The Author(s). 2021 **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article’s Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article’s Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

In general, with any genome editing method or strategy being used, the efficiencies at different genomic loci are often highly variable. In the 2013 proof of concept paper, we showed the feasibility of generating floxed allele at *Mecp2* locus using CRISPR. To assume the efficiency we demonstrated at *Mecp2* locus will be directly translated to the success rate at other genomic loci seems premature.

We agree with the Gurumurthy et al.'s comment that the "one-donor method" offers higher success rate for generating floxed alleles in general, while the efficiency of "one-donor method" is also variable depending on the genomic loci and donor plasmid design. Before the publication of Gurumurthy et al., we also noted this, and developed a "one-donor method," termed "Tild-CRISPR" method [12], and demonstrated the feasibility and high efficiency in generating CKO mice. With the fast improvement of genome editing technologies, we and many others constantly optimize our protocols. We welcome all discussions about the choice of optimal strategy for particular applications, however, we think the reproducibility of any published work can only be validated by using the exact same experimental methods and technical parameters.

#### Acknowledgements

Not applicable.

#### Authors' contributions

HY, HW, and RJ wrote the paper. The authors read and approved the final manuscript.

#### Declarations

#### Competing interests

The authors declare that they have no competing interests.

#### Author details

<sup>1</sup>Institute of Neuroscience, State Key Laboratory of Neuroscience, Key Laboratory of Primate Neurobiology, CAS Center for Excellence in Brain Science and Intelligence Technology, Shanghai Research Center for Brain Science and Brain-Inspired Intelligence, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai 200031, China. <sup>2</sup>State Key Laboratory of Stem Cell and Reproductive Biology, Institute of Zoology, The Chinese Academy of Sciences, Beijing, China. <sup>3</sup>Whitehead Institute for Biomedical Research, Cambridge, MA, USA. <sup>4</sup>Department of Biology, Massachusetts Institute of Technology, Cambridge, MA, USA.

Published online: 07 April 2021

#### References

1. Gurumurthy CB, O'Brien AR, Quadros RM, Adams J Jr, Alcaide P, Ayabe S, Ballard J, Batra SK, Beauchamp MC, Becker KA, et al. Reproducibility of CRISPR-Cas9 methods for generation of conditional mouse alleles: a multi-center evaluation. *Genome Biol.* 2019;20(1):171. <https://doi.org/10.1186/s13059-019-1776-2>.
2. Yang H, Wang H, Shivalila CS, Cheng AW, Shi L, Jaenisch R. One-step generation of mice carrying reporter and conditional alleles by CRISPR/Cas-mediated genome engineering. *Cell.* 2013;154(6):1370–9. <https://doi.org/10.1016/j.cell.2013.08.022>.
3. Horii T, Morita S, Kimura M, Terawaki N, Shibutani M, Hatada I. Efficient generation of conditional knockout mice via sequential introduction of lox sites. *Sci Rep.* 2017;7(1):7891. <https://doi.org/10.1038/s41598-017-08496-8>.
4. Pritchard CEJ, Kroese LJ, Huijbers IJ. Direct generation of conditional alleles using CRISPR/Cas9 in mouse zygotes. *Methods Mol Biol.* 2017;1642:21–35.
5. Bishop KA, Harrington A, Kouranova E, Weinstein EJ, Rosen CJ, Cui X, Liaw L. CRISPR/Cas9-Mediated Insertion of loxP Sites in the Mouse Dock7 Gene Provides an Effective Alternative to Use of Targeted Embryonic Stem Cells. *G3 (Bethesda).* 2016;6:2051–61.
6. Ma X, Chen C, Veevers J, Zhou X, Ross RS, Feng W, Chen J. CRISPR/Cas9-mediated gene manipulation to create single-amino-acid-substituted and floxed mice with a cloning-free method. *Sci Rep.* 2017;7(1):42244. <https://doi.org/10.1038/srep42244>.
7. Nakagawa Y, Sakuma T, Nishimichi N, Yokosaki Y, Yanaka N, Takeo T, Nakagata N, Yamamoto T. Ultra-superovulation for the CRISPR-Cas9-mediated production of gene-knockout, single-amino-acid-substituted, and floxed mice. *Biol Open.* 2016;5(8):1142–8. <https://doi.org/10.1242/bio.019349>.
8. Wang H, Yang H, Shivalila CS, Dawlaty MM, Cheng AW, Zhang F, Jaenisch R. One-step generation of mice carrying mutations in multiple genes by CRISPR/Cas-mediated genome engineering. *Cell.* 2013;153(4):910–8. <https://doi.org/10.1016/j.cell.2013.04.025>.
9. Yang H, Wang H, Jaenisch R. Generating genetically modified mice using CRISPR/Cas-mediated genome engineering. *Nat Protoc.* 2014;9(8):1956–68. <https://doi.org/10.1038/nprot.2014.134>.

10. Yao X, Wang X, Hu X, Liu Z, Liu J, Zhou H, Shen X, Wei Y, Huang Z, Ying W, Wang Y, Nie YH, Zhang CC, Li S, Cheng L, Wang Q, Wu Y, Huang P, Sun Q, Shi L, Yang H. Homology-mediated end joining-based targeted integration using CRISPR/Cas9. *Cell Res.* 2017;27(6):801–14. <https://doi.org/10.1038/cr.2017.76>.
11. Yao X, Liu Z, Wang X, Wang Y, Nie YH, Lai L, Sun R, Shi L, Sun Q, Yang H. Generation of knock-in cynomolgus monkey via CRISPR/Cas9 editing. *Cell Res.* 2018;28(3):379–82. <https://doi.org/10.1038/cr.2018.9>.
12. Yao X, Zhang M, Wang X, Ying W, Hu X, Dai P, Meng F, Shi L, Sun Y, Yao N, Zhong W, Li Y, Wu K, Li W, Chen ZJ, Yang H. Tild-CRISPR allows for efficient and precise gene knockin in mouse and human cells. *Dev Cell.* 2018;45(4):526–36 e525. <https://doi.org/10.1016/j.devcel.2018.04.021>.

### **Publisher's Note**

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.