

CORRECTION

Open Access



Correction to: Redefining mouse transgenesis with CRISPR/Cas9 genome editing technology

Gaetan Burgio

Correction

In the recent Research Highlight [1], it has been highlighted that part b of Fig. 1 was incorrectly labelled as “sgRNA + tracrRNA” instead of “sgRNA (crRNA + tracrRNA)”. An updated Fig. 1, including also the amended figure legend has therefore been provided below.

Additionally, in the section entitled, “Rapid and efficient generation of conditional alleles using Easi-CRISPR”, there is a sentence currently written:

“This technique, called efficient addition with ssDNA inserts-CRISPR (Easi-CRISPR), involves targeting by two sgRNAs which flank the endogenous exon and are complexed with Cas9 to form a ribonucleoprotein complex for cellular delivery”.

This is incorrect and should read:

This technique, called efficient addition with ssDNA inserts-CRISPR (Easi-CRISPR), involves targeting by two synthetic sgRNAs (crRNA/tracrRNA) which flank the endogenous exon and are complexed with Cas9 to form a ribonucleoprotein complex for cellular delivery.

I apologise for these errors which have been acknowledged and corrected in this Correction article.

Published online: 26 March 2018

Reference

1. Burgio G. Redefining mouse transgenesis with CRISPR/Cas9 genome editing technology. *Genome Biol.* 2018;19(1):27.

Correspondence: Gaetan.burgio@anu.edu.au

Department of Immunology and Infectious Disease, The John Curtin School of Medical Research, The Australian National University, Canberra, Australia



© The Author(s). 2018 **Open Access** This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. 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.

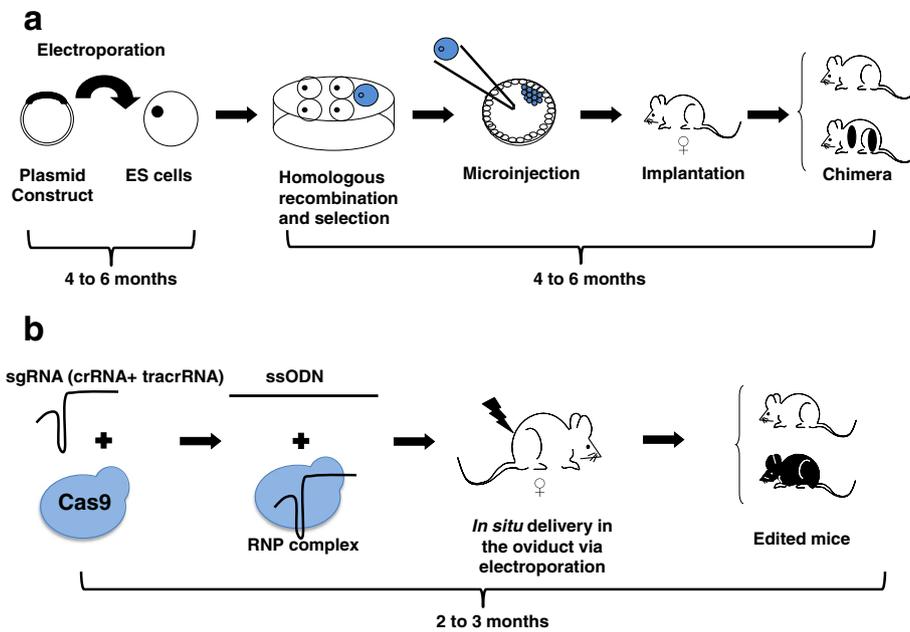


Fig. 1 a Generation of knockout and knockin alleles using embryonic stem (ES) cell technology in mice. A cloning procedure is undertaken to insert the construct into a plasmid vector as a template to replace the endogenous locus. This template could be a drug-selection cassette only (knockout) or an exon flanked with two loxP sites, or a more complex feature (knockin). These vectors contain a positive and negative selection cassette. The plasmid is then electroporated into the ES cells and then drug selected *in vitro*. After verification that the sequence is correctly inserted, the cells are microinjected into a blastocyst, before being surgically transferred into pseudopregnant females. The chimeric progenies will be genotyped to ensure the expected construct is correctly inserted into the genome by homologous recombination. **b** Generation of complex alleles using improved-genome editing via oviductal nucleic acid delivery (*i*-GONAD) technology. One or two single guide RNAs (sgRNA) are designed to either disrupt a critical exon (knockout) or remove an entire exon for replacement with a repair template (knockin). The sgRNAs (crRNA/tracrRNA) are synthesized, or *in vitro* transcribed, and then complexed with the tracrRNA and then Cas9 protein to form a ribonucleoprotein (RNP) complex. The RNPs are *in situ* electroporated with a long single-stranded oligonucleotide repair template (ssODN) into the oviduct of a pregnant female. The progenies are genotyped to ascertain successful editing of the gene of interest