Efficient generation of a single-copy \textit{eft-3p::TIR1::F2A::BFP::AID*::NLS} allele in the \textit{C. elegans ttTi5605} insertion site through recombination-mediated cassette exchange

An A. Vo\textsuperscript{1}, Max T. Levenson\textsuperscript{1}, James Matthew Ragle\textsuperscript{1} and Jordan D. Ward\textsuperscript{1§}

\textsuperscript{1}Department of Molecular, Cell, and Developmental Biology, University of California – Santa Cruz, Santa Cruz, CA, USA

\textsuperscript{§}To whom correspondence should be addressed: jward2@ucsc.edu

Abstract

The auxin-inducible degron (AID) system is a widely used system to conditionally deplete proteins. Using CRISPR/Cas9-based genome editing in \textit{C. elegans}, we recently generated a set of single-copy, tissue-specific and pan-somatic TIR1-expressing strains carrying a BFP reporter inserted in single-copy into two commonly used, well-characterized genetic loci. However, we were unable to obtain a strain carrying a pan-somatic \textit{eft-3p::TIR1::F2A::BFP::AID*::NLS} transgene inserted into the chromosome II \textit{ttTi5605} insertion site. Using recombination-mediated cassette exchange (RMCE) we were able to efficiently obtain this knock-in. The resulting strain displayed equivalent depletion of an AID*::GFP reporter compared to our previously generated \textit{eft-3p::TIR1::F2A::BFP::AID*::NLS} transgene knocked into the chromosome I \textit{ttTi4348} insertion site. This work highlights the power of RMCE for generating new reagents for the AID system and provides an \textit{eft-3p::TIR1::F2A::BFP::AID*::NLS} allele on chromosome II which will simplify genetic crossing schemes when using the AID system.
Methods
generation of single-copy transgenes at defined loci (Nonet 2020). Our chromosome I was almost undetectable after two hours of exposure, similar to what we reported for control animals, but dropped significantly in animals exposed to 4 mM auxin displayed a severe reduction of BFP and GFP by 120 minutes post-treatment (Figure 1A). We confirmed these results with an anti-GFP western blot (Figure 1B). GFP levels were stable in control animals, but dropped significantly in animals exposed to 4 mM auxin. We then generated an integration vector containing an RMCE uses a germline-expressed Flp recombinase to insert transgenes into specialized integration landing sites (Nonet 2020). We developed a TIR1::F2A::BFP::AID*::NLS transgene (Ashley et al. 2021) which in an F2A ribosome skip sequence allows production of separate TIR1 and BFP::AID*::NLS proteins from a single mRNA transcript (Ryan and Drew 1994; Ryan et al. 1999; Donnelly et al. 2001; de Felipe et al. 2003; Ahier and Jarriault 2014). The use of a BFP reporter allows for depletion experiments while imaging red and green fluorescent proteins (Ragle et al. 2020). TIR1 expression can be monitored by nuclear-localized BFP and the AID* sequence allows detection of TIR1 activity by auxin-dependent BFP depletion (Ashley et al. 2021). We previously inserted tissue-specific (germline, intestine, neuron, muscle, hypodermis, seam cell) TIR1::F2A::BFP::AID*::NLS transgenes into standardized genetic loci on chromosomes I and II (ttTi4348 and ttTi5605). We attempted to generate a chromosome II single-copy TIR1 strain through recombination-mediated cassette exchange (RMCE), an alternate genome editing method (Nonet 2020). RMCE uses a germline-expressed Flp recombinase to insert transgenes into specialized integration landing sites (Nonet 2020). As there are now a number of landing sites, a single integration vector can be used to generate insertions into multiple genomic loci. We generated an integration vector containing an eft-3p::TIR1::F2A::BFP::AID*::NLS transgene, inserted it into a strain carrying a landing pad in the ttTi5605 insertion site in chromosome II (M. Nonet, https://sites.wustl.edu/nonetlab/rmce-insertion-strains), and recovered a single knock-in from 30 injected animals on our first attempt. We expect that we can improve on this knock-in rate and move closer to the reported efficiency of injecting seven animals to achieve a knock-in. We then generated an eft-3p::TIR1::F2A::BFP::AID*::NLS transgene and performed a depletion time course to validate the TIR1 allele. At the 0 minute timepoint, we observed nuclear-localized BFP, indicating that the eft-3p::TIR1::F2A::BFP::AID*::NLS transgene was being transcribed and translated (Figure 1A). In control treated animals we observed no detectable change in BFP or GFP by microscopy (Figure 1A). In contrast, animals exposed to 4 mM auxin displayed a severe reduction of BFP and GFP by 120 minutes post-treatment (Figure 1A). We confirmed these results with an anti-GFP western blot (Figure 1B). GFP levels were stable in control animals, but dropped after 30 minutes of auxin exposure and were almost undetectable after two hours of exposure, similar to what we reported for our chromosome I eft-3p::TIR1::F2A::BFP::AID*::NLS transgene (Ashley et al. 2021). This new TIR1 strain should complement our original chromosome I eft-3p::TIR1::F2A::BFP::AID*::NLS strain and provide a new allele on a separate chromosome to facilitate genetic crossing schemes. This work also highlights the effectiveness of the RMCE method for generation of single-copy transgenes at defined loci (Nonet 2020).
Request a detailed protocol

Worm culture

Animals were maintained on MYOB (Church et al. 1995) seeded with OP50, similar to previously described methods (Brenner 1974). 4 mM auxin plates were made by diluting 20 µl of 1 M K-NAA (1-Naphthaleneacetic Acid, Potassium Salt, Phyto-Technology Laboratories, N610)(Martinez and Matus 2020; Martinez et al. 2020) in 100 µl of M9 and adding to a well of a 6-well MYOB plate seeded with OP50 (5 ml volume). The plate was allowed to dry for two hours before use. For the time course experiments in Figure 1, JDW346 animals were synchronized by alkaline bleaching and released on 10 cm MYOB plates at a density of 2000 worms/plate for 26 hours at 25°C. Animals were then shifted to 6-well plates (control or 4 mM auxin). 480 animals/well were plated to collect for western blots, 72 animals/well were plated to collect for imaging. Animals were collected at 0, 30, 60, and 120 minutes following the shift onto control or auxin plates. Animals were late L3 at the start of the time course as determined by animal size and examining vulval precursor cells.

Imaging and analysis

Animals were picked into a 20 µl drop of M9+5 mM levamisole on a 2% agarose pad and secured through a cover slip. Images were acquired using a Plan-Apochromat 63x/1.40 Oil DIC lens on an AxioImager M2 microscope (Carl Zeiss Microscopy, LLC) equipped with a Colibri 7 LED light source and an Axiocam 506 mono camera. Acquired images were processed through Fiji software (version: 2.0.0-rc-69/1.52p).

Western blotting

Western blots were performed as described in Ashley et al., 2021. At each timepoint 480 animals were washed out of a well of a control or auxin plate with 1 ml of M9+0.05% gelatin. Animals were transferred to a 1.5 ml tube, washed twice in M9+0.05% gelatin, pelleted, resuspended in 40 µl of M9+0.05% gelatin, and freeze-cracked in liquid nitrogen twice. Laemmli sample buffer was added to 1X and samples were heated to 95°C for 10 minutes. Ten microliters of lysate were resolved by SDS-PAGE using a precast 4-20% Mini-Protean TGX Stain Free Gel (Bio-Rad) before being transferred to a polyvinylidene difluoride membrane by semi-dry transfer with a TransBlot Turbo (Bio-Rad). Total protein, pre- and post-transfer, was monitored using the stain-free fluorophore as described (Posch et al. 2013; Ward 2015). Stain-free imaging of total protein was used to confirm equal loading. The blot was sequentially probed with rabbit anti-GFP antibody (Abcam, #ab290) diluted 1:1000 and a goat anti-Rabbit-HRP (Kindle Biosciences LLC, #R1006) diluted at 1:1000. SuperSignal™ Western Blot Substrate (Thermo Fisher Scientific, A45916) was added and the blot was imaged with a Bio-Rad ChemiDoc imaging system.

RMCE strain

NM5340 jsSi1579 [loxp rpl-28p FRT GFP::his-58 FRT3] II; unc-119(ed3) III; bqSi711 [mex-5p::FLP::SL2::mNG + unc-119(+)] IV was a gift from Dr. Michael Nonet and will be described elsewhere. For future RMCE experiments, strain NM5402 is recommended as it has the unc-119(ed3) allele outcrossed. The sequence of the jsSi1579 landing pad can be found on the Nonet lab website (https://sites.wustl.edu/nonetlab/rmce-insertion-strains/ -last edited 6-16-2021) and is inserted at an sgRNA within 50 basepairs away from the ttTi5605 insertion site.

Generation of an eft-3p:TIR1:F2A::BFP:AIM*:NLS::tbb-2 3'UTR transgene
eft-3p:TIR1:F2A::BFP:AIM*:NLS::tbb-2 3'UTR was PCR amplified using Phusion polymerase from pJW1441 (Ashley et al. 2021) using oligos 5530+5545 and the resulting product was DpnI digested and cloned into pLF3FShC using SapTrap (Schwartz and Jorgensen 2016; Nonet 2020). The plasmid was miniprepped using a Purelink Quick Plasmid Miniprep kit (Invitrogen, K21001) and injected into NM5340 germlines at 25 ng/µl. Candidate insertions were recovered as previously described (Nonet 2020). We outcrossed our initial insertion strain (JDW309) two times against a wildtype N2 strain to remove the unc-119(ed3) allele and the bqSi711 [mex-5p::FLP::SL2::mNG + unc-119(+)] IV transgene and generate JDW324. We confirmed loss of the bqSi711 transgene by a lack of mNeonGreen expression in the germline and loss of the unc-119(ed3) allele through wild-type animal morphology and movement. JDW324 L1 larvae were then heat-shocked to remove the SEC as previously described (Dickinson et al. 2015; Nonet 2020) which generated JDW313. JDW346 was made by crossing CA1204 males to JDW324. ieSi58 and jsSi1579 wrdSi63 were both homozygosed before the self-excising cassette was removed by heat-shock. The excised transgene can be genotyped by triplex PCR with oligos 6282+6284+6285 (see Reagents table) using a 60°C annealing temperature. The WT allele produces a 541 bp band, the SEC-excised knock-in produces a 343 bp band, and the primers genotype heterozygotes

Reagents

<table>
<thead>
<tr>
<th>Strain</th>
<th>Genotype</th>
<th>Available from</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

8/3/2021 - Open Access
<table>
<thead>
<tr>
<th>Oligo</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>5530</td>
<td>5' - actataggggatagcatcgtggagctctctgtgaagacttttctgctcggccac -3'</td>
</tr>
<tr>
<td>5545</td>
<td>5' - agtcttaagctcggcctcaataagctctctgtgaagacttttctgctcggccac -3'</td>
</tr>
<tr>
<td>6282</td>
<td>5' - agctcctaccgctcgtataac -3'</td>
</tr>
<tr>
<td>6284</td>
<td>5' - attgtttgcacctgctcggccac -3'</td>
</tr>
<tr>
<td>6285</td>
<td>5' - atgcaagacacccgagggttg -3'</td>
</tr>
</tbody>
</table>

**Acknowledgments:** We thank Michael Nonet for his gift of the unpublished NM5340 strain.

**References**


**Funding:** The work was supported by the NIH/ National Institute of General Medical Sciences R01 GM138701.
Author Contributions: An A. Vo: Formal analysis, Investigation, Methodology, Validation, Visualization, Writing - review and editing. Max T. Levenson: Investigation, Methodology, Writing - review and editing. James Matthew Ragle: Investigation, Methodology, Writing - review and editing. Jordan D. Ward: Formal analysis, Funding acquisition, Investigation, Methodology, Supervision, Validation, Visualization, Writing - original draft.

Reviewed By: Jonathan Pettitt

History: Received July 12, 2021 Revision received July 20, 2021 Accepted July 21, 2021 Published August 3, 2021

Copyright: © 2021 by the authors. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International (CC BY 4.0) License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Citation: Vo, AA; Levenson, MT; Ragle, JM; Ward, JD (2021). Efficient generation of a single-copy eft-3p::TIR1::F2A::BFP::AID*::NLS allele in the C. elegans ttTi5605 insertion site through recombination-mediated cassette exchange. microPublication Biology. https://doi.org/10.17912/micropub.biology.000425