



Developing CRISPR-Cas9 based genome-editing tools in entomopathogenic nematode

Steinernema carpocapsae

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Abstract

Steinernema carpocapsae is parasitic to insects and mutualistic to bacterial symbionts *Xenorhabdus nematophila*, therefore is valuable to study naturally-occurring microbial symbiosis. As genetic tools in *Xenorhabdus* bacteria proved to be powerful to reveal the mechanisms underlying bacteria-host interactions, the lack of genetic tools on *Steinernema* nematodes hampered the study in the molecular pathways regulating the host side of the symbiotic conversation. Here we present our attempts to establish a CRISPR-Cas9 based approach to introduce mutations in *S. carpocapsae* genes predicted to encode collagens in the nematode cuticle. We are presenting our progress in genome-editing of *S. carpocapsae* and current efforts aiming to develop CRISPR-Cas9 co-conversion markers in *S. carpocapsae* by introducing mutations that cause distinctive and heritable phenotypes. Our CRISPR-Cas9 based tools will open a new revenue to study molecular pathways in host-microbes signaling particularly in naturally occurring parasitic and mutualistic symbiosis.

Figure 1. The insect-nematode-bacteria tripartite symbiosis includes both parasitic and mutualistic symbiosis.

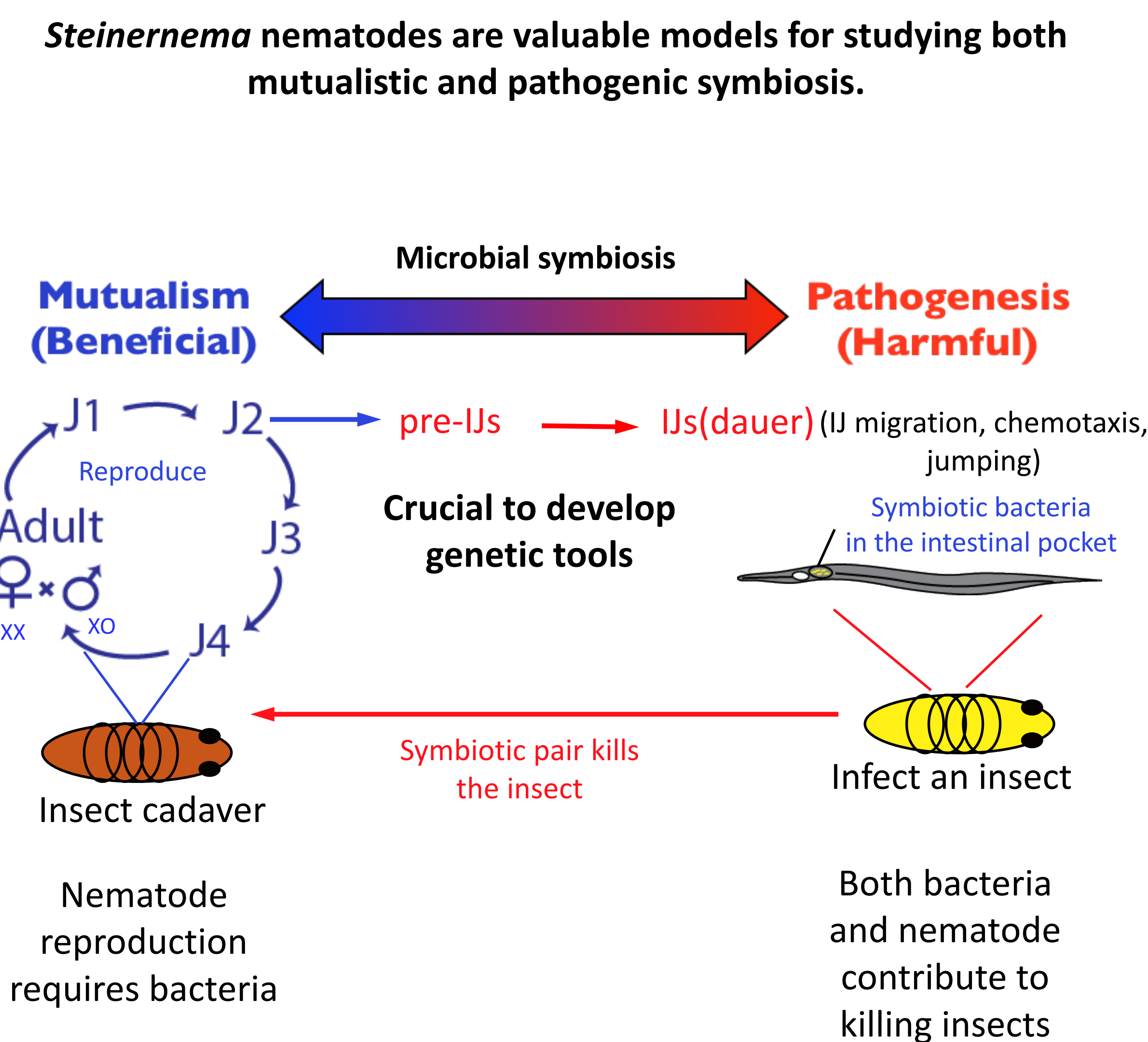


Figure 2. We choose cuticle collagen gene homologues to be targets of CRISPR-Cas9 based genome-editing in *S. carpocapsae*.

(A). We target homologous genes that might encode collagens in *S. carpocapsae* cuticle thus are likely to cause visible phenotypes.

	<i>SC-dpy-10</i> (X-linked) R70C target	<i>SC-rol-6.1</i> (non X-linked) R71C target
<i>S. carpocapsae</i>	LNELDFGKLVPLNRTERQAYN	SC GAGTASNRVRRQYGGYGATGVQPP
<i>C. elegans</i>	ALELYQGMKMRMTGNRTARGAYG	CE GAGTPSNRQRQAYGGYGATGSQPS
<i>C. briggsae</i>	ALELYQGMKMLSGNRTARGAYG	**** * * * * * * * * * *
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(B). We aim to develop a CRISPR-Cas9 method with template-based homologous repair to create missense mutations in *SC-dpy-10* and *SC-rol6.1*.

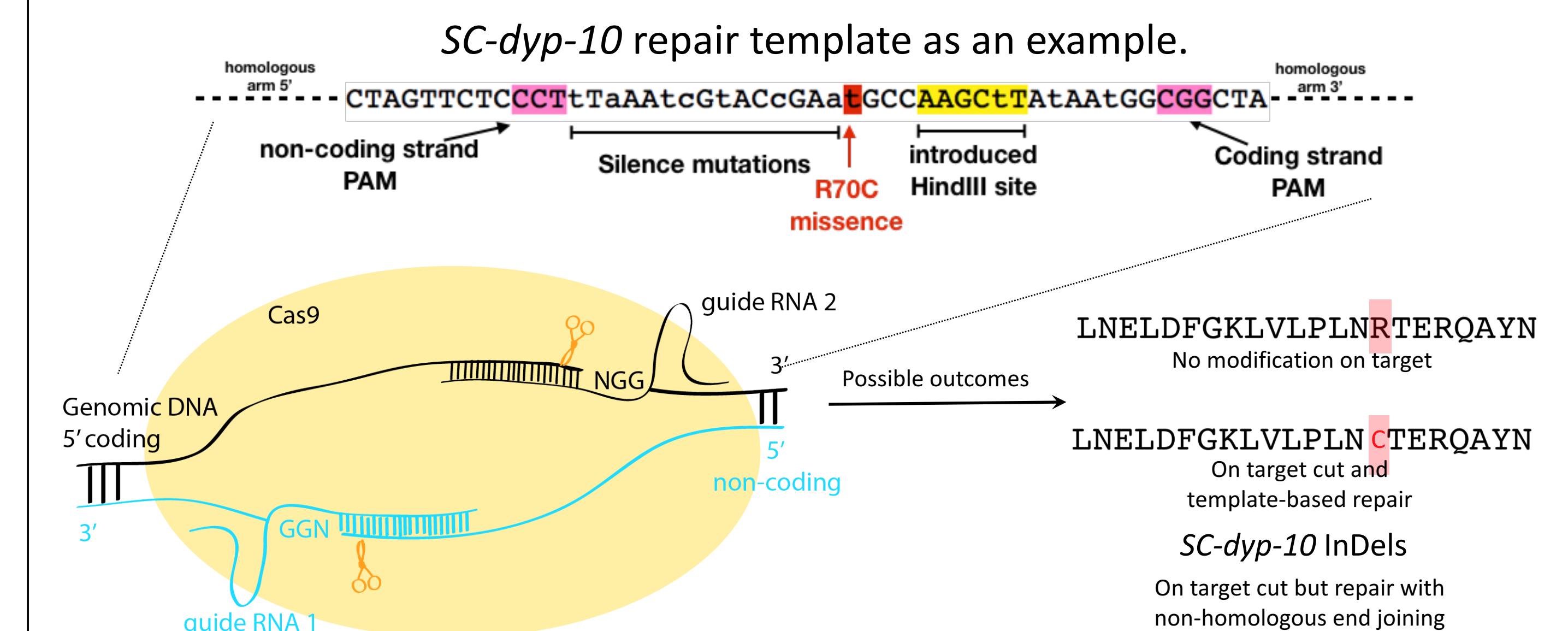
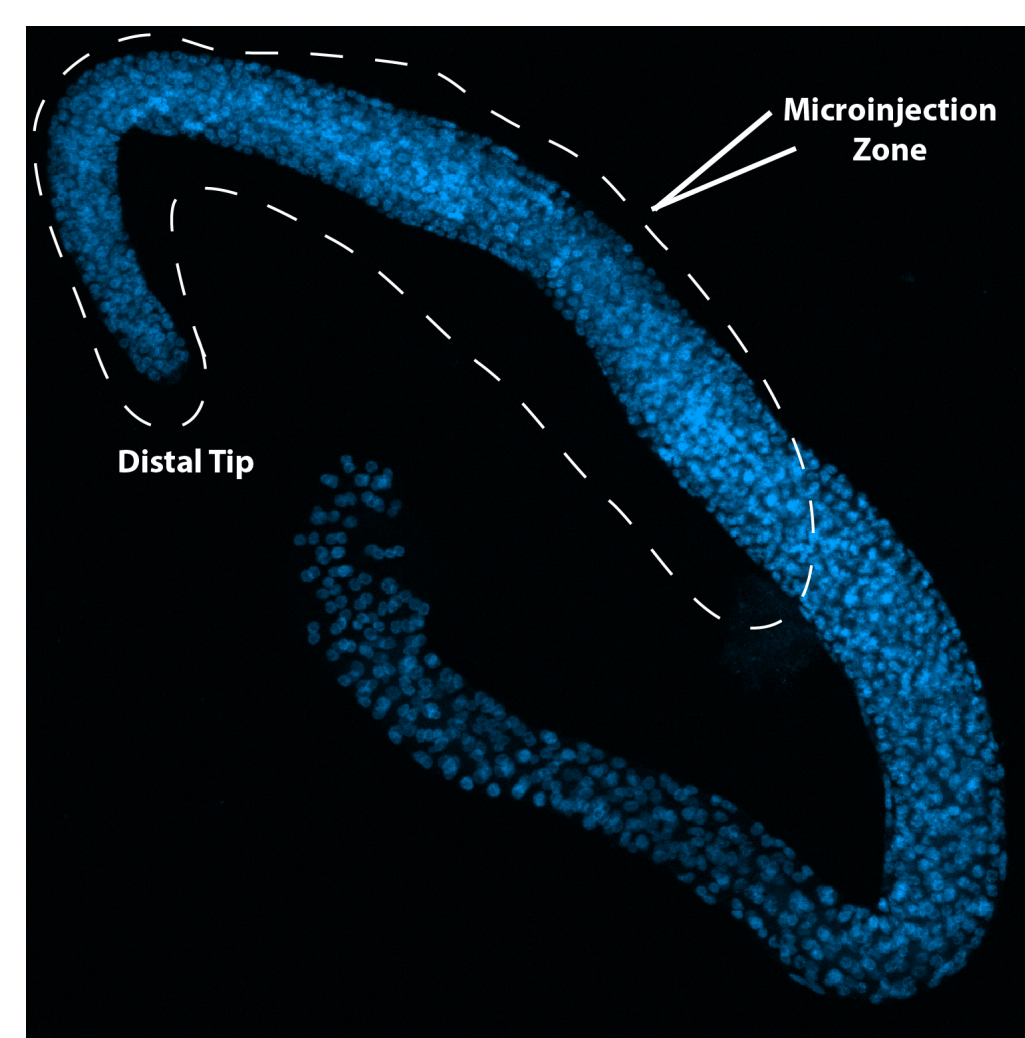


Figure 3. We perform gonadal microinjection to deliver CRISPR-Cas9 reagents.

(A). Gonadal arm of the adult female *S. carpocapsae* female might have a syncytia (z-stack video available upon request).



Left: One of the two gonadal arms dissected from an adult female stained with DAPI.

S. carpocapsae features long gonadal arms with highly packed germ cells.

Zone of microinjection in our preliminary trials is circled with dashed line.

Gonadal flow was observed during injection.

(B). A flow chart for gonadal microinjection in *S. carpocapsae* adult females.

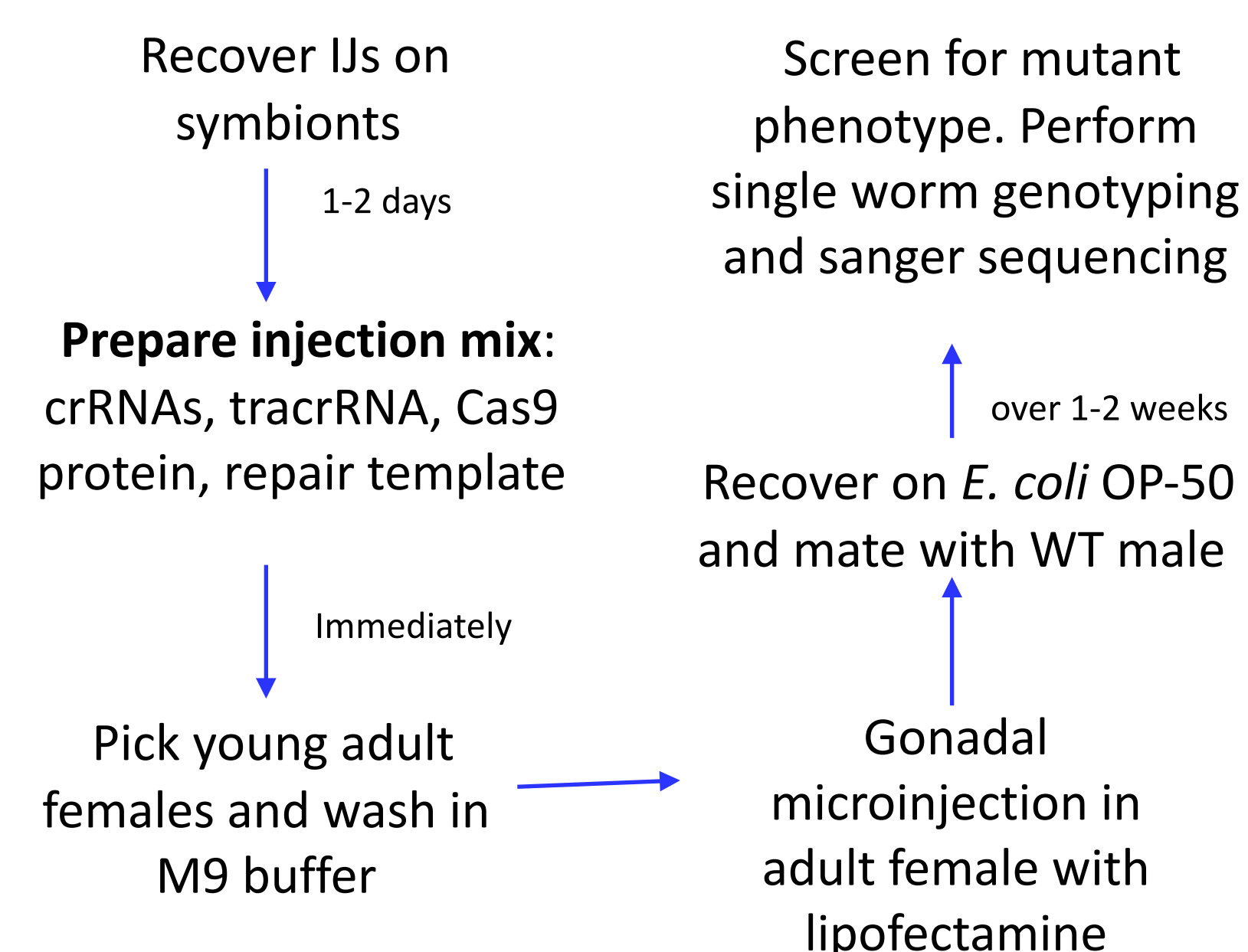


Figure 4. *SC-dpy-10* R70C mutation could be confirmed by sanger sequencing in F1 and F2 progenies.

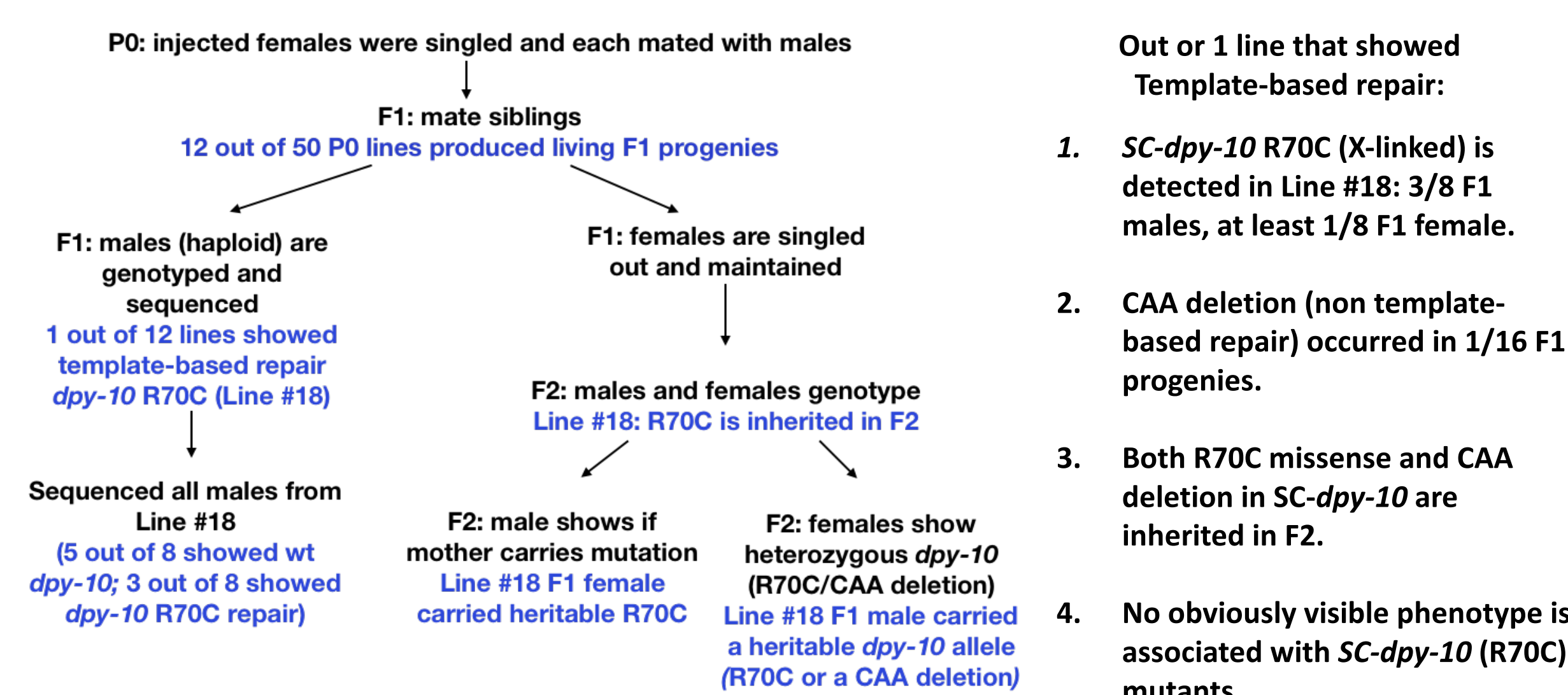


Figure 5. We observed cuticle-associated phenotypes in F1 progenies after our attempts to modify *SC-rol 6.1* by gonadal microinjection (Blisters are indicated by blue arrows).

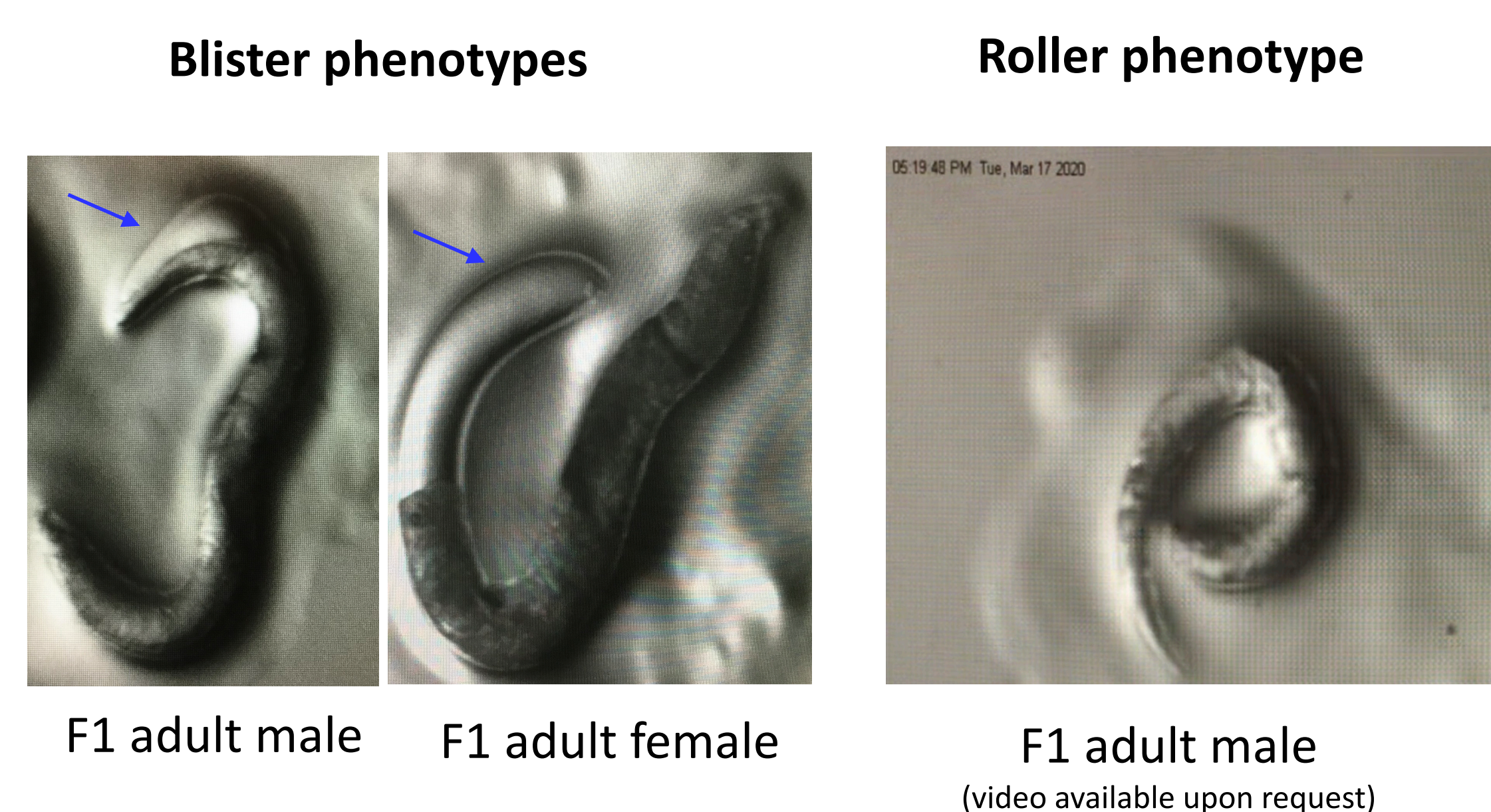


Figure 6. Current effort to better develop cuticle-associated mutants as *S. carpocapsae* Co-CRISPR markers (Alae: red arrow; Annuli: yellow arrow).

(A). Adapting the *C. elegans* "STOP-IN" cassette to create *S. carpocapsae* null mutants.

exogenous Cas9 target site stop codons in 3 reading frames NheI

5' -GGGAAGTTTGTCCAGAGCAGAGGTGACTAAGTGATAAGCTAGC-3'

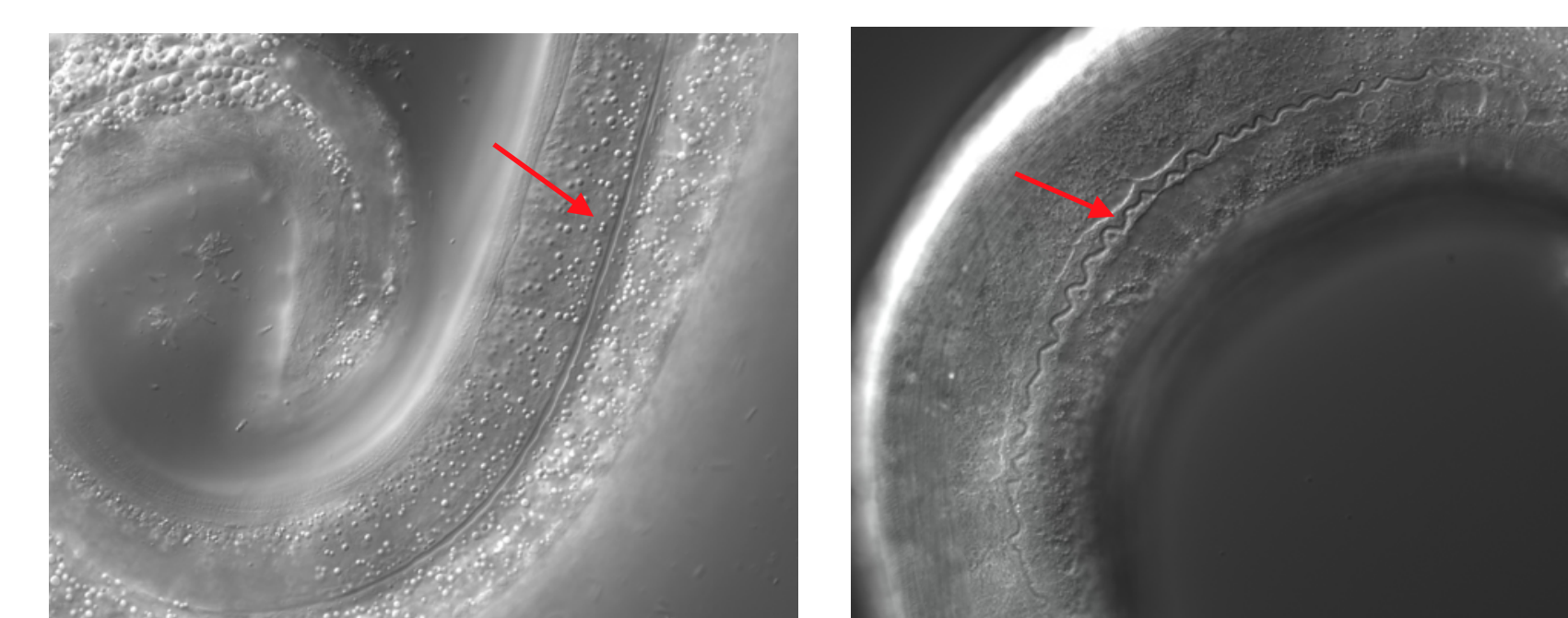
RF1: 5' -GGGAAGTTTGTCCAGAGCAGAGGTGACTAAGTGATAAGCTAGC-3'

RF2: 5' -GGGAAGTTTGTCCAGAGCAGAGGTGACTAAGTGATAAGCTAGC-3'

RF3: 5' -GGGAAGTTTGTCCAGAGCAGAGGTGACTAAGTGATAAGCTAGC-3'

Wang et al., 2018

Preliminary trial of STOP-IN in *S. carpocapsae* showed modified alae structure

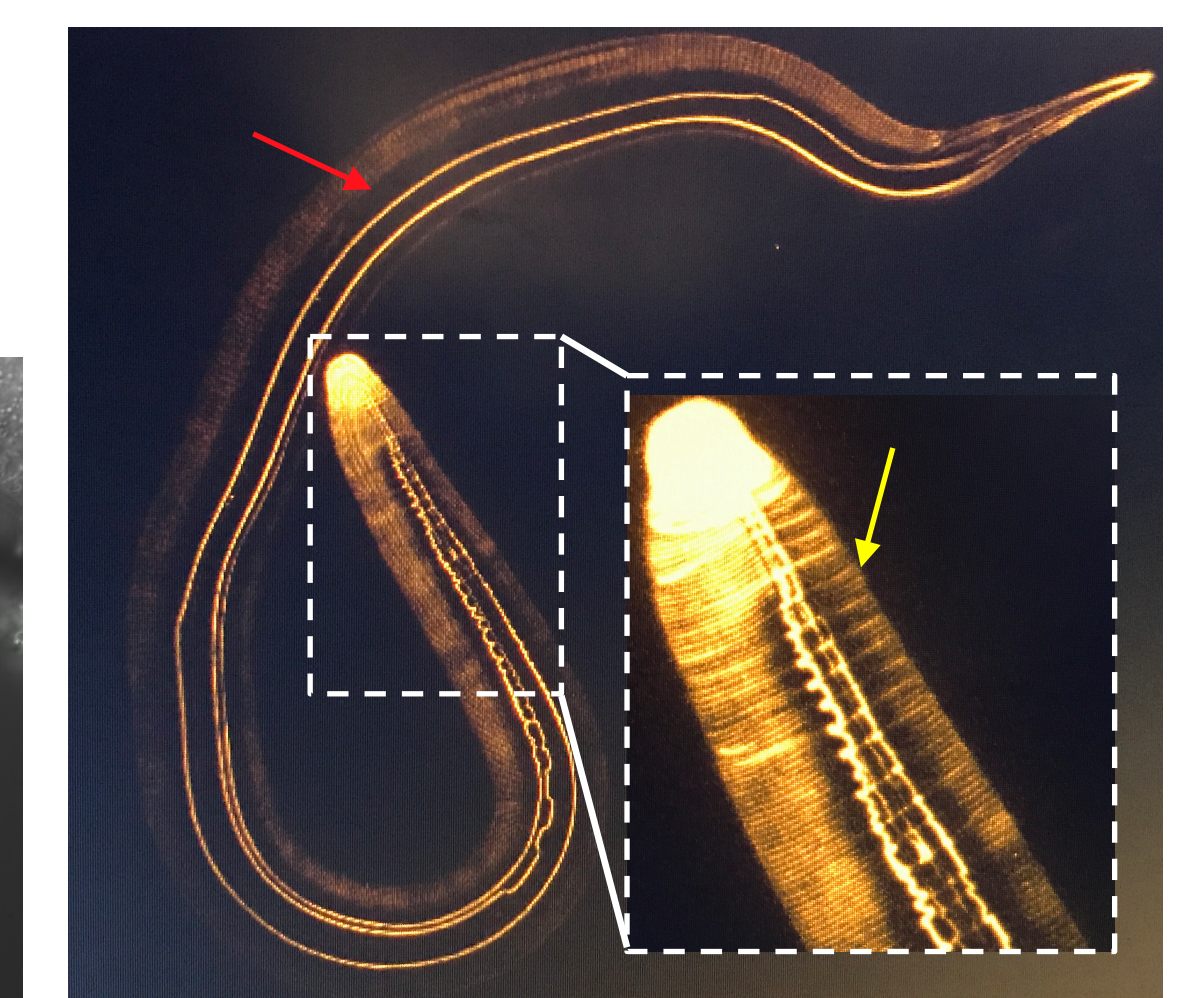


WT adult male: Continuous and straight alae

F1 adult male from *dpy-10* Stop-in microinjection: Alae is zig-zagged

(B). Developing methods to characterize cuticle structures in *S. carpocapsae* wildtype and mutants.

Preliminary trial of Dil staining *S. carpocapsae* cuticle.



A representative IJ stained with Dil showing alae and annuli.

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Acknowledgements

This work would not have been possible without Sandy Wong, Heenan Park, Lorryane Serra, Ali Mortazavi, Adler Dillman, Heidi Goodrich-Blair, Jenny Heppert, Han Wang, Hillel Schwartz, Andre Pires da Silva, and Sally Adams.

We would like to particularly thank the wonderful teams at WormBase ParaSite and WormBase.

Special thanks to all Sternberg lab members. I would have listed all your names if there is space.

Special thanks to Mr. Phillip Wong at Alhambra high school who directed research classes for Yu Jun Li.

FUNDING: NIH-F32 fellowship (1 F32 GM131570-01)