Mapping Results for a Set of cGAL Effectors and Drivers

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Description:

Recently, the GAL4-UAS system (cGAL) has been adapted for use in *C. elegans* for control of gene expression across 15°C - 25°C (Wang et al., 2017). In order to create a desired gene expression pattern, one crosses a transgenic strain containing a driver construct with another strain containing an effector gene. Here we mapped several cGAL driver and effector integrations. We first crossed each of the cGAL driver and effector strains with N2 males, picked the heterozygous male progeny, crossed them with hermaphrodites of the mapping strain (DA438), picked L4 hermaphrodites with the corresponding transgenic marker of the driver or effector strain and scored the progeny in the next generation. The DA438 strain contains six recessive mutations, each of which locates on one of the six chromosomes and produces visible phenotypes (Bli on chromosome I, Rol on II, Vab on III, Unc on IV, Dpy on V, and Lon on X (Avery, 1993). F2 progeny with each of the six phenotypes were selected and examined for the presence or absence of the dominant marker associated with the transgene. In the cases where the dominant transgene marker is unlinked to the recessive phenotypic marker, about three quarters of the F2 progeny will have the dominant marker. If the two markers are linked, very few or no animals are expected to have the dominant transgenic marker. The following tables summarize the mapping results for each cGAL strain, stating the ratios of the F2 mutant progeny with and without the dominant transgenic marker.

Effectors

15xUAS::GFP for Cell Labeling

Strain	Genotype	Location	Bli	Rol	Vab	Unc	Dpy	Lon
PS6843	*syIs300*	LGV	6:1	7:1	6:4	7:3	0:8	8:0
PS7149	*syIs390*	LGX	7:3	8:2	7:3	7:1	9:1	0:6

15xUAS::mKate2 for cell Labeling

Strain	Genotype	Location	Bli	Rol	Vab	Unc	Dpy	Lon
PS7136	*syIs378*	LGI	1:5	9:1	7:0	5:3	6:3	8:2

15xUAS::hChR2(H134R)::YFP for neuronal activation

Strain	Genotype	Location	Bli	Rol	Vab	Unc	Dpy	Lon
PS7044	*syIs341*	LGIV	8:1	8:2	11:0	1:11	6:1	7:3
PS7045	*syIs342*	LGII	6:0	0:9	5:1	6:0	7:3	7:0

15xUAS::TeTx (Tetanus toxin light chain) for blocking synaptic transmission

Strain	Genotype	Location	Bli	Rol	Vab	Unc	Dpy	Lon
PS7201	*syIs421*	LGIV	5:0	7:2	5:1	1:6	7:1	8:3

15xUAS::HisCl1::SL2::GFP for neuronal inhibition

Strain	Genotype	Location	Bli	Rol	Vab	Unc	Dpy	Lon
PS7199	*syIs371*	LGIII	9:1	6:0	0:6	4:1	6:0	4:1
PS7107	*syIs373*	LGI	0:8	7:3	10:1	6:3	10:1	8:1
PS7108	*syIs374*	LGV	8:1	7:1	7:1	7:1	0:10	7:1

Drivers

Pharyngeal muscle driver, P*myo-2*

Strain	Genotype	Location	Bli	Rol	Vab	Unc	Dpy	Lon
PS6844	*syIs301*	LGV	3:2	7:1	6:4	7:3	0:7	7:0

Heat shock driver, P*hsp-16.41*

Strain	Genotype	Mapped	Location	Bli	Rol	Vab	Unc	Dpy	Lon
PS7169	*syIs398 syIs337*	*syIs398*	LGIII	8:0	7:0	1:4	7:0	7:0	6:0
PS7172	*syIs401 syIs337*	*syIs401*	LGIII	7:0	8:0	0:8	5:3	8:2	7:1

Pan-neuronal driver, P*rab-3*

Strain	Genotype	Location	Bli	Rol	Vab	Unc	Dpy	Lon
PS6961	*syIs334*	LGX	6:1	5:1	6:1	5:1	8:2	2:7

Intestinal driver, P*nlp-40*

Strain	Genotype	Location	Bli	Rol	Vab	Unc	Dpy	Lon
PS6935	*syIs320*	LGV	7:0	7:0	5:1	5:1	0:7	6:1

Body muscle driver, P*myo-3*

Strain	Genotype	Location	Bli	Rol	Vab	Unc	Dpy	Lon
PS6936	*syIs321*	LGI	1:6	4:2	4:1	6:1	6:1	5:0

References

Avery, L. The genetics of feeding in *Caenorhabditis elegans*. Genetics. 1993 April;133(4): 897-917.

Wang H, Liu J, Gharib S, Chai CM, Schwarz EM, Pokala N, Sternberg PW. cGAL, a temperature-robust GAL4-UAS system for *Caenorhabditis elegans*. Nat Methods. 2017 Feb;14(2):145-148. doi: 10.1038/nmeth.4109.

Reagents

Effector strains:
PS6843 *syIs300[15xUAS::Δpes-10::GFP::unc-54 3'UTR + ttx-3p::RFP + pBlueScript]* V
PS7149 *syIs390[15xUAS::Δpes-10::GFP::let-858 3'UTR + ttx-3p::RFP + 1kb DNA ladder(NEB)]* X
PS7136 *syIs378[15xUAS::Δpes-10::mKate2::let-858 3'UTR + unc-122p::GFP + 1kb DNA ladder(NEB)]* I
PS7044 *syIs341[15xUAS::Δpes-10::hChR2(Y134R)::YFP::let-858 3'UTR + ttx-3p::RFP + pBlueScript]* IV
PS7045 *syIs342[15xUAS::Δpes-10::hChR2(Y134R)::YFP::let-858 3'UTR + ttx-3p::RFP + pBlueScript]* II
PS7201 *syIs421[15xUAS::Δpes-10::TeTx::let-858 3'UTR + myo-2p::NLS::GFP + pBlueScript]* IV
PS7199 *syIs371[15xUAS::Δpes-10::HisCl1::SL2::GFP::let-858 3'UTR + unc-122p::GFP + 1kb DNA ladder(NEB)]* III
PS7107 *syIs373[15xUAS::Δpes-10::HisCl1::SL2::GFP::let-858 3'UTR + unc-122p::GFP + 1kb DNA ladder(NEB)]* I
PS7108 *syIs374[15xUAS::Δpes-10::HisCl1::SL2::GFP::let-858 3'UTR + unc-122p::GFP + 1kb DNA ladder(NEB)]* V

Driver strains:
PS6844 *syIs301[myo-2p::NLS::GAL4SC::VP64::unc-54 3'UTR + unc-122p::RFP + 1kb DNA ladder (NEB)]* V
PS7169 *syIs398[hsp16.41p::NLS::GAL4SK::VP64::let-858 3'UTR + unc-122p::RFP + 1kb DNA ladder(NEB)]*
syIs337[15xUAS::Δpes-10::GFP::let-858 3'UTR + ttx-3p::RFP + 1kb DNA ladder(NEB)] III
PS7172 *syIs401[hsp16.41p::NLS::GAL4SK::VP64::let-858 3'UTR + unc-122p::RFP + 1kb DNA ladder(NEB)]*
syIs337[15xUAS::Δpes-10::GFP::let-858 3'UTR + ttx-3p::RFP + 1kb DNA ladder(NEB)] III

PS6961 *syIs334[rab-3p::NLS::GAL4SK::VP64::let-858 3'UTR + unc-122p::RFP + pBlueScript]* X
PS6935 *syIs320[nlp-40p::NLS::GAL4SK::VP64::unc-54 3'UTR + myo-2p::NLS::mCherry + pBlueScript]* V
PS6936 *syIs321[myo-3p::NLS::GAL4SK::VP64::unc-54 3'UTR + myo-2p::NLS::mCherry + pBlueScript]* I

Mapping:
DA438 *bli-4(e937)* I*; rol-6(e187)* II*; daf-2(e1368) vab-7(e1562)* III*; unc-31(e928)* IV*; dpy-11(e224)* V*; lon-2(e678)* X
Wild type N2

Please select a tag below that best describes your submission:
New findings
Methods & reagents

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