cpo

FBrf0075185

DROSOPHILA GENMAPS DATABASE RECORD PRINTOUT - 7/20/92
Return corrections to John Merriam, UCLA Biology.
Los Angeles, CA 90026-1606; FAX [redacted]

Df(3R)DG4
Df(3R)Sr16
Df(3R)Sr300.101

source_number: 1001

full_location: 90D1,4
table_numbers: 1,5,6
cross_locations:

gene_name: couch potato=PNS gene
gene_abbrev: cpo
product:

1 kb_cloned_genom: 125 vector_genomic: lambda DASH
kb_cloned_cDNA: 5 vector_cDNA: gt10, gt11

METHOD: expression: walk_jump_org: YACs: 0
microcloning: oligonucleotide:
homology: transposon_tag: xxx

clonetechtext: transposon tagging P[lArB]B52.1M3 and many others

2 rearrangement:

3 T_strain:
markers:

5 kb_seq_genomic: 3 acc_number_gen: kb_seq_old: 0
kb_seq_cDNA: 4 acc_number_cDNA:
comments:
ORF_size:
ORF_function:
ORF_domains: OPA repeat and other repeats

6 kb_trans_size: 3.3/4.6
transc_dist: PNS, 5 hr throughout development, PNS early, CNS and PNS late

7 protein_dist:

8 fusion_dist:

misc_info: Df(3R)sr-l6;Df(3R)sr-l461;Df(3R)DG4

full citation: Bellen HJ. 1991 Personal communication

contact_person: Bellen, HJ. ph [redacted] FAX [redacted]
lab_address: Baylor College of Medicine
address_line1: Howard Hughes Medical Institute
address_line2: Institute for Molecular Genetics
address_line3: Houston, TX 77030
address_line4:

keywords muscles, PNS, enhancer detectors

C. John, There seem to be two genes. 1) couch potato / 2) stripe. want to each other

source_number: 1001

full_location: 90D1,4 cross_locations:

table_numbers: 1,5,6

gene_name: PNS gene = stripe (couch potato, stripe) "PNS"

gene_abbrev: ~~sr~~ c.p.

product: ~~sr protein~~

YACs: 0

kb_cloned_genom: ~~42~~ 72.5 vector_genomic: lambda DASH

kb_cloned_cDNA: 5 vector_cDNA: gt10, gt11

expression: PNS early, CNS + PNS late ~~larvae~~

homology:

microcloning:

transposon_tag: xxx

oligonucleotide:

onetechtext: transposon tagging P[lArB]B52.1M3 & many others

earrangement:

T_strain:

markers:

kb_seq_genomic: 3 acc_number_gen: kb_seq_old: 0

kb_seq_cDNA: 4 acc_number_cDNA:

comments:

ORF_size:

ORF_function:

ORF_domains: OPA repeat and other repeats

kb_trans_size: ~~7.6~~, ~~6.5~~ 3.3/4.6.

ansc_dist: PNS, ~~6.10h of development~~ 5/6 → throughout development ←

rotein_dist:

usion_dist:

nisc_info: Df(3R)sr-l6;Df(3R)sr-~~8~~461;Df(3R)DG4

full citation: Bellen HJ. ~~1990 Drosophila conference.~~ 1991 personal Communication

contact_person: Bellen, HJ. phone_number: [redacted]

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keywords: muscles, PNS, enhancer detection

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1001

SANTA BARBARA • SANTA CRUZ

December 20, 1990

FAX: [redacted]

Bellen, HJ.
Baylor University
Howard Hughes Medical Institute
Institute Molecular Genetics
Houston, TX 77030

[redacted]

John Merriam
UCLA Drosophila Genmaps Database
DEPARTMENT OF BIOLOGY
405 HILGARD AVENUE
LOS ANGELES, CALIFORNIA 90024-1606
FAX [redacted]

Dear Colleagues:

I would like to use information from the clone list to construct a "physical map" of the Drosophila gen... have (a) clone(s) listed, as described below, so I would like to enlist your help. What I need for this project are the names and locations of chromosome rearrangement breakpoints that lie within the region of your clone/walk. Mapping breakpoints is the most reliable way of connecting the molecular with the cytological scales.

As you know, the clone list has been useful to Drosophila workers in finding starting points for their walks. The database is organized by references, so that the original cloning paper from a lab is cited as key #1, with subsequent papers cited by subject (key #5 is sequence information, for example). The clone list is therefore also a gene-by-gene literature index. The clone list is now mounted on the Indiana University BioArchive computer bulletin board in the FLY subdirectory. Use Internet address 129.79.1.101 and your local File Transfer Program.

Please take a few minutes to complete this form and return to me by FAX or mail. It will be most useful if you can update your clone sizes and make more exact your clone locations. Make any other changes you want also. List the rearrangements and which breakpoints you have identified. Any cytologically visible rearrangement (deletion, inversion, translocation, transposition, duplication) is useful. Please indicate if the same citation is the best reference, or indicate a better one (or a personal communication).

I thank you for your help as always. With your prompt and generous support I can expect to show you the results in March at the Chicago fly meeting.

List Rearrangements:		Breakpoint found:	Other breakpoints:
Df(3R) sr[6]	sr-6	No, but deletes at least 100 kb	in 90DE (some of 90F)
Df(3R) sr[461]	sr-461	" " " " " "	" " (most or all of 90D)
Df(3R)D64	D64	" " " " " "	" " "

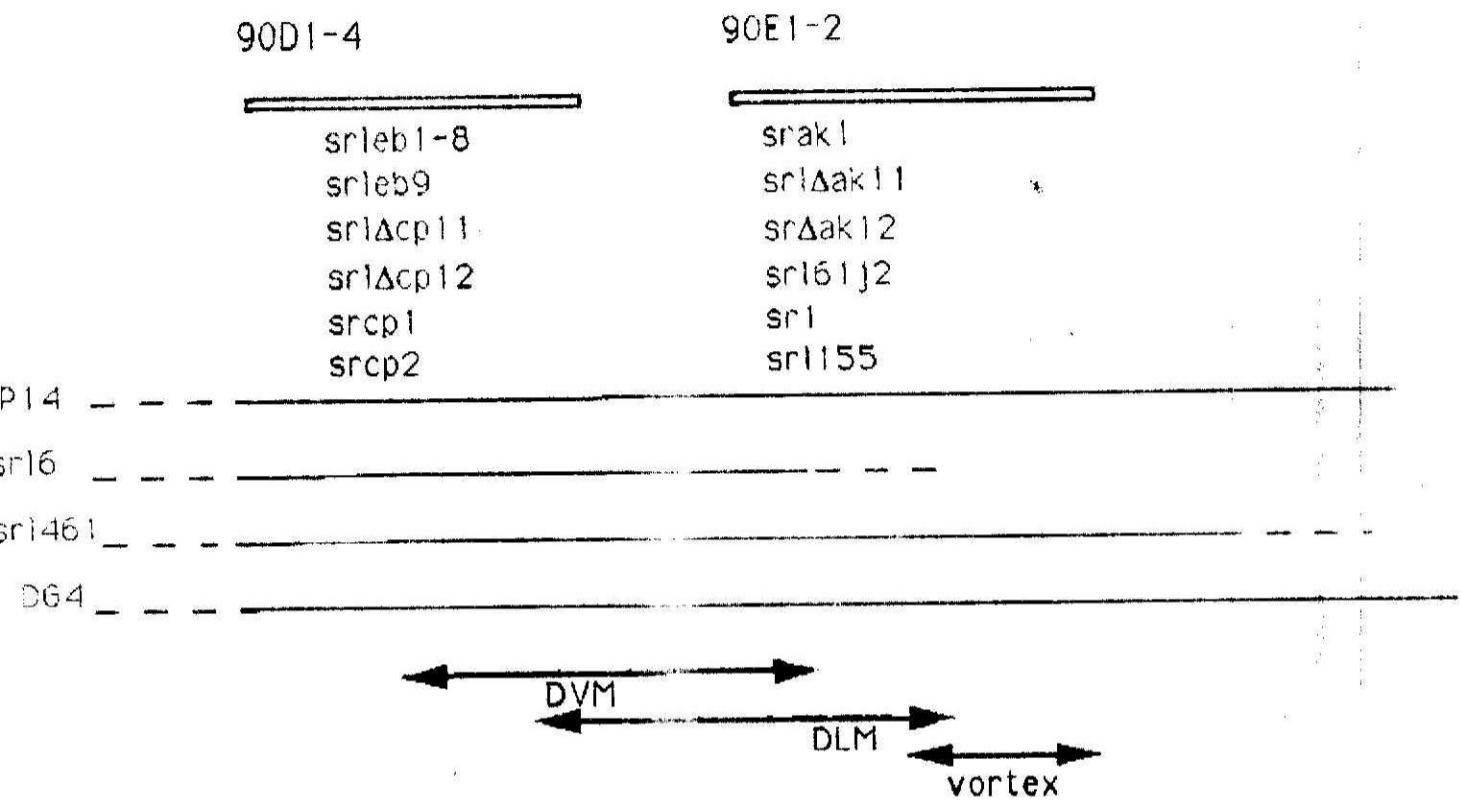
CHANGE or CONFIRM indexing for original clone cit'n: Locations __ Clone sizes __ Names/Products __

Bellen HJ. 1990 Drosophila conference.

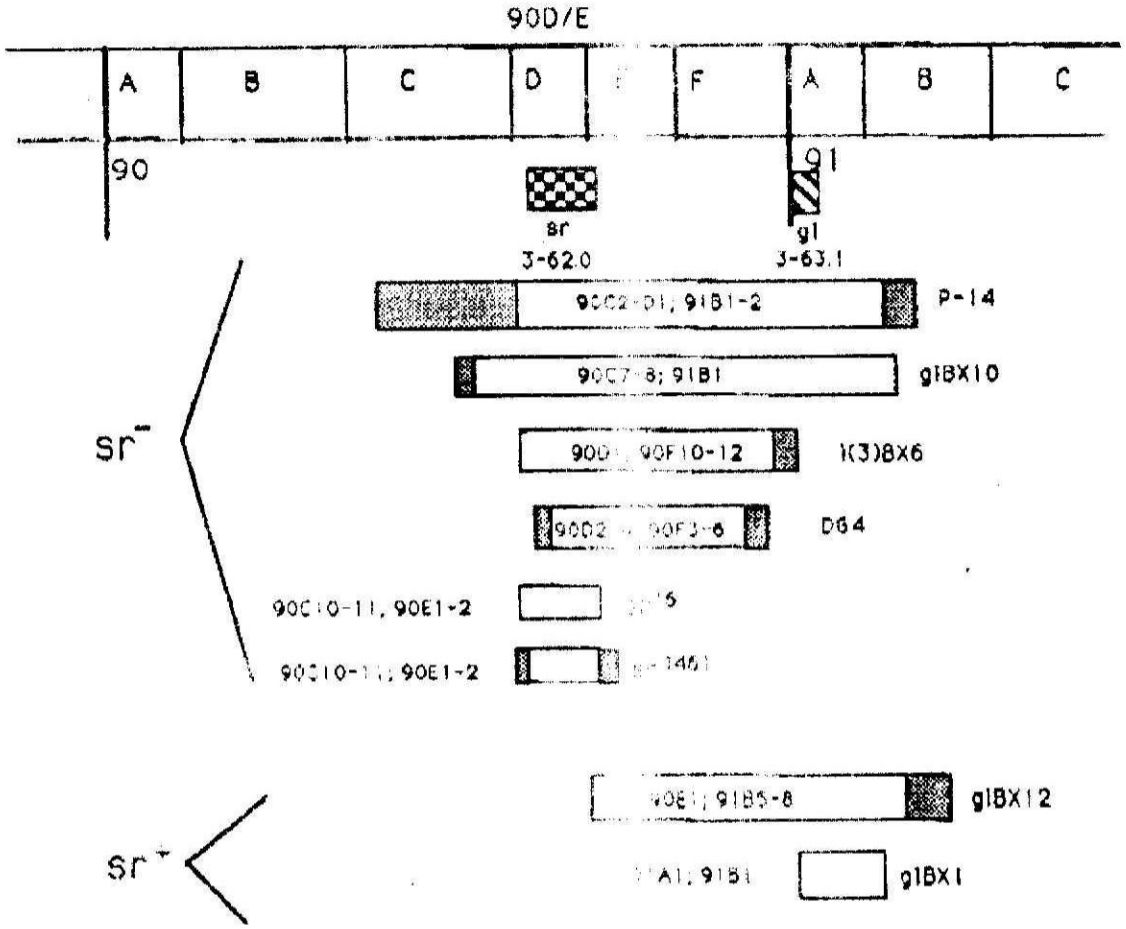
Location	Key	kb gen/cDNA	Gene name (abbreviation) product rearrangements...
90D 1-4	1,5,6	125 / 5	PNS gene = stripe, (sr) ~~deficiency data (arFop)~~
3.E1.1	1	30	stripe-distal (sr)

misc: on last page, list Df that break near sr

gure 4: Map of the *stripe* complex



e 3. Extent of some cytological visible deficiencies in the 90D/E
gion



1001

Return to John Merriam, UCLA Biology, LA 90024 FAX [redacted]
REFERENCE: _____

NAME: H. C. [illegible] PHONE # [redacted] FAX # _____

1. GENE: How do you describe the gene you are reporting on?

mutant name (if any) [illegible] = stripe couch potato

abbreviation sr ?

biochemical name (if any) _____

2. LOCATION: Where is your clone/walk located? 90D
(If you are using a clone from a more extended walk, what is the location of your gene? _____)

3. SIZE: How many kb did you clone? (round to nearest kb)

genomic 70 kb vector/library name λDASH

cDNA 5 kb vector/library name λgt10 x λgt11

4. METHOD: Describe the entry point for your clone/walk

prior clone PlArB 352.1H3 transposon tag ?

expression _____ differential screen _____

microclone _____ oligonucleotide _____ PCR? _____

homology _____

5. SEQUENCE: [redacted] the nearest 10th the kb sequenced

genomic 3 kb accession # _____

cDNA 4 kb accession # _____

PRODUCT: How many amino acids in the ORF? ?

OPA repeat + other repeats
List above the predicted function or homology group of the ORF

List above the key words that describe domains in the ORF

6. TRANSCRIPTS: round m RNA sizes to nearest 10th kb, list largest first ~~6.8kb~~/6.5kb When/where found? PNS, 5-10 h of development

7. PROTEIN (antibody detection) Where found? _____

8. LAC Z FUSION stain Where found? _____

9. MORE DETAILS: _____

12/17/91

John Merriam
UCLA Drosophila Genmaps Database

FAX:

Bellen H; Reece-Kooyer S; D'Evelyn D.
Howard Hughes Medical Institute for Molecular Genetics
Baylor College of Medecine
Houston, TX 77030

FAX [redacted]
310

Help!

Your article, listed below, is likely to have cloning or molecular information that should be listed in Drosophila Genmaps. As you know, the clone list has been useful to Drosophila workers in finding start points for their walks. The database is organized by references, so that the original cloning paper from each lab is cited as key #1, with their subsequent papers cited by subject. The clone list is therefore also a gene-by-gene literature index. The clone list is now mounted on the Indiana University BioArchive computer bulletin board in the FLY subdirectory. Use Internet address 129.79.1.101 and your local File Transfer Program.

Please take a few minutes to complete this form and return to me by FAX or mail. On separate sheet(s) we print out the information we have already from your lab on this gene. Send back to us any corrections you may have. If we missed any previous papers, make copies of this form to describe each earlier paper. Include your FAX number. If you think that one of your co-authors would be a better contact for us, feel free to send them this letter with your request to answer it.

I thank you for your help as always. With your prompt and generous support I can include your results in the next update on the bulletin board. -- John

CITATION:

Bellen H; Reece-Kooyer S; D'Evelyn D. CSH Mol. Neur. of Dros. Abstracts 1991.

--> List the Gene name:	and its Chromosome location:
Couch potato	90D2 - 90E1/2

KEYs 1-8: Please check off those boxes which describe THIS PAPER

Describe your results in detail on the reverse side.

- [x] 1 Genomic or cDNA clones obtained.
- [x] 2 Rearrangement breakpoints found in clone.
- [x] 3 New location of transformed insert.
- [x] 5 Sequence obtained.
- [x] 6 Transcript obtained.
- [x] 7 Protein described by antisera.
- [x] 8 Promoter fusion studies.
- [ ] No cloning or molecular information about gene

DROSOPHILA GENMAPS DATABASE REPORT FORM
Return to John Merriam, UCLA Biology, Los Angeles, CA 90026-1606; FAX [redacted]

location: 90D2-90E 1/2 keys for this paper: 1,6,7,8,5,2,4,4

Gene/mutant name: couch potato
abbreviation: cpo
biochemical name/product:

(1) CLONES:
kb_genomic: 100 Kb vector/library name: λDASH
kb_cDNA: 3.7 kb vector/library name: λgt11

METHOD:
prior clone: enhancer detection walk:
expression: differential screen:
microclone: oligonucleotide: PCR?
homology: transposon tag: P elements

(2) REARRANGEMENTS: small deletion by precise excision mutagenesis.

(3) TRANSFORM INSERTS: 10 kb fragment of genomic clone ✓

(5) SEQUENCE:
kb_genomic: ✓ 100 kb accession number:
kb_cDNA: 3.7 kb accession number:
ORF-size: 50-55 kD (45 kD)
ORF_function/homology group: RNA-binding protein
ORF_domains:

(6) TRANSCRIPT DESCRIPTION: ✓
transcript_size:
distribution: embryo: in sensory mother cells, in all cells of the developed embryonic PNS in many glia of PNS and CNS

(7) PROTEIN ANTIBODY: ✓
distribution: nuclear. same distribution as transcripts α β-galactosidase

(8) LAC Z FUSION STAIN: ✓
distribution: 10 kb fragment - expression in some cells as above

MISC_INFO:

.ILA GENMAPS DATABASE RECORD PRINTOUT - 7/20/92
Corrections to John Merriam, UCLA Biology,
.ngeles, CA 90026-1606; FAX [redacted]

source_number 2535

full_location 90D2-90E1/2
table_numbers 1,5,6,7,8 cross_locations

gene_name couch potato
gene_abbrev cpo
product

1 kb_cloned_genom 100 vector_genomic lambda DASH
kb_cloned_cDNA 3.7 vector_cDNA lambdagt11
METHOD: expression walk_jump_org YACs 0
microcloning oligonucleotide
homology transposon_tag xxx
clonetechtext Prior clone enhancer deletion; P elements

2 rearrangement

3 T_strain
markers

5 kb_seq_genomic 100 acc_number_gen kb_seq_old 0
kb_seq_cDNA 3.7 acc_number_cDNA
comments
ORF_size 50-55
ORF_function RNA-binding protien
ORF_domains poly-alanine, poly-glutamine, and P-V-S-V-P repeats

6 kb_trans_size
transc_dist embryo in sensor another cells, in all cells of the developed embryonic PNS in

7 protein_dist nuclear same distribution as transcripts alph beta-gala

8 fusion_dist 10 kb fragment-expression in same cells as above.

misc_info small deletion by. more transc_dist many glia of PNS and CNS.

full citation Bellen H; Reece-Kooyer S; D'Evelyn D. CSH Mol. Neur. of Dros. Abstracts 1991.

contact_person Bellen H. ph FAX
lab_address Howard Hughes Medical Institute for Molecular Genetics
address_line1 Baylor College of Medecine
address_line2 Houston, TX 77030
address_line3
address_line4

keywords