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December 20, 1990

su(f)

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

FAX:

O'Hare, K.
Department of Biochemistry
Imperial College of Science Technology and Medicine
London SW 7 2AZ
England, UK

Dear Colleagues:

I would like to use information from the clone list to construct a "physical map" of the Drosophila genome. You 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:

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

O'Hare, K. 1990 Crete meeting.

Location	Key	kb gen/cDNA	Gene name (abbreviation) product rearrangements...
20EF	1,5,6	50 2.6	suppressor of forked (su(f))

2,16 update of existing record of O'Hare

DROSOPHILA DATABASE REPORT FORM

Return to John Merriam, UCLA Biology, LA 90024-1606 FAX [redacted]

Please verify [___] or correct the address and citation on the reverse.

NAME:_____ PHONE #:_____ FAX #:_____

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

   mutant name (if any): P mutant, fertile

   abbreviation: P(ry+)

   biochemical name (if any) _____

2. **LOCATION:** Where is your clone/walk located? 20C1

   (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 50 vector/library name: _____

   cDNA _____ vector/library name: _____

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

   prior clone _____ transposon tag P mutant

   expression _____ differential screen _____

   microclone _____ oligonucleotide _____ PCR? _____

   homology _____

5. **SEQUENCE:** How many kb did you sequence? (round to nearest 0.1 kb)

   genomic 10.1 accession #: to be entered when paper accepted

   cDNA several accession #: leave as is

   PRODUCT: How many amino acids in the ORF? 84kD & 39kD proteins predicted

   (List above the predicted function or homology group of the ORF)

   No homologues

   (List above the key words that describe domains in the ORF)

6. **TRANSCRIPTS:** (round mRNA sizes to nearest 0.1 kb, list largest 1st):

   2.9 / 2.6 / 1.3 When/where found? throughout development

7. **PROTEIN** (antibody detection): Where found? no data on tissue dist-n. N/A

8. **LAC Z FUSION** stain: Where found? N/A

9. **MORE DETAILS:** ~~at 11, het locus~~, surrounded by repeated interval. the beta tubulin 4.

Genes RECORD NO _____ REF NO. _____

...ion 7/24/87

4. Date _____

5. Location _____ 20F _____

6. Table Num 0 1 2 3 4 5 6 _____

7. Clone Name _____

8. Genes Info suppressed for ... (Lon ...)

9. Stock Orgn _____

10. KB Size _____

11. Cross Ref _____

12. Misc Info transposon tag adjacent beta
heterochromatin, deficit. Wing blade genes;
2 exons

13. Reference _____

14. Breakpoint _____

15. BPCont1 _____

16. BPCont2 _____

17. T Strain _____

18. Markers _____

19. DIS Vol _____

20. Comments _____

21. KB Sequenced _____

22. Coordinates _____

_____

_____

please return to:

John Merriam

Biology Department
Univ California
Los Angeles, CA 90024

FAX # [redacted]

Tudor, M., Histochem
I.M. et al C. Hom

h.
Dept Biochemistry
Imperial College
of Science Technology
& Medicine
London SW7 2AZ

1987

key to Table num for this record: 0 = new data and ref on one previously entered, 1 = clone, 2 = rearrangement breakpoint, 3 = insert, 4 = walk, 5 = sequenced, 6 = transcription multiple entries ok (ie 1,2,4,5,6)

ñila clone list report form ver 12/6/89

please return to:

./update
ate_____ record #_____ reference#[redacted]

John Merriam
Biology Department
Univ California
Los Angeles, CA 90024

FAX # [redacted]
phone

key 1 2 3 5 6 7 8

location	gene name	abbrev	product	cross loc	rearrange	Tstrain	marker
20 EF	suppressor of forked	su(f)					

lk/jump_____ genomic kb seq. 11 kb accession# not yet submitted
origin

homology_____ cDNA kb seq. 2.6 accession# "
origin

transposon tag su(f) MS97 & su(f) MI252 ORF_____
name #amino acids

cDNA_____ kb transcript(s) 2.6, 2.9, 1.3
express, enrich, or +/-

oligonucleotide_____ product distribution_____
sequence

microcloning_____
PCR?

genomic kb cloned ~50 vector EMBL4

cDNA kb cloned 2.6 vector pGEM

misc (promoters, transmembrane, DNA binding, etc)_____

words beta-heterochromatin

Source_number: 639

full_location: 20EF cross_locations:

table_numbers: 1,5,6

gene_name: suppressor of forked

gene_abbrev: su(f)

product: YACs: 0

kb_cloned_genom: 50 vector_genomic: EMBL4

kb_cloned_cDNA: 2.6 vector_cDNA: gt10

expression:

homology:

microcloning:

transposon_tag: P mutant, su(f)-MS97 and su(f)-MS252

oligonucleotide:

clonetechtext: 0

rearrangement:

T_strain:

markers:

kb_seq_genomic: 10.1 acc_number_gen: kb_seq_old: 0

kb_seq_cDNA: 2.6 acc_number_cDNA:

comments:

ORF_size: 84kD; 39kD

ORF_function: proteins predicted

ORF_domains: no homologies

kb_trans_size: 2.9, 2.6, 1.3

transc_dist: throughout development

protein_dist:

fusion_dist:

misc_info: More than one cDNA sequence. Surrounded by repeated intervals of the beta heterochromatin, direct 1.5 kb repeats flank gene; 9 exons.

full citation **O'Hare, K. 1990 Crete meeting.**

contact_person **O'Hare, K.** **phone_number**

lab_address **Department of Biochemistry**

address_line1 **Imperial College of Science Technology and Medicine**

address_line2 **London SW 7 2AZ**

address_line3 **England, UK**

address_line4

keywords !