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December 20, 1990

FAX: [redacted]

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John Merriam
UCLA Drosophila Genmaps Database
DEPARTMENT OF BIOLOGY
405 HILGARD AVENUE
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FAX [redacted]

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 [redacted] 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:
Dp(1;3)sn 13a1	70D	79E

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

Paterson J; O'Hare K. 1990 Drosophila conference.

Location	Key	kb gen/cDNA	Gene name (abbreviation) product rearrangements...
7D1,2	1,2,5,6	50 3.5	singed (sn)

otherwise OK

1,2,5,6,8

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

NAME: S. Paterson K. O'Hare PHONE # [redacted] FAX # [redacted]

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

mutant name (if any) enlarged 11/28/90

abbreviation -en

biochemical name (if any) _____

X 2. LOCATION: Where is your clone/walk located? 70D-2
(If you are using a clone from a more extended walk, what is the location of your gene? 21.0)

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

genomic ~50 vector/library name λ EMBL4 / Carlson S w Oregon R

cDNA 3,5 vector/library name λ gt10 / Kamvar

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

prior clone inversion 17C – 70 transposon tag _____

expression _____ differential screen _____

microclone _____ oligonucleotide _____ PCR? _____

homology _____

5. SEQUENCE: round to the nearest 10th the kb sequenced

genomic 2,0/0,4/3,5 accession # X17548/X17549/X17550

cDNA _____ accession # _____

PRODUCT: How many amino acids in the ORF? 591

_____
List above the predicted function or homology group of the ORF

_____
List above the key words that describe domains in the ORF

Y 6. TRANSCRIPTS: round m RNA sizes to nearest 10th kb, list largest first 3,6/3,3/3,0 When/where found? maternally contributed to embryos, 3,6 only in pupae & ♂, all 3 in females

7. PROTEIN (antibody detection) Where found? ND

8. LAC Z FUSION stain Where found? In P[lacZ] insertion mutants,

9. MORE DETAILS: border cells & nurse cells stain in ovary

nothing new 7/27/92 hold

source_number: 1289
full_location: 7D1,2 cross_locations:
table_numbers: 1,2,5,6,8
gene_name: singed
gene_abbrev: sn
product: YACs: 0
kb_cloned_genom: 50 vector_genomic: EMBL4 / Canton S or Oregon R
kb_cloned_cDNA: 3.5 vector_cDNA: gt10 / Kauvar
expression:
homology:
microcloning:
transposon_tag:
oligonucleotide:
clonetechtext: inversion 17C - 7C
rearrangement:
T_strain:
markers:
kb_seq_genomic: 3.5 acc_number_gen: X17550 kb_seq_old: 0
kb_seq_cDNA: 0 acc_number_cDNA:
comments:
ORF_size:
ORF_function:
ORF_domains:
kb_trans_size: 3.6, 3.3, 3.0 .
transc_dist: maternally contributed to embryos, 3.6 only in pupae and males; all 3 in females
protein_dist:
fusion_dist: In P[lacZ] inversion mutants; border cells and nurse cells stain in ovary.
misc_info: Other genomic DNA sequences: 2.0kb (X17548); 0.4kb (X17549).

full citation **Paterson J; O'Hare K. 1990 Drosophila conference.**

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

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SANTA BARBARA · SANTA CRUZ

March 26, 1990

DEPARTMENT OF BIOLOGY
LOS ANGELES, CALIFORNIA 90024

J. Paterson and K. O'Hare

FAX # [redacted]

Dear Contributor to the 1990 Drosophila conference:

I will include the molecular information about the clones/genes you presented last week in the next version of the "Clone List." This list began to help cloning or walking in chromosome regions. It still serves that purpose even with YAC and microdissected cosmid libraries. In addition, there is a need to keep track of the molecular aspects of genes. Ultimately the Drosophila community wants a vertically integrated data base descending in layers from chromosome region to nucleotide sequence. The original clone list format is appropriate for this purpose since the data are listed by chromosome region; the format has evolved as you can see to add new molecular fields.

With the volume of reports coming out I need your help in collecting this information. I am in the process of creating an electronic report form that can be added directly to the data base. In the meantime, the abstracts from the 1990 meeting, and self reports, represent the most accurate way of getting information. The response frequency this year to a focused questionnaire about your previous reports was extremely impressive (well over 50%), so I am persuaded to try it with the new abstracts.

On the opposite page you will find the new report form with the information collected from your presentation. Please fill in the additional information requested by the X's, and any additional information you may have obtained. The reference will be the 1990 meeting unless you replace it with a published citation. FAX or mail the form back to me in the addressed envelope as soon as possible. You can update the information by sending me a reprint when it is published and drawing my attention to any additions or changes.

I would appreciate receiving your comments about the kinds of information you would like to see in a data base or handbook format. I invite your questions about information in the data base that can be FAXed back to you. Include your FAX number.

Sincerely,

Jack Merriam