Scot Munroe
[redacted]
will return mid-May

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To LYNN CROSBY | From K. COOK
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To FLYBASE CURATORS | From K. COOK
Co./Dept. | Co. STOCK CENTER
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Department of Developmental Biology
Stanford Medical Center
Stanford, CA 94305-5329
April 16, 1998

Dr. Kathy Matthews
I.U. Bloomington Drosophila Stock Center
Department of Biology
Indiana University
Bloomington, IN 47405-6801

FBf 0102541

Dear Dr. Kathy Matthews,

Here are the fly stocks from the Hogness lab fly collection that you have requested. Below is a brief description of their history; I have also enclosed several figures that show additional information.

w ; Df(3L)663/TM3
w ; Df(3L)294/TM6B
w ; Df(3L)E1/TM6B
w ; Df(3L)1-11/TM6B

w ; EcRE-lacZ-4 (on II)
w ; EcRE-lacZ-3 (on III)

w ; L63[81]/TM6B

w ; Sb129/TM3
w ; Sb200/TM3
w ; Sb64/TM3
w ; Tb96/TM6B
w ; Tb255/TM6B

Df(3L)663 and Df(3L)294 were made by Stephanie Paine-Saunders during her graduate work in Jim Fristrom's lab on the Imp-E2 gene. Df(3L)E1 and Df(3L)1-11 were made by Steve Stowers in the Hogness lab by simultaneous excision of two P elements. Steve has mapped at least one of the breakpoints of each Df by in situ hybridization with genomic phage clones and subsequently by Southern blot. The uncertainty in this mapping is in most cases just a few kilobases. This information comes from Steve Stowers' dissertation: Stowers, R. Steven. (1997). Molecular and Genetic Analysis of Two 'Late' Genes of the Ecdysone Hierarchy of *Drosophila melanogaster*. Ph. D. Thesis, Stanford University, Stanford, California. Steve's work on L63 is also in a manuscript that is in preparation.

Steve Stowers also constructed the EcRE-lacZ transformants. Starting with the 7xEcRE-lacZ construct made by Michael Koelle and described in Cell 67: 59 (1991), Steve isolated a PstI-EcoRI fragment and inserted this into pCasper that had been cut with PstI and EcoRI. This information is a personal communication from Steve Stowers.

The L63[81] allele was induced by EMS by Stephanie Paine-Saunders. Steve Stowers showed that it was an allele of the L63 gene by rescuing its lethality with a hs-L63 cDNA transgene. Anne Rascle in the Hogness lab sequenced an RT-PCR product and found a 48 bp deletion that removes 16 codons from the L63 open reading frame. Because there are multiple potential initiation codons for this open reading frame (see the gene structure summary on page 93 enclosed), it is not straightforward to assign amino acid numbers to the residues deleted. In the sequence published by Sauer *et al.*, Mol. Biol. Cell 7: 1759, accession number X99512, these would be amino acids 213 to 228. Steve Stowers outcrossed the original mutant chromosome from Paine-Saunders and removed at least one additional lethal. Animals homozygous for the chromosome we have sent die predominantly before the end of the third instar; only a very small

number pupariate. This information comes from Steve Stowers' dissertation and a personal communication from Anne Rascle.

The final five chromosomes were created by Anne Rascle in a hunt for more mutants in L63. Her screen and complementation data are on enclosed pages. These data indicate that none of these mutants lie in L63 but rather they are in adjacent genes. This information is a personal communication from Anne Rascle.

If you have any questions or need additional information, please inquire. After late May, when I leave Stanford, please address them to Dave Hogness.

Scot Munroe

Chapter 2-Figure 2. Genomic map of 63E region.

The genomic phage inserts from the 63E region and their approximate cytological locations are shown as is the location of yeast artificial chromosome (YAC) 527. The transcription units identified by reverse Northern analysis are shown relative to the genomic phage to which they hybridize.

from:

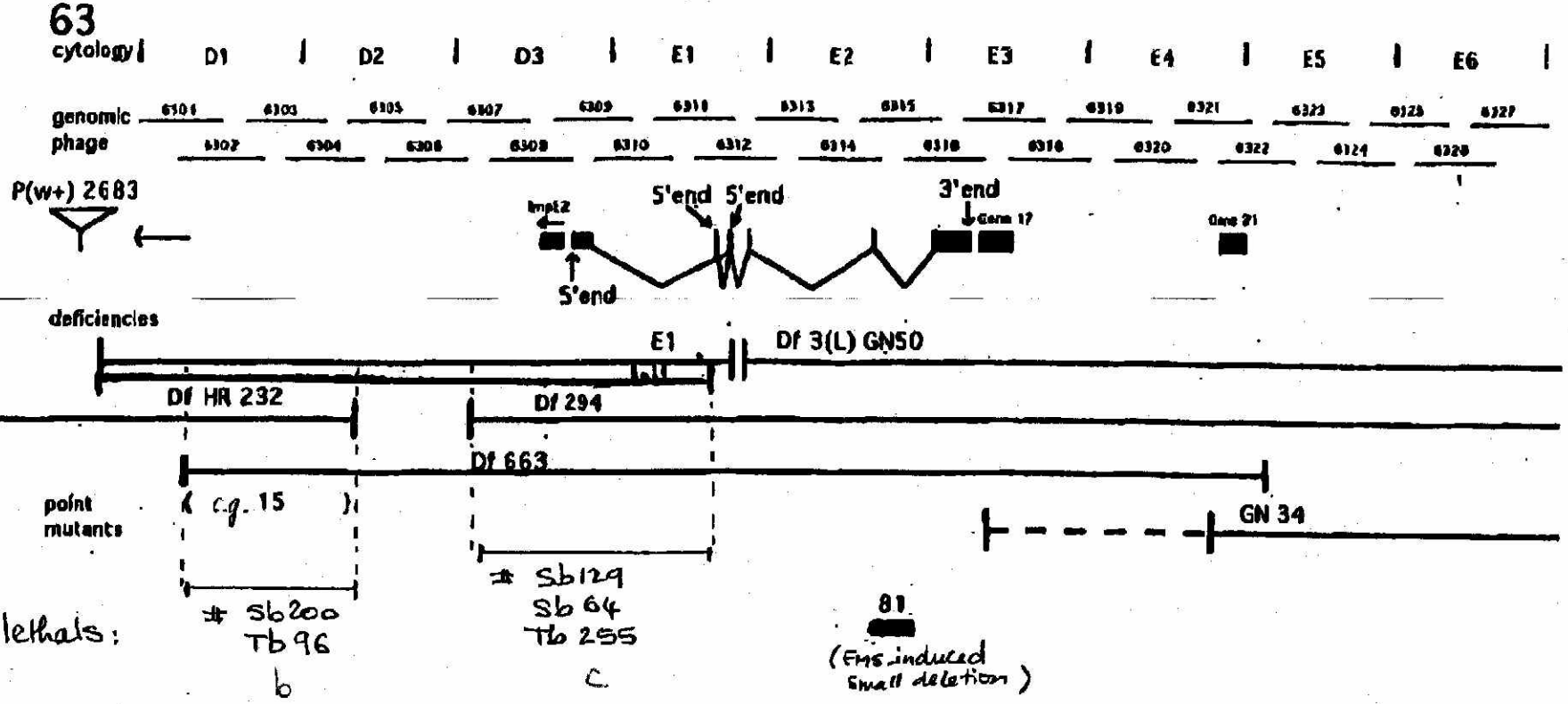
Stowers, R. Steven. (1997). Molecular and Genetic Analysis of Two 'Late' Genes of the Ecdysone Hierarchy of *Drosophila melanogaster*. Ph. D. Thesis, Stanford University, Stanford, California.

Chapter 2-Figure 3. L63 gene structure.

Schematic diagram of the *L63* gene structure showing the exon locations of the nine known *L63* mRNAs relative to 63E region genomic phage and breakpoints of 63E region deletion mutants. *L63* mRNAs are grouped and colored according to the known or suspected *L63* transcription start sites from which they originate. The sizes of the exons are accurate relative to each other but they are larger than the scale indicated at the bottom right of the diagram. Possible translation start sites are indicated as green ATGs while translation stop is indicated as a red TAA. Solid lines indicate sequences that are absent in the deficiencies. Deletion chromosomes in which the 63E puff is active are shown in green and are marked with a (+) while those in which the 63E puff is not active are shown in red and are marked with a (-). The 81 and 204h2 mutants are alleles of L63. A restriction map is also indicated at the top of the diagram for *Eco RI*, *Sal I*, and *Xho I*.

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FAX NO.
MAY-12-98 TUE 11:42 AM KAUFMAN LAB

63E Genetics



*:
Sb129: w; ImpE2-129 / Tm3
Sb200: w; *15-200 / Tm3
Sb64: w; ImpE2-64 / Tm3
Tb96: w; *15-96 / Tm6b
Tb255: w; ImpE2-255 / Tm6b

Complementation data of the EMS-induced lethals (screened first for lethality over Df663)

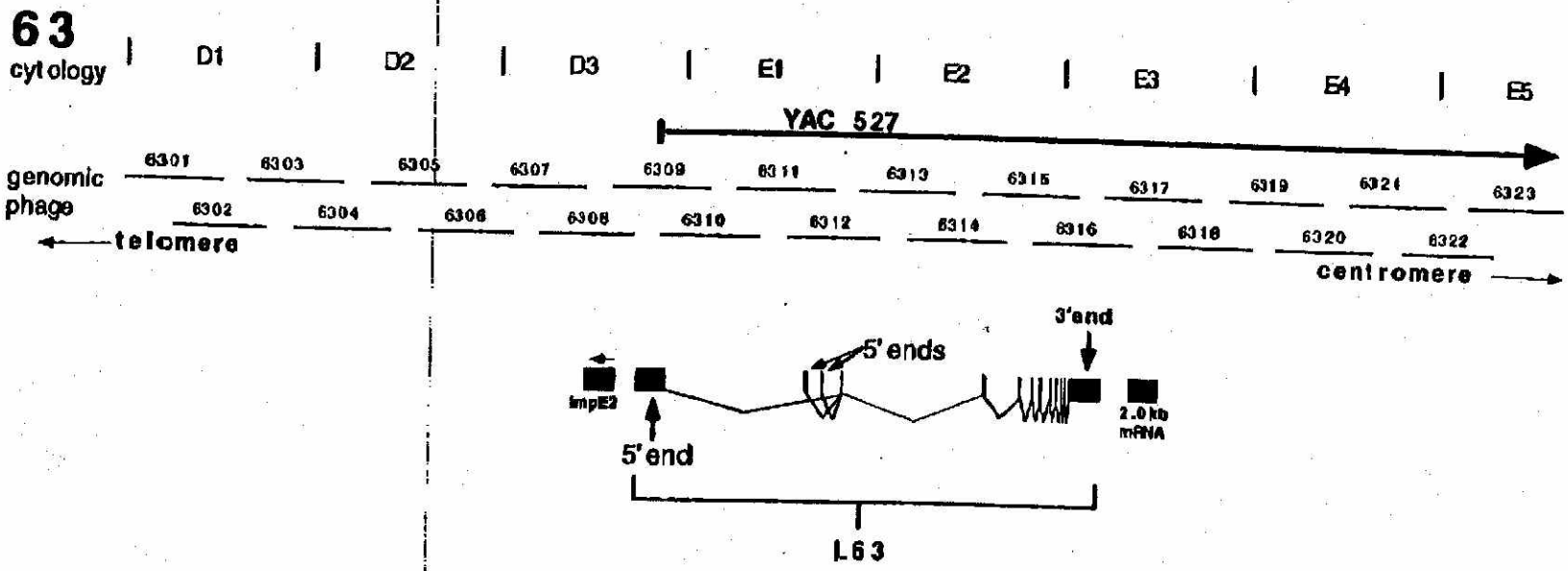
*	itself	Df663	81	Df294	DfGN50	Df1-11	DfE1	Df HR232	DfGN34	Gene (?)
Sb129	-	-	+	-	+	-	-	+	+	ImpE2 (?)
Sb200	-	-	+	+	+	-	-	-	+	c.g. 15
Sb64	-	-	+	-	+	-	-	+	+	ImpE2 (?)
Tb96	-	-	+	+	+	-	-	-	+	c.g. 15
Tb255	-	-	+	-	+	-	-	+	+	ImpE2 (?)

c.g. 15 : complementation group #15

+ : complementation
— : No complementation

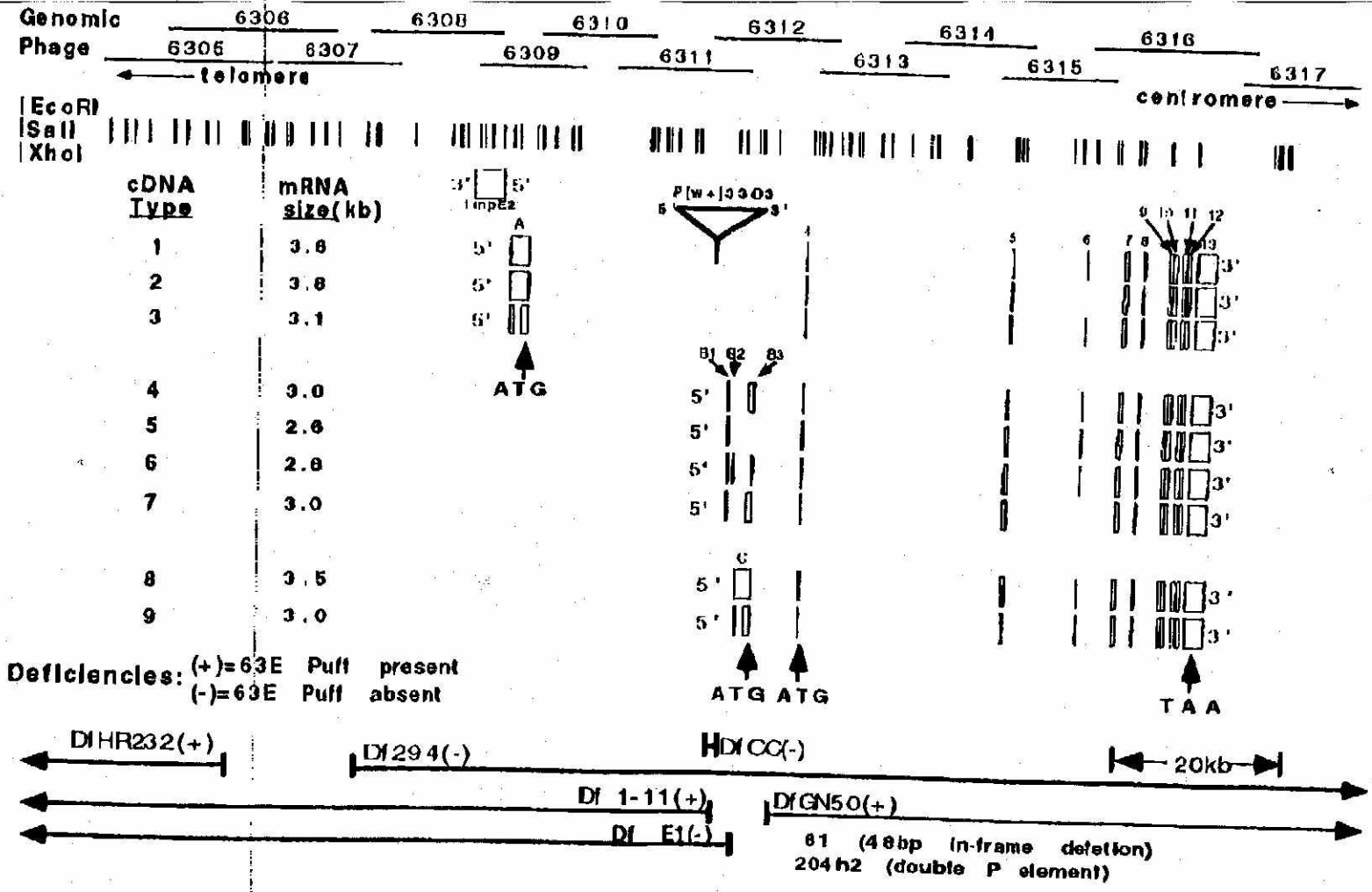
Anne Rascle

63 E Genomic Map

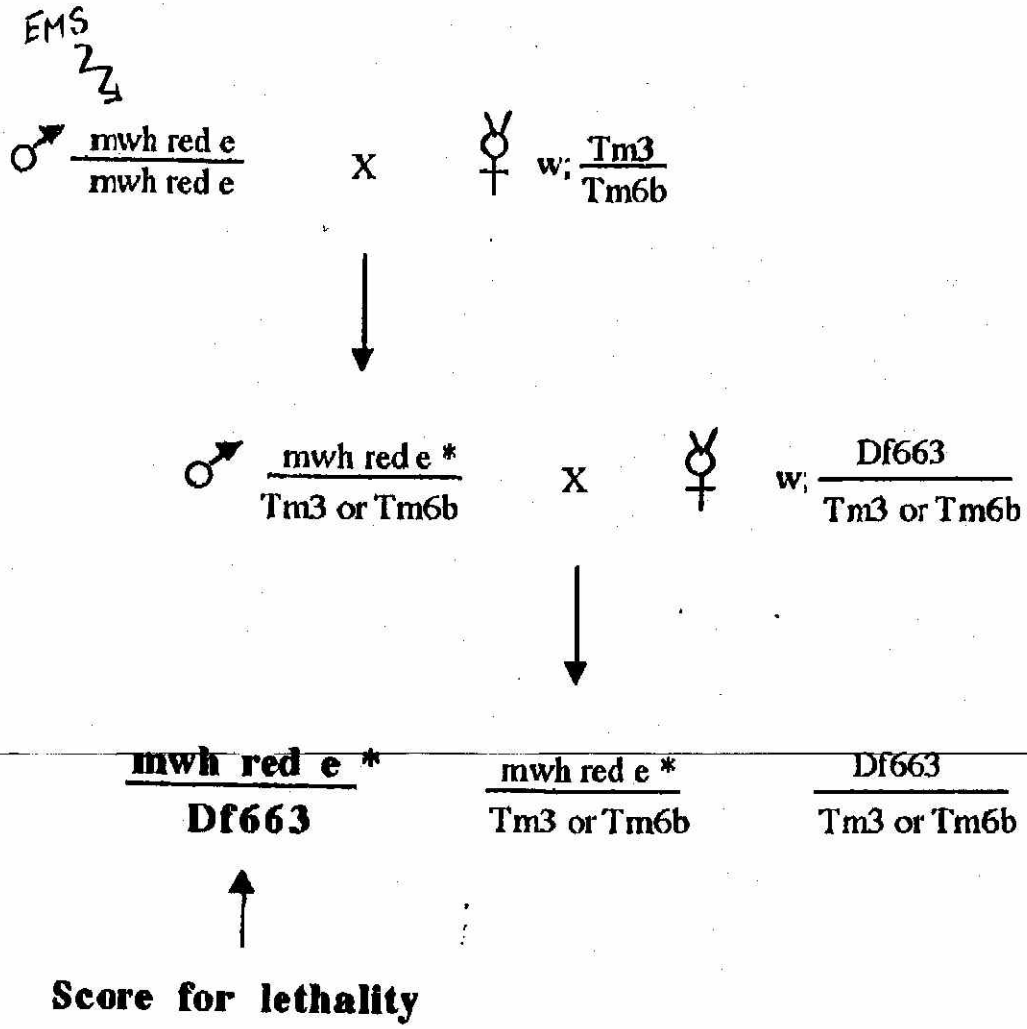


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L63 Gene Structure



Identification of new 63E mutants: F2 EMS screen



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