

LINKAGE DATA

Perkins, D. D. and N.E. Murray. New
markers and linkage data.

The following mutants that were previously un-
assigned to linkage groups have now been located:

- K7 cys-4 : cysteine-4 (IV R). U V; Y8743. cf. Murray 1960.
- C124 me-9 : methionine-9 (VII). U V; Abb4 X 25a. Extracted from 44303.
Responds to methionine only (G. R. Dubes 1953), whereas me-7 responds
to cystathionine, homocysteine, or methionine. 0/341 recombinants
with me-7 (K79).
- Y154M37 ad-9 : adenine-9 (I R). X-ray; 74A. Blocked between GAR and FGAR
(N. J. Nelson and M. E. Case).
- 20705 ad(-2) : adenine (III R). X-ray; LA X La. 0/29 recombinants with
ad-2 (70004t).
- 33026 val : valine (V). U V; 1A X 19a. 0/45 recombinants with val (45201),
which is close to iv-1.
- 35001 cys-5 : cysteine-5 (I L). U V; 1A X 25a. Both 35001 and cys (85518)
respond to sulfite, and N. H. Horowitz (unpublished) had previously
shown that cys (85518) is linked to mating type. 0/111 recombinants
from an intercross of 35001 X 85518.
- T (III; VI) 1: First translocation between III and VI. Recovered by
P. St. Lawrence from a cross 74A X rg cr a; apparently spontaneous.
- 47904 T (V; VI), inos. Translocation between V and VI, not separated from
inos requirement allelic with inos (V). (N. H. Giles, 1951)

hist (PI43h) was reported as a possible second hist-4 allele (Murray and Glassey, NN. #1). Recent data confirm a location distal to pan-1. Chromatographic studies of the accumulation products of single and double mutants show that PI43h differs from hist-4 (C14l) only in that it is temperature sensitive. At 25° PI43h is not stimulated by histidine and no imidazole accumulation products were detected; at 34° PI43h is leaky but the imidazole products accumulated were characteristic of the hist-4 allele, C14l. Three-point data are tabulated on the following page using the conventions of Perkins et al. (1962, Canad. J. Genet. Cytol. 4:192; 1959, Genetics 44:1191). Cross numbers prefixed S designate data of the second author.

Cross No.	Zygote Genotype and Recombination %	Parental Combinations	Recombinations			Total; per cent Germi-nation; Link-age Groups	Marker Isolation Numbers
			Singles Region 1	Singles Region 2	Doubles Regions 1 and 2		
S667	+ cys-5 A leu-3 + a 7.8 5.2	40 27	2 4	1 3	0 0	77 83% I	47313 35001 sex
1646	+ + ad-9 thi-1 csh + 12.2 5.4	34 27	4 5	4 0	0 0	74 74% I	56501 STL8 Y154M37
1684	+ + me-6 nit-1 ad-9 + 7.0 3.5	51 -	- 4	2 -	- 0	57 (ad ⁺ only) 89% I	34547 Y154M37 35809
S504	+ ad-4 leu-1 me-8 + + 1.4 1.4	122 155	3 1	0 4	0 0	285 71% III	P53 44206t 33757
S574	+ + cys-4 pan-1 mat + 11.5 918	48 41	6 7	5 6	0 0	113 75% IV	5531 B57 K7
S531	+ + hist-4 me-2 pan-1 + 4.6 1.7	79 82	4 4	2 1	0 0	172 86% IV	H98 5531 P143ht
1649	+ pab-2 pl leu-5 + + 28.3 7.9	43 40	19 15	3 5	1 1 C=0.7	127 84% V	45208t H193 B118
1682	+ bis + leu-5 + pab-2 29.9 7.2	34 29	14 13	4 1	1 1 C=1.0	97 98% V	45208t B6 H193
1669	+ T + ylo + thi-4 3.9 32.5	29 22	0 1	8 15	1 1 C=2.1	77 81% III;V	Y30539y T(III;VI)1 85902
1713	+ + (T)ylo leu-1 tryp-1 (+)+ 20.2 31.0	30 34	10 15	22 17	0 1 C=0.1	129 78% III;V	33757 10575 /T(III;VI)1/ Y30539y
1680	+ inos T + chol-2 + tryp-1 0 36.2	30 30	0 0	22 12	0 0	94 94% V;VI	47904 T(V;VI)46802 10575
1705	+ inos T + chol-2 + ad-8 6.2 6.2	27 30	2 2	2 2	0 0	65 88% V;VI	47904 T(V;VI)46802 Y226M58

--Department of Biological Sciences, Stanford University, Stanford, California.