



Linkage maps of *D. simulans*: An update of Sturtevant (1929) with additional loci.

Barker, J.S.F.¹, and J.J. Moth². ¹ School of Rural Science and Natural Resources, University of New England, Armidale NSW 2350, Australia. ² PO Box 570, Cessnock NSW 2325, Australia.

Sturtevant (1929) presented the results of extensive experiments on linkage relationships and mapping of 45 visible mutant loci, although some of the map positions were very tentative. Subsequently, Sturtevant (1934), Puro (1971), Rux and Coyne (1991), Jones and Orr (1998), and Ciecko and Presgraves (1999) have given some mapping results for 20 loci, including 10 additional to Sturtevant (1929). Here we combine Sturtevant's (1929) data with our results for 25 loci, including 11 not in Sturtevant's maps, to produce new maps for *D. simulans* with a total of 51 loci.

For loci on Sturtevant's (1929) map, we use the same symbol, except for peach (*p* in Sturtevant), where we use *p^p* (pink-peach) to conform with the *D. melanogaster* symbol. The 11 additional loci that we include have no (or limited) previous mapping data, viz. X chromosome – *v* (vermilion – mapped to 32 by Sturtevant, 1934); Chromosome 2 – *net*, *bw* (brown, Rux and Coyne, 1991) and *up* (wings up – 14.1% crossover with polychaete, Puro 1971); Chromosome 3 – *rd* (rugged – 10 units from *ju*, Puro, 1971), *ju* (javelin, Sturtevant, 1934, Jones and Orr, 1998), *e* (ebony, Jones and Orr, 1998), *Ubx* (Ultrabithorax, Puro, 1971), *ae* (aeroplane – wings held at 90° to body axis), “brown” (eye colour – may be homologous to sienna in *D. melanogaster* – see J. Coyne stock list in

Table 1. Recombination value (RV) estimates and standard errors (SE) used for linkage mapping, and number of flies (N) scored for each estimate.

Loci	RV (%)	SE	N	Loci	RV (%)	SE	N
X Chromosome				Chromosome 3			
y w	8.41	0.80	1200	rd ju	13.29	1.41	579
y v	22.93	1.48	807	ju se	7.13	1.28	406
w v	19.54	1.22	1055	ju st	35.51	1.42	1129
w f	42.10	1.49	1100	se st	29.95	2.02	514
v f	26.65	2.14	428	st ae	15.01	1.73	426
Chromosome 2				st H	24.10	1.58	730
net b	45.06 ⁿ	2.95	284	st e	23.12	1.19	1254
net py	49.23 ⁿ	3.08	264	st DI	25.06	2.31	351
d b	32.57	3.15	221	st Ubx	32.82	1.13	1718
d py	49.66 ⁿ	2.04	602	st “brown”	45.18 ⁿ	2.57	374
b py	29.08	2.31	385	st p ^p	45.12	0.94	2790
b sd	35.55	2.48	374	st pm-l	47.53 ⁿ	2.27	484
b bw	36.66	1.62	889	ae p ^p	40.60	2.38	426
b up	39.88	1.84	707	H p ^p	37.68	1.29	1409
sw py	21.63	1.26	1072	e p ^p	36.91	1.36	1254
sw bw	29.96	1.71	714	Ubx “brown”	24.06	2.21	374
sw up	37.86	1.92	639	Ubx p ^p	28.83	1.32	1179
py sd	6.34	1.18	425	Ubx pm-l	45.65 ⁿ	2.26	484
py up	15.27	1.11	1054				
py pm	32.13	2.45	364				
sd pm	27.85	2.77	262				

ⁿ – not significant, * P<0.05, all others P<0.000

FlyBase, 1999) and *pm-l* (plum-like eye colour – no apparent homologous locus in *D. melanogaster*). The second chromosome locus plum (*pm* in Sturtevant, 1929) is now known to be a recessive allele of the Punch locus (Sugaya and Fuyama, 1995). In addition to results in Sturtevant (1929), loci that have been shown to be allelic to *D. melanogaster* are: X chromosome – prune (*pn*), ruby (*rb*) and rudimentary (*r*) (Rux and Coyne, 1991); Chromosome 2 – *net* (our data), straw (*sw*, Sturtevant and Novitski, 1941), *bw* (Rux and Coyne, 1991); Chromosome 3 – *juv* (Sturtevant and Novitski, 1941), *e* (our data), and *Ubx* (Puro, 1971).

Preliminary test crosses located mutants to chromosome 2 or 3. Recombination fractions were estimated using 2- or 3-point testcrosses. Results from 3-point test crosses were used in defining locus order, but only recombination fractions between adjacent loci were then used in constructing linkage maps. Our data are given in Table 1.

Table 2. Map positions for each locus on each chromosome.

X Chromosome		Chromosome 2		Chromosome 3	
Locus	Position	Locus	Position	Locus	Position
pn	0.0	net	0.0	rd	0.0
E	1.4	T	19.0	cu	11.7
y	4.0	d	25.3	juv	12.5
w	8.2	b	70.6	se	19.1
	10.7	a-w	79.7	rh-b	36.4
rb	14.4	sw	87.4	d-l	38.4
cv	19.3	S-a	90.3	st	53.1
vs	25.7	py	108.2	ae	67.4
sn	26.0	vg	113.9	H	74.2
v	28.5	sd	115.0	e	76.5
dy	42.3	bw	118.9	DI	78.2
tb-b	47.7	up	124.7	Ubx	90.3
g	49.5	pm	143.9	ap	91.3
r	60.1			bp	92.5
f	64.1			“brown”	115.1
tb-a	66.0			p ^p	121.4
fu	68.5			rg	125.4
bb	75.1			M	153.3
				ca	154.8
				pm-l	157.3

For each testcross, recombination values were estimated using the program LINKAGE-1 (Suiter *et al.*, 1983). Linkage maps were constructed from the pairwise recombination data (combining our data with that of Sturtevant, 1929) using the program GENMAP (Lalouel, 1977), with application of the Kosambi (1944) mapping function. For the X chromosome, Sturtevant’s (1929) data for *w vs* and for *vs sn* (both based on only 79 flies) fitted poorly, and were deleted. Map positions for the loci on each chromosome are given in Table 2.

Acknowledgments: Much of the data was collected some years ago, and is presented with apologies to those colleagues who have received preliminary results that are changed here.

References: Ciecko, S.C., and D.C. Presgraves 1999, *Dros. Inf. Serv.* 82: 120-121; FlyBase 1999, *Nucleic Acids Research* 27: 85-88. <http://flybase.bio.indiana.edu/>; Jones, C.D., and H.A. Orr 1998, *Dros. Inf. Serv.* 81: 137-138; Kosambi, D.D., 1944, *Ann. Eugen.* 12: 172-175; Lalouel, J.M., 1977, *Heredity* 38: 61-77; Puro, J., 1971, *Dros. Inf. Serv.* 46: 50; Rux, J.G., and J. Coyne 1991, *Dros. Inf. Serv.* 70: 282; Sturtevant, A.H., 1929, *Carnegie Inst. Wash. Publ.* 399: 1-62; Sturtevant, A.H.,

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