



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

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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<sup>p</sup>* (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 *jv*, Puro, 1971), *jv* (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							
<i>y w</i>	8.41	0.80	1200	<i>rd jv</i>	13.29	1.41	579
<i>y v</i>	22.93	1.48	807	<i>jv se</i>	7.13	1.28	406
<i>w v</i>	19.54	1.22	1055	<i>jv st</i>	35.51	1.42	1129
<i>w f</i>	42.10	1.49	1100	<i>se st</i>	29.95	2.02	514
<i>v f</i>	26.65	2.14	428	<i>st ae</i>	15.01	1.73	426
				<i>st H</i>	24.10	1.58	730
Chromosome 2							
<i>net b</i>	45.06 <sup>n</sup>	2.95	284	<i>st Dl</i>	25.06	2.31	351
<i>net py</i>	49.23 <sup>n</sup>	3.08	264	<i>st Ubx</i>	32.82	1.13	1718
<i>d b</i>	32.57	3.15	221	<i>st “brown”</i>	45.18 <sup>n</sup>	2.57	374
<i>d py</i>	49.66 <sup>n</sup>	2.04	602	<i>st p<sup>p</sup></i>	45.12	0.94	2790
<i>b py</i>	29.08	2.31	385	<i>st pm-l</i>	47.53 <sup>n</sup>	2.27	484
<i>b sd</i>	35.55	2.48	374	<i>ae p<sup>p</sup></i>	40.60	2.38	426
<i>b bw</i>	36.66	1.62	889	<i>H p<sup>p</sup></i>	37.68	1.29	1409
<i>b up</i>	39.88	1.84	707	<i>e p<sup>p</sup></i>	36.91	1.36	1254
<i>sw py</i>	21.63	1.26	1072	<i>Ubx “brown”</i>	24.06	2.21	374
<i>sw bw</i>	29.96	1.71	714	<i>Ubx p<sup>p</sup></i>	28.83	1.32	1179
<i>sw up</i>	37.86	1.92	639	<i>Ubx pm-l</i>	45.65 <sup>n</sup>	2.26	484
<i>py sd</i>	6.34	1.18	425				
<i>py up</i>	15.27	1.11	1054				
<i>py pm</i>	32.13	2.45	364				
<i>sd pm</i>	27.85	2.77	262				

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