Table 2. Disjunction data for chromosomes 1 and 4 from females with unmarked fourth chromosomes mated to $Y^{S}X.Y^{L}$, In(1)En, v f B/0; C(4)RM, ci ey^{R}/0 males.

Female X Chromosomes	Constitution of Ova Producing Recovered Progeny: X,4+ X,44	XX,4+ XX,44	0,4+ 0,44	X,0	XX,0	0,0	Total Progeny	Percent Exceptions: X	4
y tw^3 su(w^a) w^a/ y tw^3 su(w^a) w^a	8094	2	2	2	1	0	8101	0.06	0.04
tw/tw	2425	4	13	3	1	0	2446	0.74	0.16
tw/y tw^3 su(w^a) w^a	112	0	0	0	0	0	112	0.0	0.0

were not marked, diplo-4 and mono-4 ova were indistinguishable. Homozygous tw^3 females produced 0.06% X exceptions and 0.04% nullo-4 exceptions, rates which are remarkably close to control rates (0.06% X exceptions and 0.05% nullo-4 exceptions - see Table 1 in Davis 1971). However, homozygous tw females produced exceptions at rates which were 12 times (18/2446 = 0.74%) and 3 times (4/2446 = 0.16%) the control rates for the X and fourth chromosomes respectively. Although these rates of nondisjunction are modest compared to those of meiotic mutants which have been studied, they are significantly higher than control rates.

Females heterozygous for tw and tw^3 were also mated to the tester males. No exceptional progeny were recovered, although only 112 total progeny were scored. Heterozygous females mated to Canton S wild type males produced 231 progeny with no X exceptions. Fourth chromosome exceptions would not have been recognized. The low number of progeny scored prevents firm conclusions, but the data suggest that meiosis in heterozygotes is more like homozygous tw^3 than like homozygous tw.

A total of 335 tw/tw females mated to C(3L)RM, se h rs^2; C(3R)RM, sbd gl e^s males produced 7 progeny while 207 tw/tw females mated to C(2L)RM, dp; C(2R)RM, px males produced 3 progeny. Since viable euploid zygotes can only result from aneuploid ova, these females are also showing some low frequency of nondisjunction for the large autosomes. Crosses of 57 tw^3/tw^3 females to C(3L)RM, se h rs^2; C(3R)RM, sbd gl e^s males produced no progeny.

Since tw/tw females show chromosome nondisjunction while tw^3/tw^3 females do not, an attempt was made to separate the morphological and nondisjunctional phenotypes. One generation of free recombination between the chromosome bearing tw and a Canton S wild type X was allowed. Twenty-three recombinant chromosomes with tw and 21 recombinant chromosomes with tw^+ were isolated in male progeny. Stocks were made of all 44 recombinant chromosomes, from which homozygous females were selected and tested for nondisjunction by mating to the same tester males used previously. Overall, the tw lines produced 21 X chromosome exceptions (0.31%) and 3 fourth chromosome exceptions (0.04%) among 6763 progeny while the tw^+ lines produced 29 X chromosome exceptions (0.23%) and 8 fourth chromosome exceptions (0.06%) among 12,824 progeny. Individual lines varied from no exceptions to about 1% exceptions in both groups. Thus the meiotic nondisjunction in females appears to be caused by genes which are independent of the twisted locus.

References: Davis, B.K. 1971, Molec. Gen. Genetics 113:251-272; Davis, B.K. 1975, Genetics 80:s25; Davis, B.K. 1979, DIS this issue; Lindsley, D.L. and E.H. Grell 1968, Genetic Variations of D. melanogaster, Carnegie Inst. Wash. Publ. No. 627.

De Salle, R., J.S. Yoon* and L.H. Throckmorton. University of Chicago, Chicago, Illinois, and *Bowling Green State University, Bowling Green, Ohio. Karyotypes of two new species of the virilis group of Drosophila.

Recently, two new species have been discovered in the virilis group, one from Japan and one from western Canada. Their descriptions will be published shortly (Watabe and Higuchi, in publication; Throckmorton and Yoon, in preparation). A cytological study of them is underway. With respect to karyotypes, it shows the following. The species from Japan has a rod-shaped X, a submetacentric Y, one pair of small metacentrics, three pairs of rods, and a pair of dots. Preliminary analysis of the salivary gland chromosomes identifies the small metacentric as chromosome 2 of earlier workers, and the karyotype of this species may be the hypothetical primitive III of Hsu (1952) or very near to it. Approximately half of the male lar-

vae of our stock carry an extra Y chromosome, with the two Y's identical to each other in all respects. The females may also carry a supernumerary Y, but that condition occurs less frequently than in the males.

The species from western Canada proves to have a rod-shaped X, a submetacentric Y, one pair of small metacentrics, one large metacentric pair, one pair of larger rods and one pair of small rods. With the exception of the small rods in place of dots, this karyotype is very similar to that published for the European D. littoralis. We are grateful to Dr. E. Momma for providing us with the stock of the new Japanese species and to the National Drosophila Species Resource Center, the University of Texas, for providing us with a strain of the new species from Canada. This work was supported in part by National Institute of Health grant GM 23007 to L. H. Throckmorton.

References: Hsu, T.C. 1952, Univ. of Texas Publ. 5204:35-72; Watabe, H. and C. Higuchi (in publication), submitted to Annot. Zool. Japan. (Z); Throckmorton, L.H. and J.S. Yoon (in preparation).

Dewees, A.A. Sam Houston State University, Huntsville, Texas. Lethal-bearing genomes from a Texas population of D. melanogaster.

Second and third chromosomes were sampled directly from a natural population near Huntsville, Texas, and analyzed simultaneously for the presence of lethal genes. The A_1B_{18} marker stock, supplied by Dr. Bruce Wallace, was used to produce flies isogenic for both second and third chromosomes (Wallace, Zouros and Kimbras 1966). This stock contains two reciprocal translocations, designated (Cy L; Ubx)/(Pm; Sb), and allows second and third chromosomes to be handled simultaneously. The mating scheme was initiated by crossing single wild-caught males to virgin (Cy L; Ubx)/(Pm; Sb) females in shell vials. From each parental mating a single F_1 male (Cy L; Ubx)/(+;+) was mated with a (Cy L; Ubx)/(Cy; Pm) female. Virgin F_2 (Cy L; Ubx)/(+;+) brothers and sisters were mated in half pint bottles to produce an F_3 generation (in some F_2 matings (Pm;Sb)/(+;+) flies were used). The expected proportion of viable F_3 flies, assuming lethal-free wild type chromosomes, is 2 (Cy L; Ubx)/(+;+): 1 +/+;+/+.

Second and third chromosomes, "genomes", from a total of 78 wild-caught males were carried through to the F_3 generation. An average of 105 F_3 flies was examined for the 78 genomes. The distribution of genomes into viability classes is presented in Table 1 for each of two collecting periods. The results from a 2x4 contingency chi-square analysis ($\chi^2_3 = 0.42$; $0.9 < P < 0.975$) indicate no difference in distributions over the two months. The total percentage of lethal plus semilethal genomes was 89.7% (70/78), based on pooling the three lowest viability classes. These results are similar (2x2 contingency $\chi^2_1 = 3.4$; $0.05 < P < 0.1$) to genome lethal plus semilethal frequencies reported by Wallace et al. (1966). Using the same balancer stock for the detection of viability differences in a Bogota, Colombia, population, they reported 79.8% (95/119) lethal plus semilethal genomes. Although no effort was made in the present study to localize the lethal effects of a genome to the individual chromosomes, some predictions can be made based on the findings of Wallace et al. (1966). They reported that their genome lethals were nearly equally distributed between second and third chromosomes. Band and Ives (1963) also reported similar lethal plus semilethal frequencies for these two chromosomes tested separately. Under the assumption of equal chromosome frequencies, lethal plus semilethal frequencies in the Huntsville, Texas, population can be individually determined for the second and third chromosomes as follows: Let p = frequency of lethal plus semilethal chromosomes; then $(1-p)^2$ = expected frequency of genomes having both second and third chromosomes free of lethal and semilethal genes. Eight of 78 genomes were in this category; therefore, the estimate of p is $1-\sqrt{8/78} = 0.68$.

Ives (1945) reported second chromosome lethal plus semilethal frequencies from 34% to 67% for eastern U.S. populations of D. melanogaster, with the highest frequencies obtained for Florida populations. The southeast Texas population sampled in the present study appears to be quite similar in its frequency of lethal plus semilethal chromosomes to Florida and Colombia populations.