Koliantz, G. Teachers Training College, Tehran, Iran. Recombination changes in D. melanogaster.

Generation	Low line	High line
1	16.6	18.1
2	16.2	18.4
3	15.9	18.6
4	16.1	18.2
5	16.1	18.2
6	15.9	18.6
7	15.9	18.5
8	16.1	18.6
9	16.0	18.7
10	15.9	18.7

The recombination value between Bl-L^2, derived from Bl L^2/al^2 Cy lt^v sp, was studied under artificial selection. Virgin Bl L^2/+ + females were crossed in two lines with Gayaneh wild type males. In the F_1 four recombination classes (Bl-L^2, +, Bl and L^2) were obtained. In each selected line, Bl L^2/+ + females were made to cross with their wild-type brothers in over ten generations. All flies were raised in Mostashfi medium and reared at 23 ± 1°C.

Results and conclusion: The table shows the recombination values within ten generations.

For each selected line a plateau was formed, which shows slight variability in the recombination classes.

No changes in fecundity of Bl L^2/+ + females were observed in either line.

In the 12th generation, a reciprocal cross was made between the two selected lines. The average 16.9 for Bl L^2/+ +♀L x + +/+ +♂H and 17.1 for Bl L^2/+ +♀H x + +/ + +♂L was observed, which does not show a significant dominance of one over the other.

Reference: Kidwell, M.G. 1972, Genetics 70:419-443.

Evans, W.H. Western Washington State College, Bellingham, Washington. Non-random segregation in Drosophila females.

In the course of experiments designed to show the extent of major autosome nondisjunction in inversion heterozygous females a case of non-random segregation was found.

XX;Sm1/+;CxD/+ females 2 to 4 days of age were mass-mated to attached 2 males (C(2)L, dp;C(2)R, px). Tallies of offspring genotypes are given in Table 1.

These results show that patroclinous-2 progeny are predominantly +/+ for the third chromosomes while most matroclinous-2 progeny receive the CxD chromosome from their mothers. The non-randomness is in the tendency for the CxD chromosome to be included in diplo-2 eggs beyond expectation ($P < .05$).

Table 1. Progeny from XX;Sm1/+;CxD/+ ♀♀ x C(2)L, dp;C(2)R, px ♂♂.

Matroclinous-2		Patroclinous-2	
Sm1/+;+/+	4	dp, px;+/+	19
Sm1/+;CxD/+	14	dp, px;CxD/+	5
Total	18	Total	24

The simplest model that could account for these results would be that the Sm1 and CxD chromosomes tend to the same pole during meioses that are nondisjunctional for the second chromosomes. If this were so one would expect a similar but reciprocal tendency for the Sm1 chromosome to be included in diplo-3 eggs. As shown in Table 2, the results of such a test do not conclusively support this model.

Table 2. Progeny from XX;Sm1/+;CxD/+ ♀♀ x C(3)L, ri;C(3)R, sr ♂♂.

Matroclinous-3		Patroclinous-3	
+/+;CxD/+	31	+/+;ri, sr	38
Sm1/+;CxD/+	38	Sm1/+;ri, sr	24
Total	69	Total	62

Another model that fits the results better is this: All three unpaired major autosomes may compete for pairing sites on the arms of the non-inverted third chromosome. The CxD chromosome often pairs with its homolog, at least along one arm. However, either of the second chromosomes may pair along the other arm. The remaining second chromosome is assumed to remain univalent. During segregation this situation, as often as it occurs, leads to the formation of diplo-2 eggs that are CxD or nullo-2 eggs that are not.

The inconclusive results shown in Table 2 indicate that if the non-inverted second chromosome has similar pairing sites they are less effective than those of the third chromosome in finding pairing partners. Perhaps this could be simply because the second chromosome is shorter. A question naturally arises as to why the CxD chromosome cannot pair with more than one partner as well as its non-inverted homolog. It may be that in the CxD chromosome one of the pairing sites has been disrupted. Further work is underway to test the validity of the multiple pairing site idea.