a T(2;3)-1, having a break in polytene section 42A6-10, and a T(2;3)-3 ♀, having a break in 43F-1, showed complementation. In referring back to Figure 1, it is evident that this proximal region of 2R euchromatin is associated with a high proportion of homozygous lethal translocations.

Examples of other inter se combinations having similar breakpoints which also complemented include: T(2;3)-5♂ x t(2;3)-13♀ , 2Rh/2Rh ; T(2;3)-10♂ x T(2;3)-3♀, [84D3-8/83D5-E1]; T(2;3)-14♂ x T(2;3)-46♀, [79E2-5/78B]; T(2;3)-42♂ x T(2;3)-1♀, [89A1-3/87D4-13]; T(2;3)-13♂ x T(2;3)-3♀, [83E/83D5-E1]; T(2;3)-57♂ x T(2;3)-20♀, [51F/51D2-7]; T(2;3)-57♂ x T(2;3)-5♀, [61C7-9/62E3-8]; T(2;3)-19♂ x T(2;3)-3♀, [43B1-C1/42A6-19].

Table 2, however, also lists several exceptional combinations which were noted. Four different inter se combinations appeared to be sterile. In each of these combinations, T(2;3)-13♂ x T(2;3)-52♀, T(2;3)-42♂ x T(2;3)-10♀, T(2;3)-42♂ x T(2;3)-19♀, and T(2;3)-10♂ x T(2;3)-20♀, eggs were laid in a dispersed pattern indicating that fertilization had occurred, yet none had appeared to have hatched. It is also interesting to note that one of the reciprocal crosses T(2;3)-13♀ x T(2;3)-52♂ was not sterile and produced progeny according to the expected frequencies. This result was rechecked by repeating each of the reciprocal crosses and again yielded the same results. Two additional inter se combinations involving the crosses T(2;3)-42♂ x T(2;3)-50♀, and T(2;3)-42♂ x T(2;3)-3♀ proved to complement; however, all of the trans-heterozygotes scored (approximately 40 or more in each case) were males. Meiotic segregation per se does not appear to be involved, as each translocation heterozygote male (T(2;3)/bw;ve st e) segregated euploid products (i.e., T(2;3) or t;ttt) in equal proportions. It is possible however that segregation may have been unusual in conjunction with TM3 and/or in translocation heterozygote females. Unfortunately, we can offer no explanation for these results.

The only cross which failed to show complementation was T(2;3)-6♂ x T(2;3)-1♀. In analyzing the significance of this result, it should be noted that only 23 F1 progeny were recovered. Also, upon examining the breakpoints of these translocations, we find that T(2;3)-6 is a complex rearrangement, including an inversion which bears a breakpoint in the same polytene section as T(2;3)-1. It is therefore possible that this lethality, or failure to complement, may be due to common breakpoints within one gene, rather than the type of chromosome configuration produced by this inter se combination. Unfortunately, these exceptions cannot be further analysed since all crosses involve at least one, if not both of the translocations which are no longer available as stocks.

Research is presently ongoing to obtain and analyse additional translocations. This may allow us to identify any important regions of association. Despite the fact that much additional information is still required, a picture is starting to emerge. The results presented here document that many major linkage associations need not be maintained. Some observations, however, suggest that certain regions involving the proximal and distal extremities of each linkage group may require a linear integrity.

A.J.Hilliker was responsible for cytological determination of all polytene chromosome translocation breakpoints. Synthesis and subsequent genetic analysis of the translocations was done by S.N.Trusis.

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Ukil, M., K.Chatterjee and A.S.Mukherjee. University of Calcutta, India. Cytophotometric analysis of in situ binding of non-histone protein to the chromatin in Drosophila melanogaster.

The role on non-histone chromosomal protein in the control of gene activity has been reported earlier (Paul & Gilmour 1968; Spelsberg & Hnilica 1969). Since hyperactivity of the X chromosome in Drosophila male is a consequence of relatively higher net transcription of the X chromosome, it is conceivable that the non-histone protein may have a role in mediating the hyperactivation of the X linked genes. Conversely, it may be predicted that non-histone protein may bind differently with X chromosomal DNA sequences in male and female and to substantiate this presumption we carried out the cytophotometric analysis.

Table 1.

Experiment	No. of observed nuclei	Integrated absorbance ratio 433/547 (Mean ± SE) Proximal segment of X chromosome	Distal segment of X chromosome	Autosome
1. CONTROL				
Male	10	1.78 ± 0.18*	1.97 ± 0.19**	1.32 ± 0.11
Female	10	1.33 ± 0.11	1.32 ± 0.07	1.24 ± 0.13
2. ONLY BUFFER				
Male	15	1.13 ± 0.33	1.16 ± 0.05	1.08 ± 0.06
Female	15	1.05 ± 0.03	1.03 ± 0.05	1.15 ± 0.04
3. BUFFER + NHP				
Male	20	1.75 ± 0.03***	1.73 ± 0.03***	1.23 ± 0.03
Female	20	1.30 ± 0.03	1.31 ± 0.04	1.25 ± 0.04

* $p < 0.05$

** $p < 0.01$

*** $p < 0.001$

First, the non-histone chromosomal proteins (NHP) were isolated separately from male and female Drosophila melanogaster by following standard methods (Elgin & Hood 1973; Phillips & Forest 1973; Chiu et al. 1976) with certain modifications. Formaldehyde-fixed slides were prepared from third instar larval salivary glands, and grouped as follows: (1) treated with 2M NaCl, 1M urea in phosphate buffer (pH 7.6) for 90 min and subsequently with non-histone proteins (Conc. 1 mg/ml); (2) treated with only 2M NaCl, 1M urea in 50 mM phosphate buffer (pH 7.6) for 90 min; (3) control slides without any treatment.

The treated and control slides were stained with Schiff's reagent for 90 min and counter-stained with Napthol-Yellow S for 60 min. The slides were scanned cytophotometrically by using interference band filters at 547 nm for DNA measurements and at 433 nm for NHP measurements. Two area-one wave length method was used for cytophotometric measurements and the values were transformed into AE (integrated absorbance). Results are shown as ratios of AE for 433/547 nm.

Data reveal that the ratio at 433:547 nm is always greater in the male than in the female. Results also reveal that the extraction buffer (2M NaCl, 1M urea in 50 mM phosphate buffer, pH 7.6) unequivocally removes the non-histone proteins from both X chromosome as well as autosomes, although the extraction is non-random. Interestingly, the relatively higher proportion of NHP binding to X chromosome of male is observed in control as well as NHP bound chromatin. Results clearly show that the single X chromosome in the male has a higher binding affinity than that in the female. These data corroborate the proposition that DNA-NHP-Histone organization of the chromatin of X chromosome is mainly responsible for evoking a hyper-template activity of the X chromosome in male Drosophila (Mukherjee 1982).

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