G-banding patterns of the housefly, *Musca domestica*, autosomes and sex chromosomes

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Summary. G-banding patterns were found on the X-chromosomes of the housefly. This indicates the presence of major gene loci on these chromosomes, i.e. sex-linked genes. G-banding patterns were also found on the Y-chromosome of 2 preparations. The first polyploid cell (a tetraploid, 2n=24) for *Musca domestica* was observed in one of the banding preparations.

The usual housefly karyotype comprises 6 pairs of metacentric or submetacentric chromosomes. Males have an X- and a Y-chromosome, and females 2 Xs. Both sex-chromosomes have long been considered to be entirely heterochromatic, the housefly thus lacking any sex-linked major genes[2,3]. That all visible mutant markers found so far are autosomal accords with this view[3].

We used G-banding to analyze a Y-autosome translocation characterizing an Australian strain (Kingsford). The procedure utilized larval cerebral ganglia and pharate adult testes, and is based on the air-drying Giemsa method of Imai et al.[4] and the trypsin-pretreatment G-band technique of Seabright[5]. The colchicine-hypotonic pretreatment was for a period of 30–40 min. The optimal trypsin-pretreatment period varied between the strains; Kingsford *(KIN)* strain preparations usually required 15 sec as against 10 sec for the *WHO* strain preparations. We used a 0.15% solution of trypsin in phosphate buffer (0.005 M, pH 6.8). C-banding was attempted unsuccessfully, using the denaturing agents; 5 M urea, hot standard sodium citrate (SSC) and trypsin.

The nature of G-bands is still uncertain, but it seems clear that the technique reveals heterochromatin as well as heterogeneity between euchromatic regions[6]. We found distinct bands on the X-chromosomes (figure 1). These bands strongly suggest that there are euchromatic regions in the X-chromosome yet to be identified. The intensity of banding varied from one part of a preparation to another, sometimes within a single cell, but the banding patterns of the different X-chromosomes studied (*KIN* and *WHO* strains) appeared similar, given the variation in intensity of staining.

In *Musca domestica*, the presence or absence of a Y-chromosome determines the sex of the individual, whether there is a separate Y-chromosome or whether a translocation has attached this element to an autosome, whose markers then show holandric inheritance[3]. The Y-chromosome does therefore have some genetic activity, perhaps including major genes. In 2 of the *WHO* preparations (out of a total of 70 male brain preparations), the Y-chromosome had a banding pattern (figure 2) suggesting that major loci may occur on this chromosome in addition to the autosomes and X-chromosome. Further information is

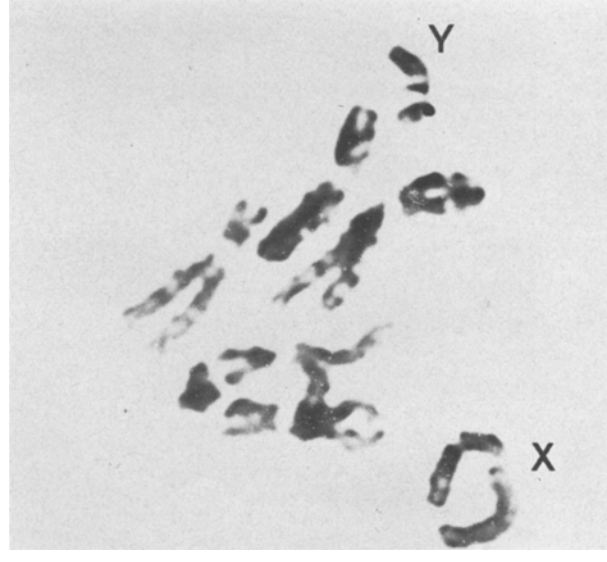

Fig. 2. G-banding patterns of a normal male *WHO* 'brain' preparation. The Y-chromosome exhibits an unusual banding pattern found in only 2 male preparations.

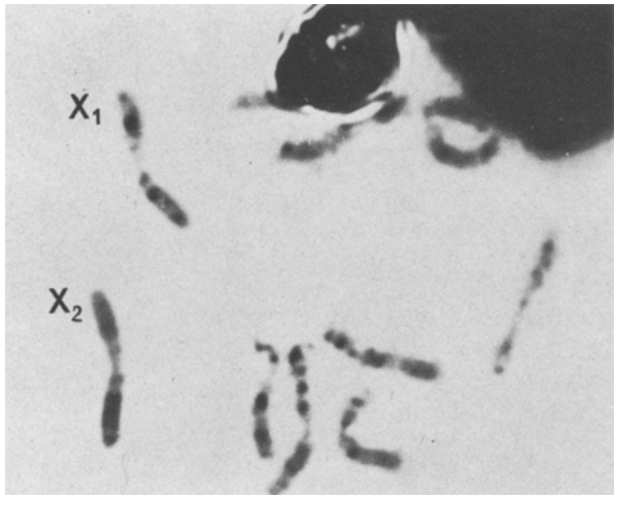

Fig. 1. G-banding patterns of the X-chromosomes of the housefly strain, *WHO*. The preparation is from a female 'brain'.

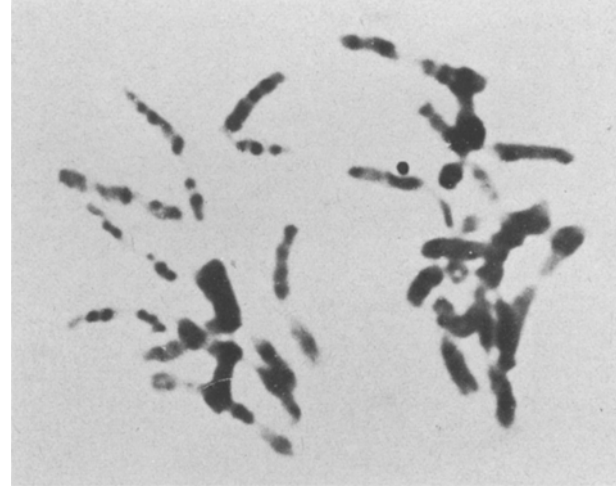

Fig. 3. A tetraploid (2n=24) cell found in *WHO* 'brain' G-banding preparation. This polyploid was considered to be naturally-occurring and was the only polyploid cell found in this preparation.

needed before confident conclusions can be reached concerning the genetic nature of the Y-chromosome.

A tetraploid cell was noted in a 'brain' (supraesophageal ganglion) preparation of *WHO*, the first reported for *M. domestica* (figure 3). Such cells are well-known in other insects (e.g. polyploidy occurs readily in hymenoptera[7]) and aneuploidy is known for both sex chromosomes and autosomes in the housefly[3]. We doubt that the colchicine-hypotonic treatment preceding the air-drying step could have spuriously produced this cell, as this treatment was only applied for 30 min.

G-banding, as described here, should prove a useful tool in correlating the genetic and cytological maps of the housefly. Furthermore, our discovery of bands on the X-chromosome should reorientate thinking on the mapping of new mutants, and the possibility of sex differences in insecticide resitance. Although sex-linked markers seem rare among visible mutants[3,8], this might not be so in the case of allozymic loci.

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Recombination in the male housefly, *Musca domestica*

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Summary. Autosome II recombinations of up to 30.7% were found in male houseflies bearing a Y-chromosome translocation on autosome II. This is the highest recorded rate of recombination found in male houseflies, therefore indicating another possible source of genetic variation. The male crossover rates were related to map distances and resulted in an inaccurate estimate for one of the loci. Explanations are provided. Male crossing-over is related to cytogenetics of the Y-chromosome.

The housefly has a high degree or genetic variability which contributes to its great adaptability to new environments[2]. Recombination plays a major role in genetic variability of most organisms, but, as is the case in *Drosophila*, the housefly male has exhibited a virtual lack of crossing-over thus reducing the potential of recombination as a factor producing variability. Autosome III of the housefly male (there are 5 autosome pairs, 2n = 12) has been shown to have crossover values of 0 to 11% between the loci *bwb* (brown body) and *ge* (green eyes). These 2 loci are between 20.3 and 28.2 map units apart[3]. Crossing-over is considered fairly common for this autosome in females, with recombination frequencies of up to 40% for some loci. A very low frequency of recombinants (0.2%) has been found for autosome II in males, but actual recombination values found for the male houseflies may have been due to genetic mechanisms other than crossing-over, for example, nondisjunction[4].

In a recent examination of a Y-autosome translocation strain (identified by genetic and cytogenetic techniques[5]) from Kingsford, Australia, exhibiting holandric inheritance, recombination rates of up to 30.7% were found in males of this strain when crossed with multimarker stock females. Only a recombination involving autosome II was identified as it was this autosome which had 2 markers, the visible mutant marker or the Y-translocation. All recombinants were found in the F_2-generations.

The procedure was as follows: Kingsford *(KIN)* males were crossed with virgin females from a multimarker stock *608Q*, in which 4 autosomes were marked, each with one visible recessive gene (*ac* = alicurve, chromosome I; *ar* = aristapedia, chromosome II; *bwb* = brown body colour, chromosome III; and *ocra* = ocra eye colour; chromosome V)[6]. The F_1 male progeny (phenotypically wild type but heterozygous for the marker loci) were then backcrossed to virgin females of the homozygous multimarker stock. The experiment was repeated using a 2-marker stock, *WTIN* (*stw* = stubble wings, chromosome II; *w* = white-eye colour, chromosome III). The cross involving *608Q* showed 30.7% recombination between the aristapedia locus and the Y-chromosome translocation (table 1). The cross involving *WTIN* exhibited 9.27% recombination between the stubby wing locus and the Y-translocation (table 2). If these recombination rates are converted to map distances, the stubble wing and the aristapedia loci are 21.43 map units apart, which is a similar result to that obtained in previous studies on crossover suppressors[2]. The stubble wing locus is 9.27 map units from the point of attachment of the Y-chromosome fragment. The inconsistency of this distance with the map distances between various other markers on the same chromosome arm[2] may be explained by the loss of the segment of autosome II during the process of the reciprocal translocation with the Y-chromosome[5].

An explanation for the high rate of recombination in the *KIN* male is that the segment of the Y-chromosome lost

Table 1. Recombination in the cross, *608Q* × *608Q/KIN*

	Males	Females
Recombinant groups	*ar*	+
Number of recombinants	5	465
Total number of flies	1531	
Percent recombination	30.7	

Table 2. Recombination in the cross, *WTIN* × *WTIN/KIN*

	Males	Females
Recombination groups	*stw, wstw*	+, *w*
Number of recombinants	1	362
Total number of flies	3913	
Percent recombination	9.27	