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# Copy-number dependent transpositions and excisions of the mdg-1 mobile element in inbred lines of *Drosophila melanogaster*

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**The chromosomal location of the mobile element mdg-1 was studied in 17 highly-inbred lines of *Drosophila melanogaster*. Although some lines were stable for their pattern of insertion sites from the 15th to the 27th and 35th brother–sister generations, others showed a high rate of gain of new insertion sites or a high rate of excision (loss of elements). In one line, 8 new insertion sites on the third chromosome were associated with an inversion on this chromosome; there is evidence that the rearrangement occurred premeiotically, thus suggesting a "transposition burst" in this line. There was no correlation between the rate of gain of new insertions and the rate of excision, this latter rate being higher. We have strong evidence that transposition is replicative. Excisions and, to a lesser extent, gains of insertions have been found to be copy-number dependent, suggesting that this is a main mechanism for copy-number regulation. Most inbred lines tended toward an optimal mdg-1 copy number for which they no longer showed transposition or excision (they became stable). These results may explain the instability sometimes reported in inbred lines.**

## INTRODUCTION

It is now well established that the genome of eukaryotes contains many mobile DNA sequences. Their role in the organism is, however, far from being elucidated and only their influence on mutation rates and chromosomal breakages (Green, 1976; Berg, Engel and Kreber, 1980; Brégliano *et al.*, 1980; Kidwell, 1983; Engels and Preston, 1984) and hence on the genetic load (Mukai and Yukuhiro, 1983; Biémont *et al.*, 1985) is widely accepted. Very little is known about the regulation and control of transposition. The transposition rate is estimated to be around $10^{-3}$; higher values are observed only in the offspring of matings between certain strains of *Drosophila melanogaster* (the hybrid dysgenesis phenomenon: Engels and Preston, 1981; Thompson and Woodruff, 1981; Bingham *et al.*, 1982; Brégliano and Kidwell, 1983; Gerasimova *et al.*, 1984). We also have evidence against a high rate of transposition under "normal conditions" (Young and Schwartz, 1981; Pierce and Lucchesi, 1981) and against a generally high mutation rate on highly homozygous lines (Woodruff *et al.*, 1984; Junakovic *et al.*, 1984). However, highly inbred populations of *Drosophila* may show genome reshuffling when submitted to mass matings (Belyaeva *et al.*, 1982) and inbred lines of maize may have unstable mutations produced by the Mu transposable element (Strommer, 1983). We show here, by *in situ* hybridisation on salivary gland chromosomes of *Drosophila melanogaster*, that some highly inbred lines had a high incidence of transpositions or excisions of the mdg-1 mobile element, though other lines remained stable; this phenomenon depended on the mdg-1 copy number of the genome of the lines.

## MATERIALS AND METHODS

A laboratory population of *Drosophila melanogaster* was established from about 50 flies captured in Azerbaidjan (USSR) in the end of 1983. The population so formed was maintained in the laboratory by mass culture at 25° before 17 inbred lines were established in October 1984. The lines were then maintained by one sib pair every generation. At generations 15, 27 and 35, each inbred line was analysed for their number and localisation of the mdg-1 mobile element (see Ilyin *et al.*, 1980 and Tchurikov *et al.*, 1981 for mdg-1

characteristics) by *in situ* hybridisation of a biotinylated DNA probe on giant salivary chromosomes (Rigby *et al.*, 1977; Langer-Safer *et al.*, 1982). Four to six nuclei were analysed per larva. It was verified that the number and location of mdg-1 elements were constant between different nuclei of the same salivary gland.

## RESULTS

### *Distribution pattern of mdg-1 elements*

Figure 1 presents the distribution pattern of mdg-1 along the chromosomes for the 17 inbred lines analysed at the 15th generation. Two to three larvae were analysed for each of these 17 lines; it was found that, for a given generation, the pattern of hybridisation was identical for every individual of a particular line. For all the 17 inbred lines, 315 insertions were detected on 113 cytologically distinguishable labelled sites. As already reported for mdg-1 element, there are some regions of the chromosomes in which more insertions were found than in others; these regions appeared to be the same regardless of the population studied (Belyaeva *et al.*, 1984; Biémont *et al.*, 1985; Biémont, 1986). Many sites appeared in high frequency (19F, 22A, 52A, 53AB, 67F, 73B, 82F, 92DE, 96F) and may represent hot spots. This is also reflected in fig. 2, which represents the number of occurrences of mdg-1 mobile elements (the frequency spectra) in the 17 inbred lines (*i.e.*, on 17 gametes chosen randomly from the initial population).

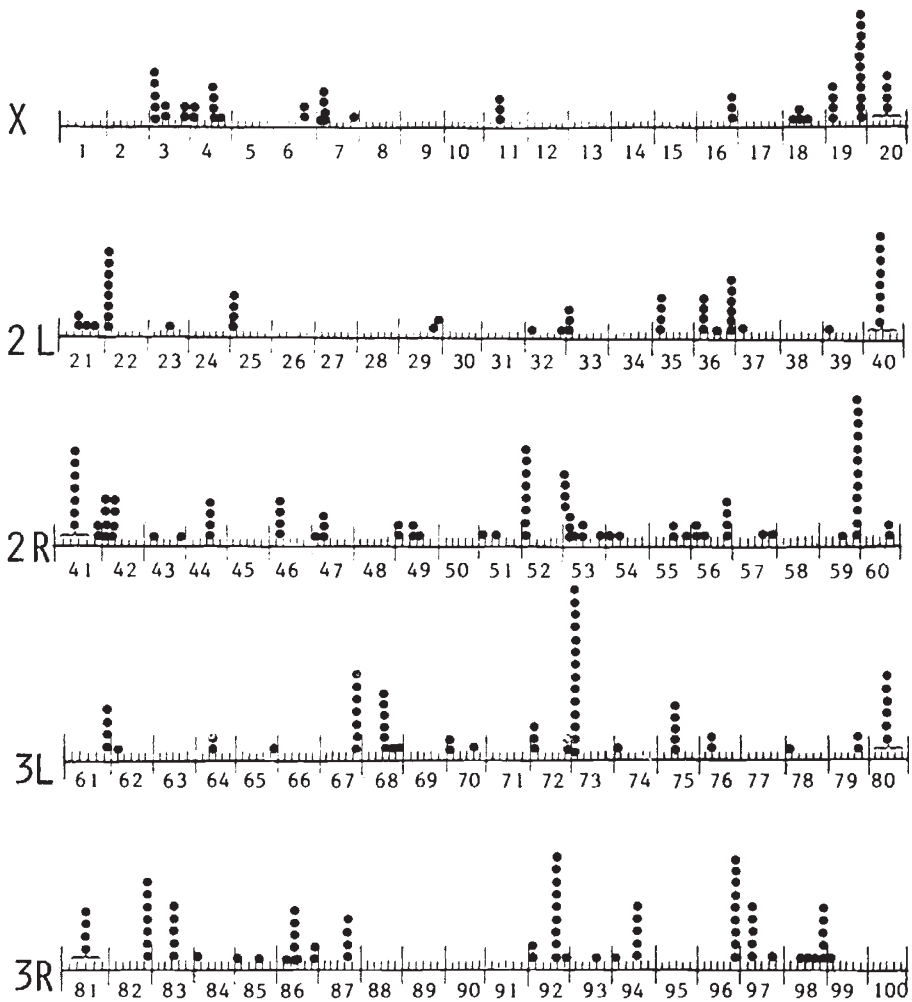


**Figure 1** Location and number of mdg-1 insertions (frequency spectra) found in the 17 inbred lines. The region numbers correspond to Bridges' subdivisions of the chromosomes.

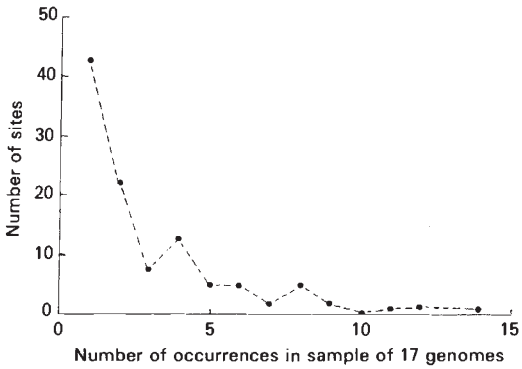


**Figure 2** Distribution of the mdg-1 element in 17 genomes (all chromosomes confounded).

### *Number of sites per inbred line*

Table 1 shows the number of insertion sites for all the chromosomes of the 17 inbred lines at the 15th generation. The average genome had a total of 19·4 insertion sites. The highest number of insertions was observed for the 2R ($n = 5{\cdot}2$) and the 3R ($n = 4{\cdot}5$) chromosome arms and the lowest for the 2L chromosome arm ($n = 2{\cdot}8$), which also showed the highest variation coefficient (61 per cent). These results are similar to previous observations done on mdg-1 elements (Biémont, 1986), but they agree neither with the facts that the right arm of the third chromosome exhibits the greatest variability (Strobel *et al.*, 1979) nor with the assumption that mobile element insertions should be less common on the X chromosome, in as much as their deleterious effects are recessive (Langley *et al.*, 1983).

Since homozygous inbred lines may be considered as a random sample of gametes from individuals of the initial population, it is possible to determine the theoretical total number of sites per genome for the 17*17 hybrids obtained from crossing all lines. We found an average value of 32·5 insertions per genome; this value is similar to that reported in the initial population (Biémont, 1986).

### *Evolution of the inbred lines over time*

At the 27th and 35th generations, the inbred lines were analysed again and insertion sites determined on all the chromosome arms. By comparing the insertion patterns of mdg-1 elements between the 15th, 27th and 35 generations, we estimated the rates of transposition (rate of gain of new insertion sites per generation) and excision (rate of loss of sites per generation) over 10 generation periods. The results are summarised in tables 2 to 5. Some lines appeared stable over time whilst others showed a high rate of gain of sites or

**Table 1** Number of labelling sites of mdg-1 insertions per chromosome arm in the 17 inbred lines studied at the 15th generation

| Chromosome arm | Line No 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | Mean | Variation coefficient |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| X | 4 | 1 | 3 | 4 | 3 | 2 | 2 | 1 | 3 | 4 | 5 | 2 | 5 | 3 | 4 | 5 | 3 | 3·17 | 0·40 |
| 2L | 1 | 3 | 0 | 3 | 3 | 4 | 3 | 7 | 5 | 3 | 0 | 2 | 3 | 3 | 4 | 3 | 1 | 2·82 | 0·61 |
| 2R | 5 | 4 | 2 | 7 | 6 | 11 | 2 | 8 | 4 | 3 | 2 | 5 | 6 | 6 | 7 | 6 | 5 | 5·24 | 0·45 |
| 3L | 4 | 5 | 2 | 1 | 2 | 3 | 4 | 5 | 5 | 5 | 3 | 4 | 5 | 5 | 2 | 5 | 2 | 3·65 | 0·38 |
| 3R | 5 | 4 | 4 | 2 | 5 | 1 | 4 | 8 | 4 | 6 | 5 | 3 | 3 | 6 | 7 | 6 | 4 | 4·53 | 0·39 |
| Total | 19 | 17 | 11 | 17 | 19 | 21 | 15 | 29 | 21 | 21 | 15 | 16 | 22 | 23 | 24 | 25 | 15 | 19·4 | 0·23 |

**Table 2** Rate of gain of new insertion sites per generation per chromosome arm in the 17 inbred lines, calculated from the 15th to the 27th generations

| Chromosome arm | Line No 2 | 3 | 4 | 5V | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | Mean | Variation coefficient |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| X | 0 | 0 | 0·11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0·10 | 0 | 0 | 0 | 0·27 | 0·028 | 2·53 |
| 2L | 0 | 0 | 0·11 | 0 | 0 | 0 | 0 | 0·10 | 0 | 0 | 0 | 0 | 0·10 | 0 | 0 | 0 | 0 | 0·018 | 2·23 |
| 2R | 0 | 0 | 0 | 0 | 0·08 | 0·08 | 0 | 0·10 | 0 | 0 | 0 | 0 | 0·20 | 0·09 | 0 | 0 | 0·09 | 0·037 | 1·56 |
| 3L | 0 | 0 | 0·22 | 0·09 | 0 | 0 | 0 | 0 | 0 | 0 | 0·09 | 0 | 0 | 0 | 0 | 0 | 0·18 | 0·034 | 2·04 |
| 3R | 0 | 0 | 0·33 | 0 | 0 | 0 | 0 | 0·10 | 0·08 | 0 | 0·09 | 0 | 0 | 0 | 0 | 0 | 0·82 | 0·083 | 2·48 |
| T (per genome) | 0 | 0 | 0·78 | 0·09 | 0·08 | 0·08 | 0 | 0·30 | 0·08 | 0 | 0·18 | 0 | 0·40 | 0·09 | 0 | 0 | 1·36 | 0·19 | 1·88 |
| T (per chromosome) | 0 | 0 | 0·16 | 0·02 | 0·02 | 0·02 | 0 | 0·06 | 0·02 | 0 | 0·04 | 0 | 0·08 | 0·02 | 0 | 0 | 0·27 | 0·042 | 1·72 |

**Table 3** Rate of excision per generation per chromosome arm in the 17 inbred lines, calculated from the 15th to the 27th generation

| Chromosome arm | Line No 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | Mean | Variation coefficient |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| X | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0·17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0·09 | 0·015 | 2·97 |
| 2L | 0·09 | 0 | 0 | 0 | 0 | 0 | 0 | 0·30 | 0·08 | 0·20 | 0 | 0 | 0 | 0·09 | 0 | 0 | 0 | 0·045 | 1·92 |
| 2R | 0·09 | 0 | 0 | 0·09 | 0 | 0·23 | 0 | 0·30 | 0 | 0·10 | 0 | 0 | 0·30 | 0·36 | 0·14 | 0·08 | 0 | 0·099 | 1·25 |
| 3L | 0·09 | 0·09 | 0 | 0 | 0 | 0 | 0 | 0·10 | 0·25 | 0 | 0 | 0·18 | 0 | 0·09 | 0 | 0 | 0 | 0·047 | 1·60 |
| 3R | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0·50 | 0·08 | 0·10 | 0 | 0 | 0 | 0·09 | 0·14 | 0·08 | 0 | 0·058 | 2·11 |
| T (per genome) | 0·27 | 0·09 | 0 | 0·09 | 0 | 0·23 | 0 | 1·20 | 0·58 | 0·40 | 0 | 0·18 | 0·30 | 0·64 | 0·29 | 0·17 | 0·09 | 0·266 | 1·16 |
| T (per chromosome) | 0·06 | 0·02 | 0 | 0·02 | 0 | 0·05 | 0 | 0·24 | 0·12 | 0·08 | 0 | 0·04 | 0·06 | 0·13 | 0·06 | 0·03 | 0·02 | 0·055 | 1·13 |

**Table 4** Rate of gain of new insertion sites per generation per chromosome are in the 17 inbred lines, calculated from the 27th to the 35th generations

| Chromosome arm | Line No 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | Mean | Variation coefficient |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| X | 0 | 0 | 0 | 0·09 | 0 | 0 | 0 | 0·09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0·09 | 0·016 | 2·23 |
| 2L | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0·13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0·008 | 4·12 |
| 2R | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0·11 | 0 | 0 | 0 | 0 | 0 | 0·006 | 4·12 |
| 3L | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0·11 | 0 | 0 | 0 | 0 | 0 | 0·006 | 4·12 |
| 3R | 0·11 | 0 | 0 | 0 | 0 | 0·13 | 0 | 0 | 0·13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0·022 | 2·23 |
| T (per genome) | 0·11 | 0 | 0 | 0·09 | 0 | 0·13 | 0 | 0·09 | 0·13 | 0·13 | 0 | 0·22 | 0 | 0 | 0 | 0 | 0·09 | 0·058 | 1·20 |
| T (per chromosome) | 0·02 | 0 | 0 | 0·02 | 0 | 0·03 | 0 | 0·02 | 0·03 | 0·03 | 0 | 0·04 | 0 | 0 | 0 | 0 | 0·02 | 0·012 | 1·16 |

**Table 5** Rate of excision per generation per chromosome arm in the 17 inbred lines, calculated from the 27th to the 35th generations

| Chromosome arm | Line No 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | Mean | Variation coefficient |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| X | 0 | 0 | 0 | 0 | 0·13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0·09 | 0 | 0 | 0·25 | 0·27 | 0·043 | 2·06 |
| 2L | 0 | 0 | 0 | 0·09 | 0·13 | 0·25 | 0 | 0 | 0 | 0 | 0 | 0 | 0·09 | 0 | 0 | 0 | 0·09 | 0·038 | 1·84 |
| 2R | 0 | 0 | 0 | 0·09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0·18 | 0 | 0 | 0·13 | 0 | 0·023 | 2·33 |
| 3L | 0 | 0 | 0·09 | 0 | 0 | 0 | 0 | 0·18 | 0 | 0 | 0 | 0 | 0 | 0·22 | 0·09 | 0 | 0 | 0·034 | 2·04 |
| 3R | 0·11 | 0 | 0·18 | 0 | 0 | 0 | 0 | 0·09 | 0 | 0 | 0·11 | 0 | 0 | 0 | 0·09 | 0 | 0·18 | 0·447 | 1·49 |
| T (per genome) | 0·11 | 0 | 0·27 | 0·18 | 0·25 | 0·25 | 0 | 0·27 | 0 | 0 | 0·11 | 0 | 0·36 | 0·22 | 0·18 | 0·38 | 0·55 | 0·184 | 0·870 |
| T (per chromosome) | 0·02 | 0 | 0·05 | 0·04 | 0·05 | 0·05 | 0 | 0·05 | 0 | 0 | 0·02 | 0 | 0·07 | 0·04 | 0·04 | 0·08 | 0·11 | 0·036 | 0·88 |

excision. There was no correlation between the two rates, and the average values of transposition was lower than that of excision ($T = 0{\cdot}19$, $E = 0{\cdot}27$ per genome, per generation, from the 15th to the 27th generation; $T = 0{\cdot}06$, $E = 0{\cdot}18$, from the 27th to the 35th generation). Among the sites that excised or appeared, some were unique sites (seen only in one line) and some were revealed in most of the lines. This suggests that deletions or insertions were at random, at least among the sites susceptible to have an element.

The absence of a relation between rates of gain and excision is in favour of the hypothesis that line instability does not concern transposition and excision simultaneously; therefore, instability was not an intrinsic characteristic of the line. Indeed, as shown in fig. 3, the rates of excision per generation (calculated over a 10 generation period) were directly correlated with the copy number of elements of the lines (the data are those from the tables 2 to 5; Spearman rank correlation coefficients, $r = 0{\cdot}78$, $P < 0{\cdot}001$ and $r = 0{\cdot}87$, $P <$

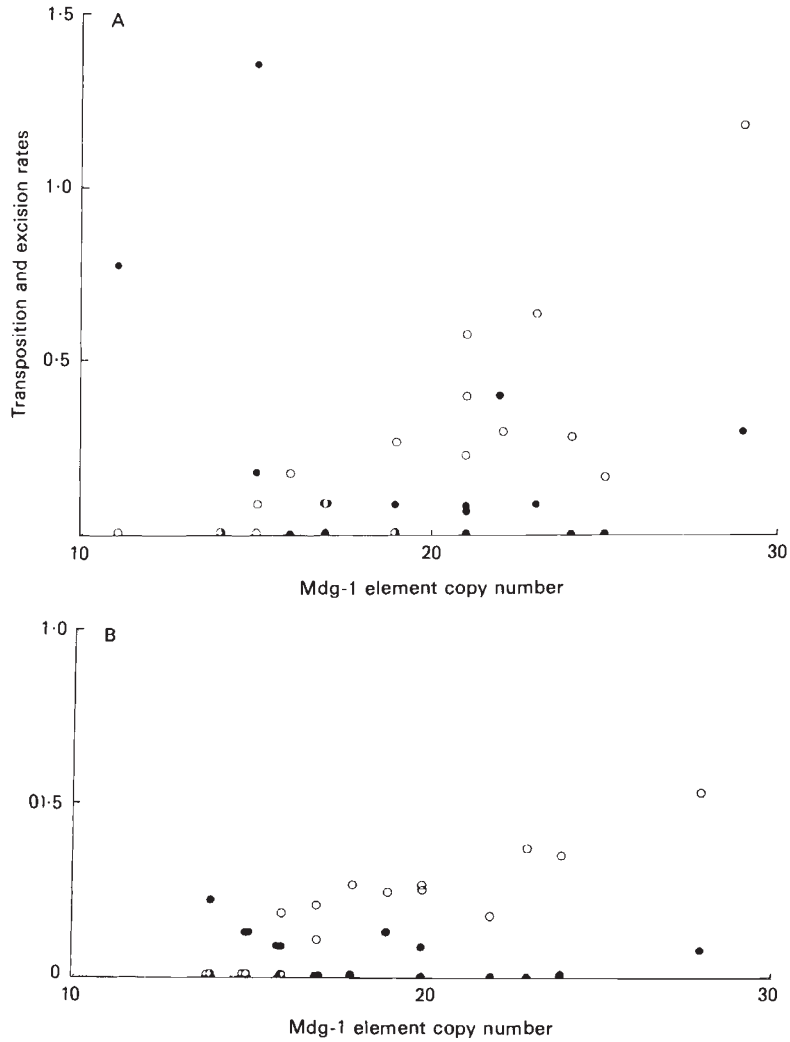


**Figure 3** Rates of gain of new insertion sites per genome per generation, and rates of excision per genome per generation, calculated over the periods from (A) the 15th to the 27th generations, (B) the 27th to the 35th generations, versus the copy number of insertions of the 17 inbred lines, (A) at the 15th generation, (B) at the 27th generation. * Rate values of gain of new insertions, ◦ excision rate values.

0·001 for the periods from the 15th to the 27th and from the 27th to the 35th generations, respectively). The relationship between the rates of gain of sites and the copy number of mdg-1 was not so clear and the Spearman correlation coefficients were not statistically significant ($r = 0{\cdot}17$ and $r = 0{\cdot}34$ for the periods from the 15th to the 27th generations and from the 27th to the 35th generations, respectively). However, the highest rate values were observed in lines having a few copy number of elements. Everything took place as if the copy number of elements of a line tended toward a value, which was a characteristic of the population and not of the line itself. Hence, when the lines had a number of mdg-1 insertions higher than this value, they showed a high rate of excision, so as to lower their copy number; lines with copy number close to this value were stable (lines 8 and 12 from the generation 15, and line 3 at generation 27), and lines with too a small copy number exhibited a high rate of insertion without excision. From these results, we conclude that excision rate of the mdg-1 mobile elements was copy-number dependent. The fact that the role of the copy number of elements was evident for regulating excisions and less clear for insertion rate may be explained by the low average number of elements the lines tended to attain (see fig. 4). Indeed, at the 15th

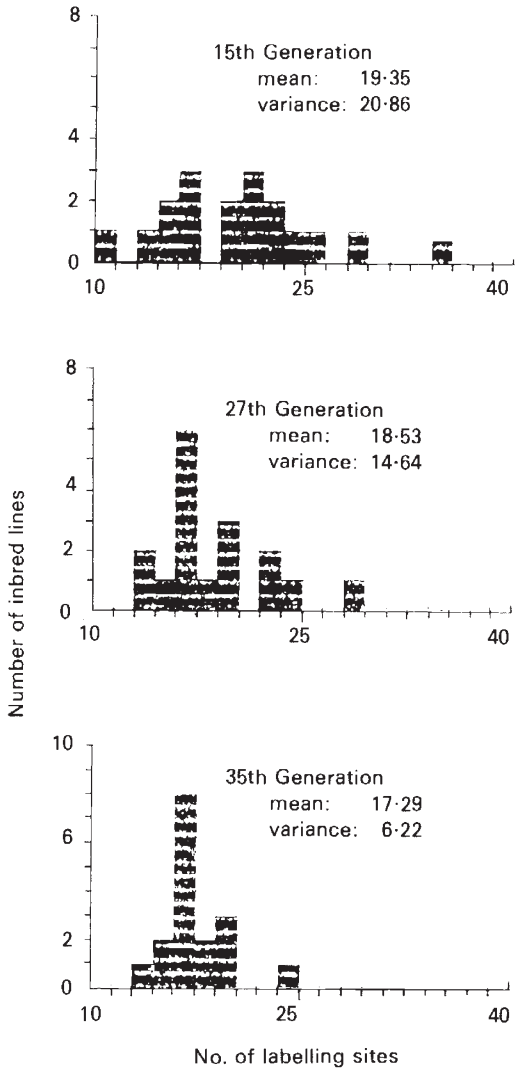


**Figure 4** Distributions of the number of labelling sites in the 17 inbred lines at the generations 15, 27 and 35.

generation, most of the lines had a number of labelling sites higher than the "optimal" value and thus may have had excisions to reduce the number until this optimal value was reached. Only a few lines had a copy number much smaller than the optimal value; these lines showed high transposition rates in succeeding generations, but this was too few a number of lines to make a correlation evident between insertion rate and copy number of elements (see fig. 3).

One can argue that the results are only artefactual, for example as the result of technical and sampling errors. In such cases, the chance of observing new insertions or excisions might increase in lines with high initial copy-number, and should be low in lines with initial small copy-number. It can be shown from tables 2 to 5 that for the lines No 9, 15, 16, 17, which had high copy number of elements at the 15th generation, the insertion rates were low while the excision rates were high. Of course, when excision and insertion rates are low, we cannot discard sampling error to explain such results. However, since such observation cannot be due to *in situ* hybridisation resolution (many nuclei of the same gland were compared, and they always showed the same mdg-1 location pattern), it may reflect heterogeneity in the insertion pattern between individuals of a line. Such heterogeneity could be due to residual heterozygosity within the lines, or to loss or new insertions of elements. Of course, as the level of inbreeding increases, the second explanation is more likely than the first. Note, indeed, that a theoretical probability of heterozygosity at any unselected locus of the inbred lines is about 0·007 at the 20th generation of inbreeding.

One striking point arises with the line 18, which showed, from the 15th to the 27th generation, a high rate of gain of new insertions. Fig. 5 illustrates that the high rate of transposition was associated with an inversion (Inv 86DE-94F). At the 27th generation, 4 larvae were analysed in the line; all

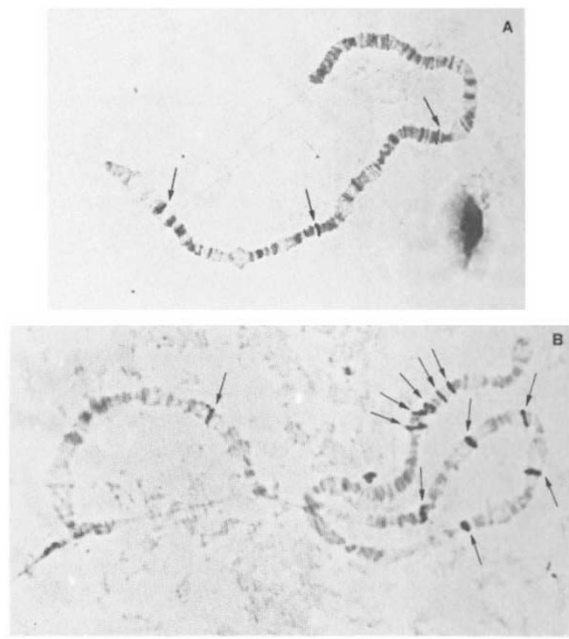


**Figure 5** The 3R chromosome arm of the line No 18. (A) without inversion, (B) with the inversion 86DE-94F. The arrows indicate sites of mdg-1 insertions.

were found heterozygous for the inversion and they showed the same pattern of mdg-1 insertions along the chromosome arms. Strikingly, 4 new insertions were observed within the inversion and 4 new ones outside it (fig. 5 and table 6). The fact that the larvae studied were heterozygous for the inversion suggests a recent event, which should have happened at a premeiotic stage. This hypothesis was corroborated by studying the line in the following generations. As seen table 6, at the 30th generation, one individual (over 4 studied) was found free of the inversion and simultaneously free of those insertion sites found associated with it. Only the sites 98F, 92DE, 87E and 81, which existed already on the 3R chromosome at the 15th generation, were observed. This suggests that these insertion sites were homozygous in the line but the 8 new ones (on the 3R chromosome, see fig. 5 and table 6) were heterozygous and must have appeared altogether and simultaneously with the inversion. This indicates a premeiotic "burst of transposition". Note that, overall, the insertion pattern in the other chromosomes remained stable throughout generations and did not depend on the inversion.

**Table 6** Examples of patterns of mdg-1 insertions in genomes of the line No 18 at generations 15 and 30

| Chromosome arm | Insertion sites | Generations 15 | 30 | 30* |
|---|---|---|---|---|
| X | 03F | 1 | - | - |
| | 04D | 1 | - | - |
| | 06A | - | 1 | 1 |
| | 16F | 1 | 1 | 1 |
| | 18BC | - | 1 | 1 |
| 2L | 22A | 1 | 1 | 1 |
| | 40 | 1 | - | - |
| 2R | 59F | 1 | 1 | 1 |
| | 53F | 1 | 1 | 1 |
| | 44D | 1 | 1 | 1 |
| | 42A | 1 | 1 | 1 |
| | 41 | 1 | 1 | 1 |
| 3L | 68D | 1 | 1 | 1 |
| | 73B | 1 | 1 | 1 |
| | 74A | - | 1 | 1 |
| | 75C | - | 1 | 1 |
| 3R | 98F | 1 | 1 | 1 |
| | 98E | - | - | 1 |
| | 98D | - | - | 1 |
| | 98B | - | - | 1 |
| | 98A | - | - | 1 |
| | 92DE | 1 | 1 | 1 |
| | 91B | - | - | 1 |
| | 89C | - | - | 1 |
| | 88E | - | - | 1 |
| | 87E | 1 | 1 | 1 |
| | 85D | - | - | 1 |
| | 81 | 1 | 1 | 1 |

* Genome heterozygous for the inversion 86DE-94F. 1 denotes presence and - absence of an insertion.

## CONCLUSION

It is now well established that many organisms contain different families of mobile elements, which have been shown to enhance the incidence of inversion, deletion and duplication of adjacent DNA sequences (Nevers and Saedler, 1977). These families are frequently associated with chromosomal rearrangements (Roeder and Fink, 1980; Engels and Preston, 1981; Shapiro, 1979) and are responsible for regulatory mutations in different organisms (Rubin *et al.*, 1982; Tsubota *et al.*, 1985). However, little is known about the rate of transposition of most elements in natural populations and on the mechanisms that regulate and control this transposition; only with *P* factors, which are involved in the phenomenon known as hybrid dysgenesis (resulting from crossing different strains of *Drosophila melanogaster*; Bregliano *et al.*, 1980; Kidwell, 1983), do we have some observations suggesting that *P* copy number and also the genomic location may, in some cases, be critical in *P* element regulation (Kidwell, 1985; Engels, 1984; Voloshina and Golubovsky, 1986). Moreover, although individuals from natural populations differ in localisation of the elements (Montgomery and Langley, 1983; Belyaeva *et al.*, 1984; Ananiev *et al.*, 1984; Biémont *et al.*, 1985; Biémont, 1986), it seems that inbred lines localisation of the elements is stable over time (Pierce and Lucchesi, 1981).

We have shown here that (a) transposition outbursts, (b) high rates of new insertions and excision (0·27 new insertions per chromosome per generation in line 18, see table 2; 0·24 losses of elements per chromosome per generation in line 9, see table 3), (c) chromosomal rearrangements, and (d) copy-number regulation of the rate of excision and transposition, are not appanages of hybrid dysgenesis only but can also be observed in inbred lines established from a natural population. Moreover, it appears that rates of gain of insertion and rates of excision are not correlated: a high gain rate does not involve a simultaneous high rate of excision. In agreement with some assumptions, this strongly suggests that transposition is replicative (Simmons and Karess, 1985) such that the original copy is retained whilst a new insertion appears.

Our results illustrate the classical assumption that inbred races and lines may possess

mechanisms that prevent reaching complete homozygosity by close inbreeding (Gowen, 1964); and the presence of a mutator factor has been supputed to explain instability in certain inbred lines (Guillaumin and Petit, 1961; Petit, 1963). The instability in some of our lines is due mainly to their tendency to regulate their number of mdg-1 elements, which was in general initially high as a result of genetic segregation in the first generations of inbreeding. As soon as the lines attain a copy number of elements close to the "optimal value", they become stable. This is compatible with the classical observation that lines with high mutation rates show rate reduction over time in the laboratory (Muller, 1941; Woodruff *et al.*, 1984).

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