SHORT PAPER

Jumping genes meet abdominal bristles: hybrid dysgenesis-induced quantitative variation in *Drosophila melanogaster*

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SUMMARY

When males from a strain of *Drosophila melanogaster* which have multiple copies of the P family of transposable elements integrated into their genome (Bingham, Kidwell & Rubin, 1982) ('P' strains) are crossed to females of strains lacking those elements ('M' strains), the F1 progeny manifest a number of aberrant traits known collectively as hybrid dysgenesis (Kidwell, Kidwell & Sved, 1977). Progeny of the reciprocal cross (P♀ × M♂) are normal. The dysgenic syndrome is characterized by a high degree of genomic instability caused by enhanced transposition of P elements. Since mutations at visible loci and chromosomal rearrangements are frequently observed in dysgenic hybrids, it was hypothesized that this phenomenon could be used to investigate the effects of transposition on quantitative characters; therefore, the progeny of dysgenic and non-dysgenic crosses were artificially selected for high and low abdominal bristle number. The response to selection, phenotypic variation, and realized heritability were all increased in the dysgenic lines, relative to the non-dysgenic control. It is postulated that these features are the result of P element-induced mutations of loci affecting bristle number, and that future work should lead to the identification of these loci, as well as elucidating the role of transposition in population differentiation for metric traits

1. INTRODUCTION

Quantitative characters, although widely recognized to be the very 'stuff of evolution' (Lewontin, 1974), have genetic properties that are amenable only to indirect statistical analysis. The multifactorial nature of inheritance of these traits precludes precise identification of the relevant loci; such identification would, however, be useful in understanding and predicting the course of natural and artificial selection. Surprisingly, the P family of transposable elements in *Drosophila melanogaster* (one of a large number of families of transposable elements comprising 17 % of the Drosophila genome (Engels, 1983)) have some peculiar biological properties which can be employed in this context.

The P family of transposable elements consists of a large 2·9 kb sequence flanked by 31 bp inverted repeats, and various smaller sequences, each of which can be derived by different internal deletions of the large element (O'Hare & Rubin, 1983). Strains of *D. melanogaster* which contain these elements ('P' strains) typically have from 30 to 50 copies per haploid genome, while other strains ('M' strains) have no functional P element (Bingham *et al.* 1982). When P males are crossed to M females, the F1 progeny are characterized by a number of abnormalities which have been embraced by the term 'hybrid dysgenesis', including temperature-sensitive sterility, male recombination, high frequency of chromosome rearrangements, and increased frequency of lethal and visible

(often unstable) mutations (Kidwell *et al.* 1977). These abnormalities do not occur in crosses of M males to P females, or in intra-P and intra-M crosses. Molecular analysis of mutations at the *white* locus resulting from a dysgenic cross indicated all were due to insertions of transposable elements; 5 of 7 *white* mutations were insertions of P elements, the other two were insertions of *copia* (Rubin, Kidwell & Bingham, 1982). The implication is that the other aspects of the dysgenic syndrome may also be explained in terms of genomic instability of dysgenic hybrids caused by high rates of transposition of P (and perhaps other) elements.
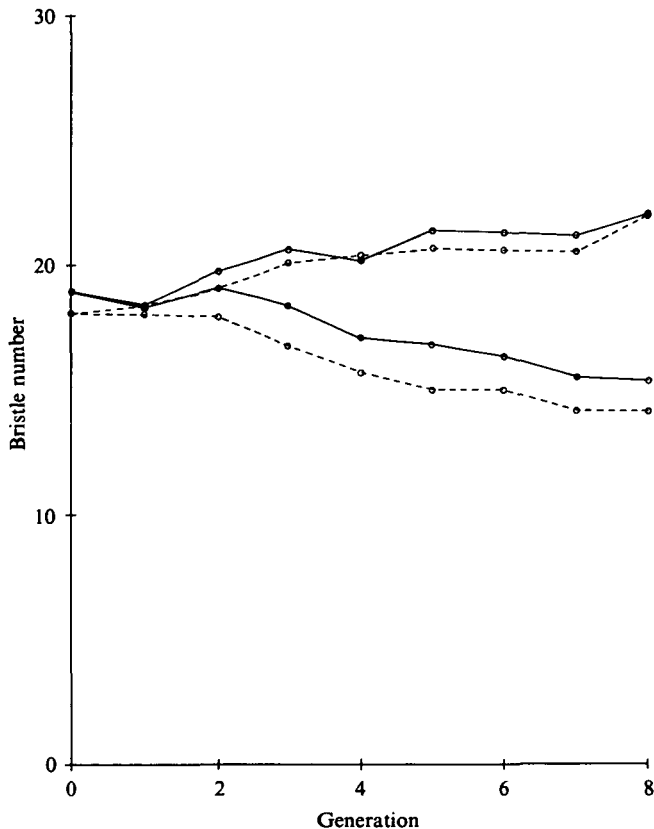

Fig. 1. Generation means of abdominal bristle score for the non-dysgenic selection lines. G0 are the progeny of a cross of 10 M males and 10 P females, which were artificially selected for bristle number according to the procedure described in the text. Solid and dashed lines depict the first and second replicates, respectively.

The rationale underlying this investigation is simple. The mutations caused by insertion and excision of P elements are as likely to alter loci controlling quantitative characters as those with major morphological consequences. Dysgenic ($M♀ \times P♂$) and non-dysgenic ($P♀ \times M♂$) hybrids will differ genetically only because of P element activity in the former cross. If one result of P element mutagenesis is to create additional genetic variation for a quantitative character, this would be manifest in an accelerated response to artificial selection for that trait in dysgenic, compared to non-dysgenic hybrids. This paper reports the results of the first eight generations of such a selection experiment.
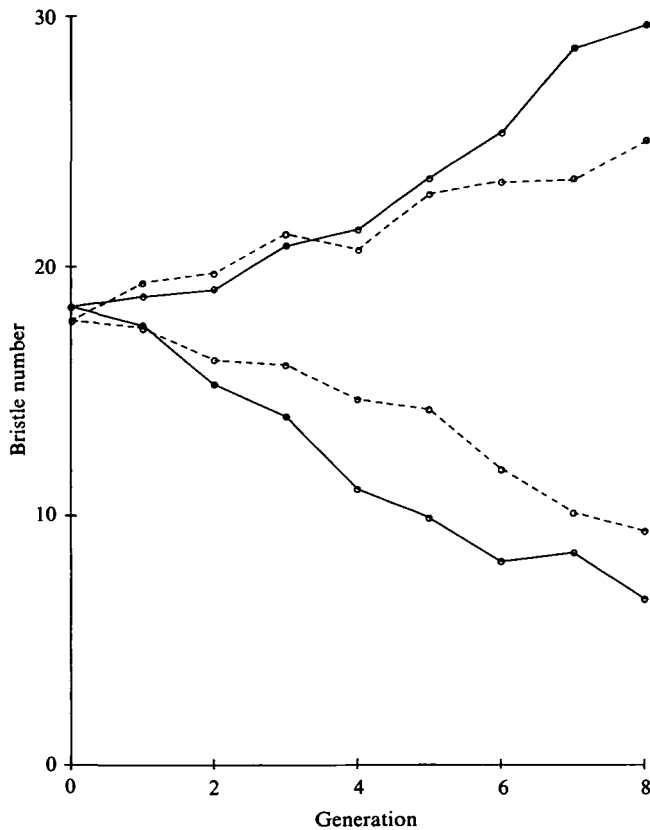
Fig. 2. Generation means of abdominal bristle score for the dysgenic selection lines. G0 are the progeny of a cross of 10 P males and 10 M females, which were artificially selected for bristle number according to the procedure described in the text. Solid and dashed lines depict the first and second replicates, respectively.

Table 1. *Phenotypic variance of abdominal bristle score in successive generations for the dysgenic and non-dysgenic selection lines*

| | Non-dysgenic crosses ($P♀♀ × M♂♂$) | | | | Dysgenic crosses ($M♀♀ × P♂♂$) | | | |
| | Replicate 1 | | Replicate 2 | | Replicate 1 | | Replicate 2 | |
Generation	High	Low	High	Low	High	Low	High	Low
0	3·67	3·67	2·53	2·53	3·72	3·72	6·87	6·87
1	4·65	2·85	4·02	3·68	4·05	6·50	4·82	3·88
2	4·87	3·60	3·47	3·29	6·42	9·58	4·54	5·79
3	3·06	3·64	3·02	3·51	5·74	12·34	5·86	4·34
4	3·45	3·52	3·24	3·19	9·97	19·97	5·24	12·72
5	5·03	3·97	3·45	4·04	10·89	15·26	8·41	14·27
6	2·93	3·19	3·80	3·22	16·68	17·69	7·84	20·81
7	4·18	4·27	5·50	4·51	23·07	19·83	8·90	22·76
8	4·59	3·45	3·93	3·82	16·98	15·43	10·14	20·24
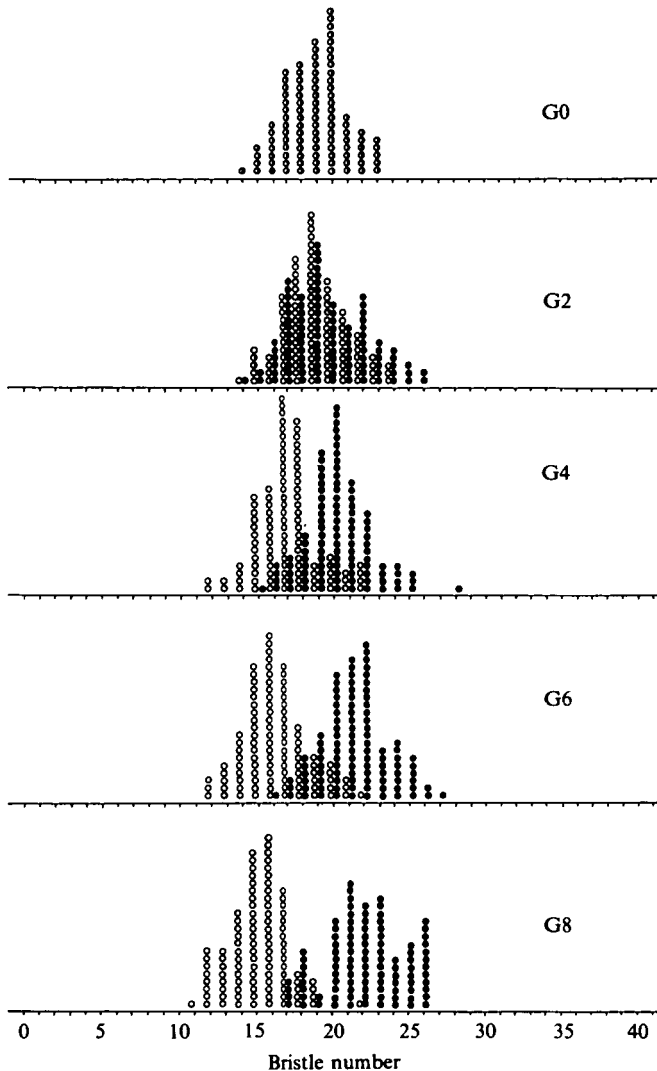
Fig. 3. Distribution of abdominal bristle score among replicate 1 of the non-dysgenic selection lines (males and females combined). Each circle represents an individual fly of the indicated phenotype, with solid circles corresponding to the high, and open circles to the low, selection lines. The second replicate, which is not shown, has a similar distribution pattern.

2. MATERIALS AND METHODS

P (Harwich) and M (Canton S) strains of *Drosophila melanogaster* were kindly donated by Dr M. Kidwell. Two replicates of dysgenic (10 M♀♀ × 10 P♂♂) and non-dysgenic (10 P♀♀ × 10 M♂♂) crosses were set up in bottle cultures. The following generation (G0), 50 individuals of each sex were scored for abdominal bristle count on the last abdominal tergite, and the 10 highest-scoring males and females, and 10 lowest-scoring males and females, were crossed *en masse* to found 'dysgenic' and 'non-dysgenic' high and low selection lines, one pair of lines for each replicate. Selection was continued in subsequent generations by choosing the 10 most extreme individuals of 50 scored of each sex, in each

line, to be parents of the next generation. The flies were reared on Edinburgh standard corn meal–agar–molasses medium, and all cultures were incubated at 20 °C, a temperature at which gonadal sterility is not appreciable in dysgenic hybrids.

3. RESULTS AND DISCUSSION

Generation means for these selection lines are depicted graphically in Figs 1 and 2, from which two features are obvious. Both response to artificial selection and variation in response between replicates are very much greater in the dysgenic, compared to non-dysgenic lines. Another unusual feature is the 3- to 6-fold increase in variance in the dysgenic lines, shown in Figs 3 and 4, and listed for each generation in Table 1. Typically phenotypic variance decreases as the population mean of a selected line changes from the original value, corresponding to a reduction in genetic variance as selection fixes desirable and eliminates undesirable alleles, but would not be expected to alter much in the early generations. The final comparison between dysgenic and non-dysgenic selection lines is that of realized heritabilities, calculated in the standard manner from the regression of divergence in response on total selection applied, cumulated over generations (Falconer, 1981). Replicate estimates of heritability are 0·199 and 0·185 for the non-dysgenic lines, and 0·317 and 0·227 for the dysgenic lines. It is not possible to attach standard errors based on variation between replicates to these heritability estimates, since the necessary assumption of homogeneity of variance (Hill, 1972) is seriously violated. The heritability of abdominal bristle score in the dysgenic crosses has increased by a factor of 1·4, as opposed to the more striking increase in phenotypic variance. The deduction is that much of this increase in phenotypic variance is due to an increase in either non-additive genetic variance, or environmental sensitivity, or both. All selection lines were of P cytotype (tested by the method described by Engels, 1979) by generation 8.

The hypothesis which most readily accounts for these observations is the mobilization of P elements in the dysgenic, but not non-dysgenic crosses. The selection response of the non-dysgenic lines follows the usual pattern for a cross between two strains, while the greater response of the dysgenic lines can be interpreted in terms of increase in frequency of new insertional mutations affecting bristle number, the greater replicate variability caused by the stochastic nature of transposition. The increase in phenotypic variability will be partly due to the increased genetic variance, and also because of the increase in variation expected as initially rare mutants attain intermediate frequencies. It would not be surprising if some of the insertional mutations affecting bristle number in dysgenic hybrids also had a deleterious effect on fitness, so that an increase in non-additive genetic variance of the character in these lines could be explained as a consequence of segregation of recessive deleterious genes.

Work is currently in progress to document the effect of insertional mutagenesis on a wide range of metric traits, as well as more detailed genetic analysis of this selection response. The beauty of this scheme is that P element-induced mutations can be localized by *in situ* hybridization of the cloned P element to polytene chromosomes, enabling the chromosomal identification of loci controlling quantitative traits. More importantly, such mutant polygenes could be used as bait to fish out the normal alleles, so that their future cloning and sequencing is conceivable (Bingham *et al.* 1982). More speculatively, the observed results pertain also to evolution. If, as has been suggested (Bingham *et al.* 1982) transposable elements are implicated in speciation, then it is feasible that the sudden bursts of phenotypic variation reported to be associated with speciation (Williamson, 1981), and the accelerated selection response reported here, are related.
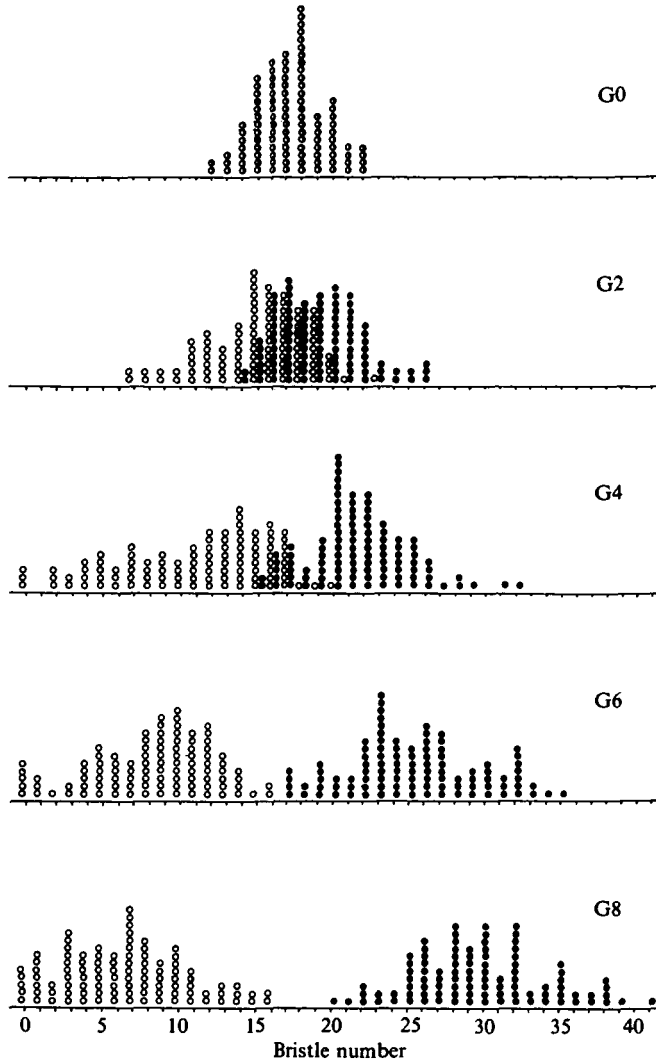
Fig. 4. Distribution of abdominal bristle score among replicate 1 of the dysgenic selection lines (males and females combined). Each circle represents an individual fly of the indicated phenotype, with solid circles corresponding to the high, and open circles to the low, selection lines. The second replicate, which is not shown, has a similar distribution pattern.

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