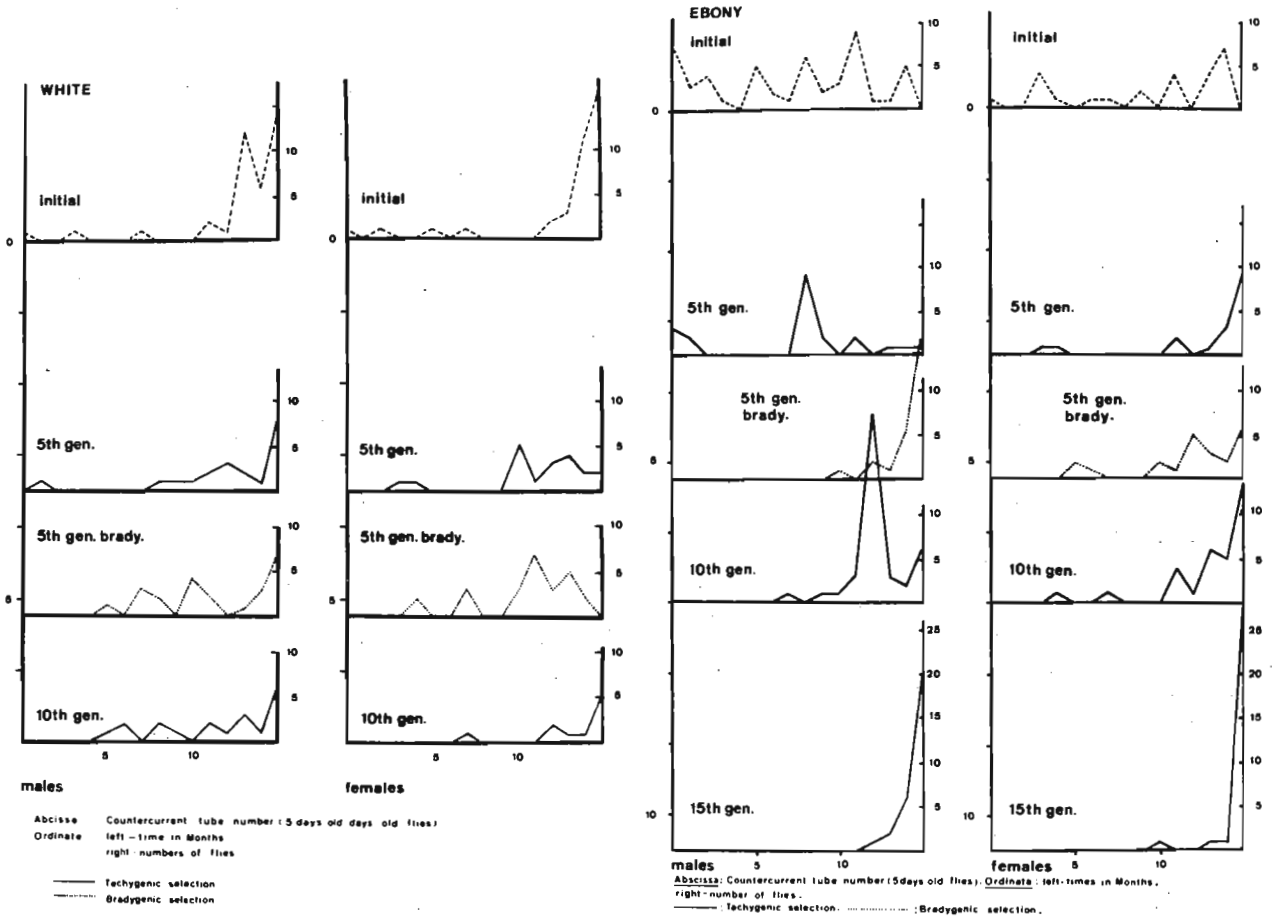
Elens, A. Facultés Universitaires N.D. de la Paix, Namur, Belgium. Parental age and efficiency of selection for phototactism.

Using the "countercurrent distribution" method of S. Benzer (1967) it is possible to fractionate populations of D. melanogaster according to their phototactic response, which changes with age and differs between strains (DIS 46:81; DIS 48:108). On the other hand, it is known that after a few generations, behavioural differences can result from the selection of "tachygenetic" and "bradygenetic" lines, i.e. by systematically choosing young or old genitors respectively (Wattiaux, J.M. 1968). The present paper concerns an attempt to combine the selection for positive phototactism with a selection for "tachygenetic" and "bradygenetic" lines.



Male and female flies were separated after eclosion and tested separately for phototactism, at 5 days of age for the "tachygenetic" line and at 30 days for the "bradygenetic" one; after the test they were allowed to mate. For the 5th and 10th generations of both "bradygenetic" and "tachygenetic" lines, flies were tested at the 5th and the 30th days after hatching, in order to permit a comparison. The figures here presented concern the behaviour of flies of 5 days, for "bradygenetic" as for "tachygenetic" lines of the white and ebony strains.

The selection for positive phototactism did not succeed in the white strain as in the ebony one. But the most interesting fact seems to be that, for the ebony males at least, the selection has been much more efficient in the "bradygenetic" line than in the "tachygenetic" one, as it can be seen by comparing the data concerning both 5th generations. It needs 15 generations of "tachygenetic" selection to obtain the same effect as 5 generations of "bradygenetic" selection, i.e., 10 months instead of 5 months.

Analogous results have been reported previously for an experiment in which the mice

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Nirmala Sajjan, S. and N.B. Krishnamurthy. University of Mysore, Manasagangotri, India. Structural variability in natural populations of Drosophila nasuta.

Natural populations of D. nasuta are highly polymorphic with regard to gene arrangements (Sajjan and Krishnamurthy 1970) Population studies revealed the presence of a total of 27 gene arrangements. These include one overlapping inversion in X-chromosome, 6 inversions in second chromosome and 19 inversions in the third chromosome (Fig. 1). Thus the third chromosome is the highly variable one and is comparable to the third chromosome of D. pseudoobscura.

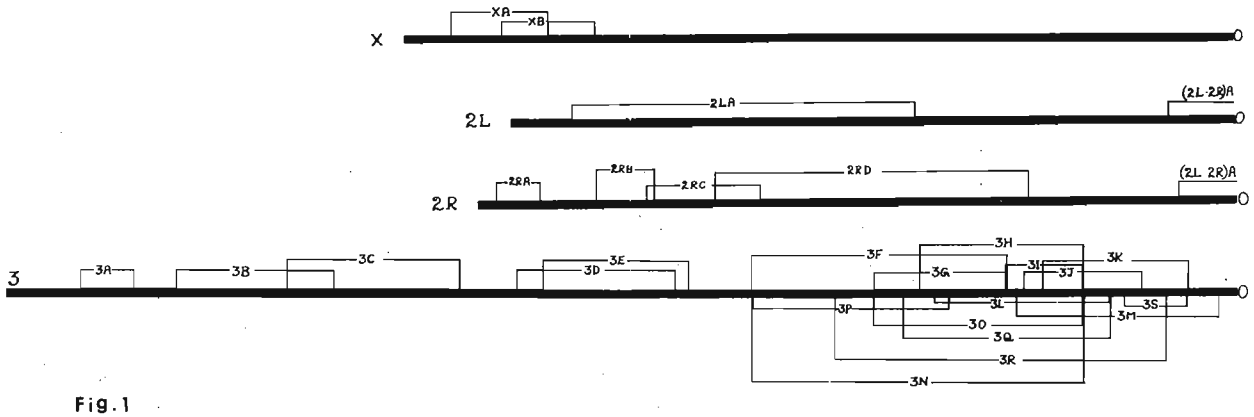

Fig. 1. Distribution of inversion break-points relative to the standard sequence. The open circles at the right ends represent the basal ends of the chromosomes.

The inversions and their distribution vary in space indicating that the chromosomal polymorphism in this species is of flexible type. Interestingly enough D. nasuta which is abundant and common species in all the localities studied, exhibits higher degree of polymorphism than the less abundant closely related form - D. neonasuta.

Another interesting feature in the present findings is that one of the 6 inversions in the second chromosome is a pericentric inversion - (2L-2R)A. It is so called because it is found between left and right arms of the second chromosome.

Acknowledgements: The writers are deeply indebted to Dr. M.R. Rajasekarasetty, Professor and Head of the Department of Zoology, University of Mysore, for many constructive suggestions and criticisms. We are also thankful to Miss A. Shashikala for preparing illustrations.

References: Sajjan, S.N. and N.B. Krishnamurthy 1970, DIS #47:121.

Hayman, D.L. and R.H. Maddern. University of Adelaide, S.A., Australia. A more precise cytological location of M(1) and su(s).

Ten deficiencies induced by X-rays and one induced by ethyl methane sulphonate selected because they exposed su(s) were all found to also expose M(1)B1d. From previous cytological studies on Df(1) svr and M(1)B1d, su(s) could be localized to the region from 1B11 to 1C2-3 and more probably from 1B13 to 1C2-3 (Bridges and Brehme 1944 "The Mutants of Drosophilia melanogaster"). The smallest M deficiency recovered after X-ray treatment was found to have its proximal break point distal to 1C1 so confining both M(1)B1d and su(s) to the region 1B11 to 1B14. The proximity of su(s) and M(1)B1d are of interest in relation to the findings of Jacobson (1971, Nature New Biology 231:17) and Atwood's earlier analogy of Minutes with tRNA genes (Ritossa et al. 1966 Genetics 54:663).

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resulting from a "bradygenetic" selection were obviously superior in learning ability to the "tachygenetic" ones (1966).

References: Benzer, S. 1967, Proc. Nat. Acad. Sc. 58:1112; Elens, A., A.N. Mouravieff and M.J. Heuts 1966, Experientia 22:186; Wattiaux, J.M. 1968, Evolution 22:406.