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.

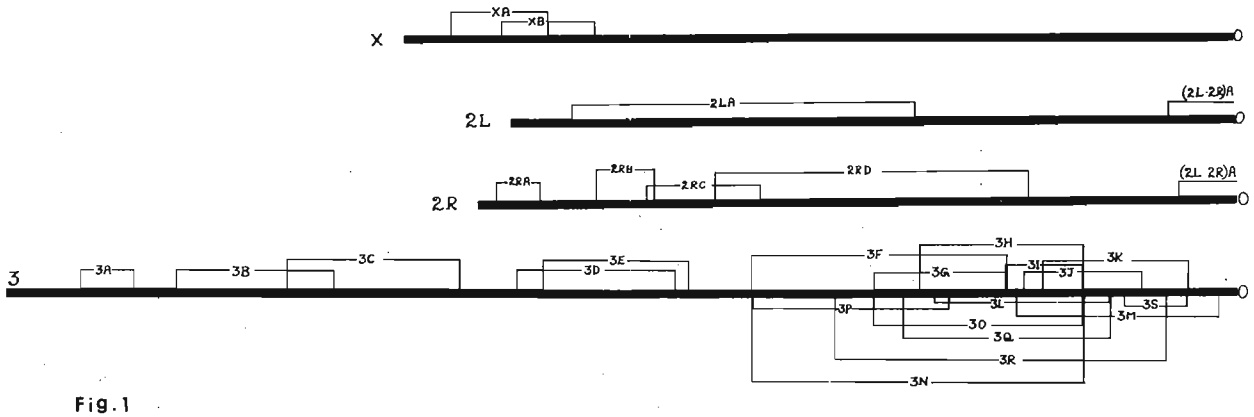

Fig. 1. Distribution of inversion break-points relative to the standard sequence. The open circles at the right ends represent the basal ends of the chromosomes.

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.

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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.