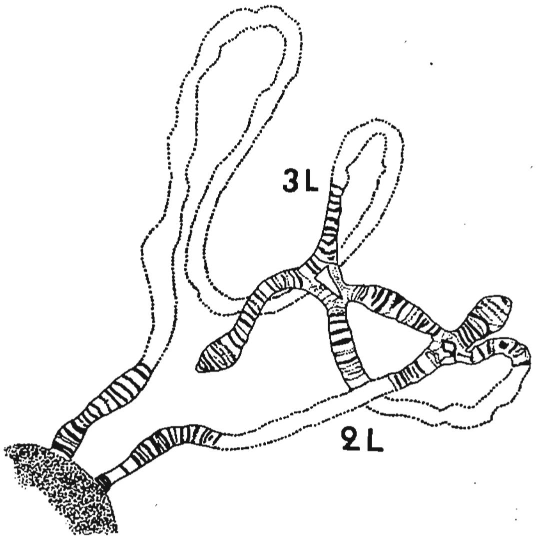
Sreerama Reddy, G. and N.B. Krishnamurthy
University of Mysore, Manasagangotri, India.

Aberrant gene sequences in D. ananassae from South India.

It is well known that the natural populations of Drosophila ananassae exhibit a high degree of chromosomal polymorphism. This is evidenced by the occurrence of coextensive inversions 2LA, 3LA and 3RA in varied frequencies in various populations and the presence of certain unique aberrations in low frequencies of 1 to 2%. Several such aberrant gene arrangements have been reported by several workers.



1

2

3

4

Aberrant gene sequences in D. ananassae: Fig. 1. Translocation (2L-3L)9; Fig. 2. Inversion XLb; Fig. 3. Inversion 2Le; Fig. 4. Inversion 2Lf.

The present note records four new arrangements in D. ananassae. Of these one is a translocation and the other three are heterozygous paracentric inversions. The translocation (Fig. 1) named here (2L-3L)9 is a heterozygous reciprocal translocation involving the left arm of the second chromosome and the left arm of the third chromosome. It is associated with the coextensive inversion 2LA and is found in a low frequency of 1% in the Merupalyam population (Niligiri Range). Its break points are located in 19A of the left arm of the second chromosome and 55 D of the left arm of the third chromosome (chromosome map by Rajeshwari, 1971). 19A lies within the inversion loop of the inversion 2LA.

Of the three paracentric inversions one is a simple inversion located in the left arm of the X-chromosome, and is found in a low frequency of 1% in Gudalur population. Its proximal break point is located in 6B and distal one in 4D. This has been called XLb (Fig. 2) and is different from XLA of Futch (1966). The second inversion called 2Le (Fig. 3) is an overlapping inversion discovered in 1% individuals of Merupalyam (Nilgiri Range). The extreme break points of this are located in 16F and 31E. The first inversion has its break points in 16F and 26F which are similar to those of the coextensive inversion 2LA. The second inversion overlapping the first has its break points at 20D and 31E. It is thus possible that the latter is of more recent origin and has not thus far been found separately. The third paracentric inversion is an included type wherein a new inversion has been included inside the coextensive inversion 2LA. This gene sequence is called 2Lf (Fig. 4) and found in Perumalmalai population (Kodaikanal Range) in a low frequency of 1%. The break points are located at 23C-26D. The new inversion found within the inversion 2LA has not been recovered independently.

The above mentioned new gene arrangements have added to our knowledge on the peculiar pattern of polymorphism exhibited by D. ananassae. Further the participation of the inversion 2LA in three of the four arrangements presented here needs a special mention. In addition to other avenues of gene rearrangements, it is possible that this species is utilizing one more avenue through the coextensive inversion 2LA in order to incorporate more novelties into the polymorphic pattern.

Acknowledgements: The authors gratefully acknowledge the help and encouragement given by Dr. M.R. Rajasekarasetty, Professor and Head of the Department of Zoology, University of Mysore. The authors are also thankful to Sri Ramakrishna Raju for his help in the preparation of microphotographs.

Sreerama Reddy, G. and N.B. Krishnamurthy University of Mysore, Mysore, India.

Two new gene arrangements in Drosophila ananassae from South India.

The rarity of translocations and pericentric inversions in the natural populations of various species of Drosophila is attributed to the production of aneuploid gametes which reduce the fecundity and fertility. Although these rearrangements are forbidden by natural selection and per se disadvantageous, that these rearrangements have played a significant role during the past in the phylogeny of several species of the genus Drosophila cannot be denied. Drosophila ananassae, a domestic cosmopolitan species is a favourable material for the analysis of gene arrangements as it harbours a wealth of chromosomal rearrangements. In addition to several paracentric inversions, certain translocations and pericentric inversions have also been reported for this species. The number of pericentric inversions and translocations found in this species out-number similar rearrangements in all the other Drosophila species so far studied.

The two new gene arrangements reported here were observed in two populations out of seven populations collected from Ooty (Niligiris) and Kodaikanal (Palani Hills) ranges. Of the two new gene rearrangements, one is a heterozygous pericentric inversion found in Gundlupet population and the other is a heterozygous translocation found in Perumalmalai population of Drosophila ananassae. The pericentric inversion (Fig. 1) is found in the second chromosome and has been named (2L-2R)9, as it is the ninth pericentric inversion reported for this species. It is a long inversion found associated with the co-extensive heterozygous paracentric inversion 2LA. Its break points are located in 26F of the left arm and 45A in the right arm of the second chromosome (chromosome map by Rajeshwari 1971). It was found in a frequency of 0.07%. The heterozygous translocation reported here involves the right arm of the X chromosome and the left arm of the second chromosome (Fig. 2) called here (XR-2L)8 as it is the eighth translocation reported in this species. The breakage points are located in 14D of the right arm of the X chromosome and 22E of the left arm of the second chromosome (chromosome map by Rajeshwari 1971). It is an asymmetrical reciprocal translocation detected, also