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Short Communication

Inversion Polymorphism in Polytene Chromosomes of *Sarcophaga* (Sarcophagidae: Diptera)

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Abstract

Cytological investigations using polytene chromosomes as a tool have demonstrated that inversion polymorphism is widespread in several members of the order Diptera. In the family sarcophagidae, which comprises several synanthropic and necrophagous filth flies however, chromosomal analysis in several species have been done, only a few cases of inversion polymorphism have been reported earlier. In the present communication some more cases of chromosomal polymorphism have been discussed.

Keywords: Sarcophagidae, Polymorphism, Polytene chromosomes, *Sarcophaga,* foot pads.

Introduction

The presence of giant polytene chromosomes in order Diptera facilitates detection of different chromosomal rearrangements such as inversions, asynchronous puffing, aberrations etc. Chromosomal polymorphisms, especially inversion polymorphism is widespread in families Drosophilidae[1-10], Chironomidae[11-15], Calliphoridae[16,17] and Simuliidae[18]. In *Drosophila melanogaster* only more than 300 inversions are known in natural populations[6]. However, in the family Sarcophagidae the cytological studies of polytene chromosomes analysis have been able to discern only a few inversion polymorphisms. The inversion polymorphism in *Parasarcophaga ruficornis* and *Parasarcophaga misera* was discussed by Kaul and Tewari[19]. Besides this a single paracentric inversion has been reported in Nepal population of *Boettcherisca peregrina* out of eight distant geographical populations[20] and in *Bercea haemorrhoidalis*[21]. In the present study, chromosomal inversions involving chromosome arm VI L of *Sarcophaga nathani*, III L of *S. peregrina* and V L of *S.dux* is described.

Materials and methods

Laboratory stocks of *Sarcophaga peregrina, S. nathani* and *S. dux* maintained at 26°C±1°C has been used in the present study. The foot pad of 7 days old male pupae were dissected out in insect saline. Chromosome preparation was made follows the method of Kaul et al[22].

Results and discussion

The polytene complement from the foot pads of all the three species shows five elements, corresponding to the five pairs of biarmed euchromatic mitotic chromosomes in neuroganglial cells. The polytene elements have been designated II-VI on the basis of their homology with the polytene elements of other Sarcophagid species[23,24]. The mitotic sex chromosomes are represented by a tiny mass of granular heterochromatin in polytene complement.

Sarcophaga peregrine: Chromosome arm III L of *S. peregrina* is easily identifiable by the bulb of region 9A, the dark regions at 9A/9B and the pattern of bands in region 7 A-C. The chromosome arm is polymorphic due to the presence of a paracentric inversion extending from the proximal limit of 7 C to 9A/B. The banding pattern of inversion heterozygote shows a typical inversion loop. The banding pattern of standard sequence, heterozygote and inversion homozygote is shown in Figure-1.

Sarcophaga nathani: Chromosome arm VI L of *S. nathani* shows a small paracentric inversion extending between the chromosome region 6B/6C to 7A/7B. The chromosome arm is identifiable by the sequence of bands in 7C/8A-C region at its telomeric end and the bands presents at 6C/7A. The banding pattern of standard sequence, heterozygote and inversion homozygote is shown in Figure-2. As the area of inversion is very small the chromosomes in heterozygote do not form a loop, instead they remain unpaired.

Sarcophaga dux: A short paracentric inversion extending between chromosome region 7C/8A to 8C/9A is found on the chromosome arm V L of *S.dux*. The chromosome arm is easily identified by the sequence of bands of region 8C-9C at its telomeric end. The heterozygote does not form a typical loop as the region involved in the inversion is too small.

The banding pattern of standard sequence and the heterozygote is shown in Figure-3. Inversion homozygote was not detected.

All the chromosomal inversions observed in the present study are of paracentric type no pericentric inversion is found. Similar inversions were reported in chromosome arm II L of *Parasarcophaga ruficornis* and Chromosome arm II R of *P.misera* [19], chromosome arm IV L of *Boettcherisca peregrina*[20] and chromosome arm V R of *Bercea haemorrhoidalis*[21]. It shows that in flies of family Sarcophagidae chromosomal inversion is restricted to paracentric may be it is right arm or left arm.

In many species of *Drosophila* it was found that chromosomal inversions respond to natural selection but the mechanism how the natural selection effects inversion is yet to understand[10]. Different chromosomal inversions involve the breaks at different position of chromosomes and simultaneously they reunite in a specific combination. During this process the position of genes as well as their controlling sequences are changed which results in the change in gene expression[9]. How this change in expression of gene is selected in the environment remains a question among researchers. The approaches to advance molecular techniques and genome sequencing of inverted regions can explore the adaptation of polymorphism to environment.

Figure-1: The banding pattern of the chromosome arm III L of *Sarcophaga peregrina* of i. Standard sequence, ii. heterozygote and iii. inversion homozygote.

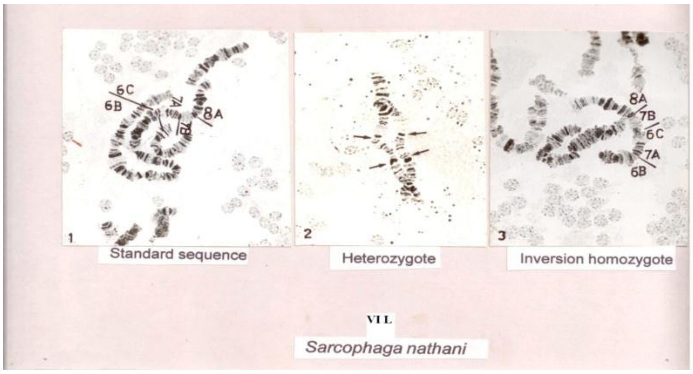

Figure-2: The banding pattern of the chromosome arm VI L of *Sarcophaga nathani* of i. Standard sequence, ii. heterozygote and iii. inversion homozygote.

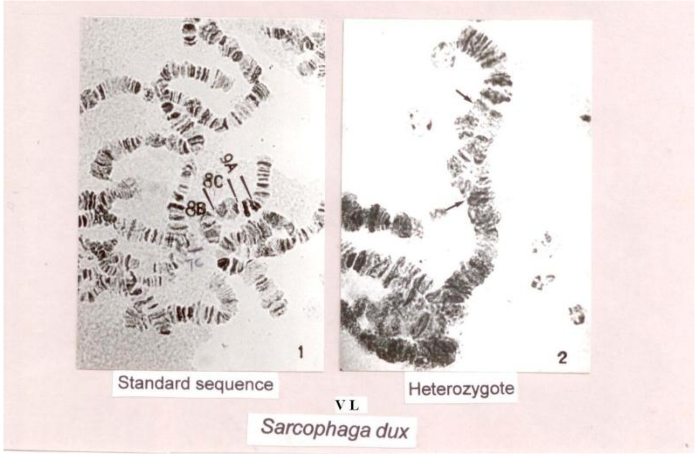

Figure-3: The banding pattern of the chromosome arm V L of *Sarcophaga dux* of i. Standard sequence and ii. heterozygote.

Conclusion

As the present study and earlier data are epitomized from only the laboratory stocks, a survey of these inversions in natural populations of different species of sarcophagidae family may provide interesting informations like, are these polymorphisms among these flies are of adaptive advantage for their future progeny or how different mechanisms evolved in these flies for adjustment to their environments.

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