

Chromosomal diversity in some common butterflies of family hesperiidae, from Akola district of Maharashtra

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ABSTRACT

The chromosomal study has been carried out in 5 commonly Hesperidae, butterflies from Akola district, in Western Vidarbha Region of Maharashtra. The aim of the study was to determine the variation in chromosome number in these butterflies. Testicular meiosis examined in all species demonstrated variation in haploid chromosome number. 4 genera, 5 species of family Hesperidae showed a range of $n = 24 - 32$. In the present study chromosome numbers are less than $n = 29 - 31$ and nearer or slightly more than 31 chromosomes. It is suggested that as in other several species of butterflies from different part of the world, the chromosome number in butterflies of Family Hesperidae in Akola district of Maharashtra might have evolved due to chromosomal aberrations. However, conventional staining analysis has not revealed its origin and these data remain open to future research.

Key words : Lepidoptera, Hesperidae, chromosome, fusions, fissions.

INTRODUCTION

Lepidoptera have a great range in chromosome number than any other group of animals. As per record, there has been numerical variations in the number of Lepidopteran species with high chromosome numbers (From $n = 7$ to $n = 220$). Chromosomal counts have been done on first metaphase which is visible as bodies rather than single chromosome. But they show a strongly marked mode at 29-31 so that the variance is much lower than in the decapods and Crustaceans. Extensive study of chromosomes from cytotaxonomic point of view has been carried out in this order. Earlier work on the chromosomes of butterflies of Europe has been published by Lorkovic, (1941) and Maeki, (1951) investigated the chromosome numbers of 31 species of butterflies of different families and reported that the haploid chromosomes in primary and secondary ranged from 14 to 31. Saitoh *et al.*, (1981) studied karyotype differences between 2 related species of the genus *Neope* (Lepidoptera, Satyridae) from Japan. Mohanty and Narang and Gupta, (1982) while studying chromosomes in 16 species of Indian Pyralid moths revealed that the evolution in chromosome numbers tends toward the lower numbers from a model haploid number $n = 31$ of the family. Kaur, (1988) studied the chromosome numbers of thirty-one species of Indian Lepidoptera and obtained elongated karyotypable chromosomes in 26 species. She observed diploid and haploid chromosome numbers in 20 species 62 and 31,

respectively, which is the ancestral or primitive number of the order (Brown *et al.*, 1992, 2004).

Recently Lukhtanov *et al.*, (2003) and Brown *et al.*, (2007) have given elaborate description of new species of the "brown" *Agrodiaetus* complex from south-East Turkey (Lycaenidae), they have also studied the evolutionary patterns in chromosome number in Neotropical Lepidoptera including Family Nymphalidae.

These workers have revealed a consistent haploid number of $n = 21$ in the genus *Heliconius* and $n = 31$ in the more primitive genera. Hesperidae is the family of small to large sized, butterflies, between 20mm and 80mm, usually dull, drab brown in color. Sturdy, robust bodies with a large, heavily muscled thorax are frequently confused with moths. Very few species of Hesperidae have been reported from Akola district of Maharashtra, which motivated us to analyze the chromosomal diversity in this family.

MATERIALS AND METHODS

The butterflies were captured with the help of insect net in and around Akola district from July 2010 to Feb 2011. Most of the butterflies were collected in the early hours of the day from 8 am to 12 noon. The collected butterflies were safely and carefully put in to a plastic box and brought to the laboratory. Species of butterflies, considered to be rare were handled with the permission of the district Forest Officials and only dead specimens were obtained for the necessary studies in the laboratory. The butterflies were identified by their physical appearance using an updated field guide and reference book (Kaur, 1988).



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Chromosomal study was performed from the testis of the collected male butterflies. The male butterflies were dissected and testes were taken out. A pretreatment was given to the testis by keeping it in a hypotonic solution. The testes were then transferred into a solution containing 1 part Ringer solution and 3 parts distilled of water. This treatment was continued for 30 minutes to one hour and in some cases i.e. depending upon the size, the testicular pieces were left in the solution for 1 to 2 hours. It was followed by the fixation in 45% acetic acid for 1 to 2 hours. The pre-treated testis was crushed in 45% acetic acid and a suspension was prepared. The suspension containing broken cells of the testis were spread on a clean slide and allowed to become dry. The dried slides were then stained with freshly prepared acetocarmine for 20-30 minutes then allowed to dry for 2 to 8 hrs. The stained dried slides were mounted and observed under self illuminated microscope. Chromosomal analysis of at least 5 individuals was examined for each species. The number of chromosome was counted to calculate the average number of chromosome for the particular species.

RESULTS AND DISCUSSION

In the present study, 5 species belonging to 4 genera of family Hesperidae have been identified which were collected feeding on different types of vegetations in the sanctuary areas. We have recorded *Caltoris kumara*, *Parnara naso*, *Pleopides muthias*, *Barbo bevani*, *B. cinnara*. 12 to 15 cells were used for counting, the chromosomal diversity in these butterflies. Most chromosomes have been found in bivalent form in the images, (Table 1).

Chromosomal diversity was studied, preferably during meiotic pairing of chromosome in the males which are mostly univalent, bivalent and some time multivalent in nature. The chromosomes were observed as dots and were found to be rod shaped. Only haploid chromosome number and relative sizes of bivalents of the species chromosomes have been commonly used in butterfly cytogenetic analysis.

We have focused on the chromosome number because it can be easily analyzed in a comparative study. However, we do not know the true number of chromosomal rearrangements separating their karyotypes. Species with conserved chromosome numbers can still have chromosomal rearrangements fixed between them that will be invisible to our analysis. Therefore, the true number of chromosomal rearrangements among butterfly taxa is probably underestimated in our study. The bivalent forms of chromosome are separated from each other followed by the univalent form of chromosomes. The chromosomes are counted as per the procedure and the results are documented in the table.

The number of chromosomes counted from *Pelopides mathias* was 26. Chromosome count from *Borbo bevani* was 32 and that from *B. Cinnara* was 28. The number of chromosome in *Caltoris kumara* was 30 and the same number of chromosome are counted from *Parnara naso*. The images for the studied species are captured and displayed in the plate-Although the classification of butterflies and skippers is based on morphology of specimen, traditionally butterflies and skippers have been placed into two super families and 5 families.

The skippers belonging to Hesperidae family and they are placed in their own super family Hesperioidea, while all other butterflies are placed in Papilionoidea. Both the super families have been considered sister taxa. Among the skippers extreme variation in chromosome number have been reported in 3 species of remarkable giant skippers. It was found that they have haploid chromosome number of 21, 27, and 50 chromosomes (Maeki and Remington, 1960). Maeki and Ogata (1971) reported the haploid chromosome number $n = 28$ in *Ocybadistes walkeri* so this and $n = 31$ in *Trapezites eliema*. In the study slight differences in 2 species of *Borbo cinnara* and *B. bevani* were observed in haploid number of chromosome. *Parnara naso* and *Caltoris kumara* have $n = 30$ chromosome number.

The lowest number of chromosome ($n = 26$) was in found *Pelopidas mathias*. Overall range of chromosome in this family among the 5 species of 4 genera was between 26 and 32. The Lepidopteran in general are characterized by stable chromosome number and majority of butterflies and moths have haploid chromosome number ranging from $n = 29$ to $n = 31$ with $n = 31$ found as the most common number across Lepidoptera (Robinson, 1971; Williams, 1973; Werner, 1975). This suggests that the divergent number of chromosome of various genera of different families should have derived from the Lepidopteron model of $n = 29 - 31$. The karyotypes of several butterflies as a constant total volume of chromosome hence fissions and fusions are more responsible for change in chromosomal number than polyploidy (White, 1978; Brown *et al.*, 2004).

In the present study all species have the chromosome number less than $n = 29 - 31$ and nearer or slightly more than 31 chromosome number. It can be thus concluded that the chromosome number in butterflies of study area might have evolved due to the fusions and fissions as in other several species of butterflies from different parts of the world. However to support these finding more detailed analysis of chromosome numbers is needed with improved techniques so as to minimize the errors in the counting of chromosomes.

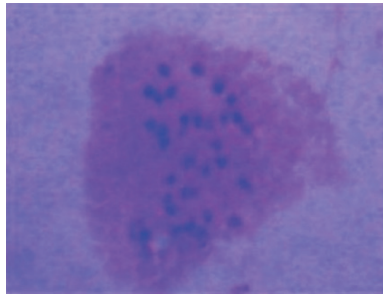
Table 1 : Chromosome diversity of Butterflies from family Hesperidae

Sr.No.	Common Name	Scientific Name	n =
1	Bevan's Swift	<i>Borbo bevani</i>	32
2	Rice Swift	<i>Borbo cinnara</i>	28
3	Straight Swift	<i>Parnara naso</i>	30
4	Blank Swift	<i>Caltois kumara</i>	30
5	Small-branded Swift	<i>Pelopidas mathias</i>	26

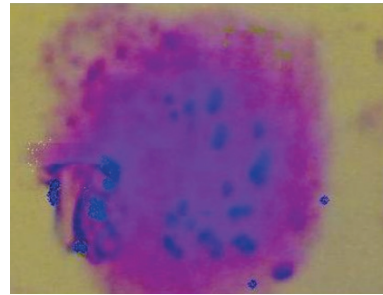
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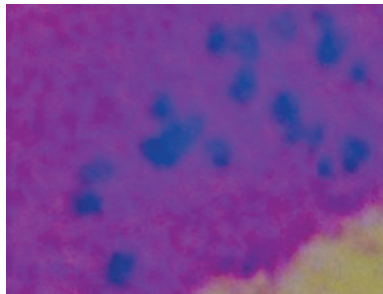
Chromosome diversity of Butterflies from family Hesperiidae



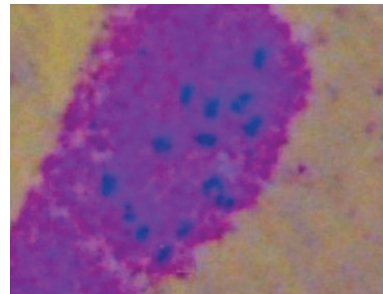
Borbo bevani



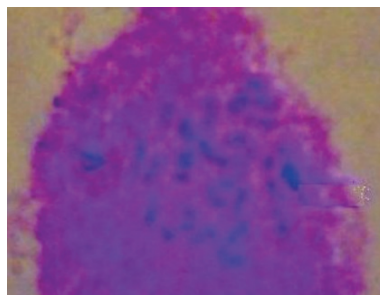
Borbo cinnara



parnara naso



Pelopidas mathias



Caltoris kumara