chromosomes prevent identification of other than gross morphological changes in mitotic chromosomes. The level of damage encountered differed between the 2 treatment levels. At 2 kR simple numerical changes predominated; most embryos examined fell in the chromosome number range 2n=57 to 2n=66 (figure 1). Much more extensive damage was found in the 10 kR series, the presence of numerous chromosome fragments making exact determination uncertain in many cases.

Sampling of larvae from F1 families descended from irradiated males confirmed the presence of inherited numerical modifications, as well as revealing morphological changes undetectable in mitotic cells. Meiotic analysis disclosed altered chromosome configurations ranging from simple trivalents and quadrivalents in the 2 kR series to fragments, complex multivalents and heteromorphic bivalents in the 10 kR series (figure 2). In general, the extent of inherited chromosome aberrations predicted for each family on the basis of embryonic sampling was closely confirmed by meiotic analysis, indicating that embryo sampling is useful in detecting both presence and extent of inherited aberrations.

From a 2 kR family known by embryonic and meiotic analysis to be carrying low frequencies of aberrations, 6 males were identified by testis sampling as heterozygous for 1 or 2 chromosome fusions. Of the 4 that became adults, 3 mated successfully with normal females. Egg hatch was reduced in all 3 families, and embryonic sampling gave the following chromosome number classes: family 1, ♂ parent n=28 II+1 III, 12 embryos with 2n=60, 14 with 2n=59; family 2, ♂ n=28 II+1 III, 16 embryos with 2n=60, 9 with m=59; family 3, ♂ n=26 II+2 III, 5 embryos with 2n=58, 7 with 2n=59 and 4 with 2n=60. Establishment of segregation ratios in F2 embryos demonstrates 2 points; the techniques can be used to establish translocation-bearing strains in 1 generation, and embryo sampling can be used to investigate meiotic behavior of translocations in the holokinetic chromosome system of Lepidoptera, hitherto not studied in detail.

1 T.J. Ennis, Can. J. Genet. Cytol. *20*, 427 (1978).
2 A. Retnakaran and J. French, Can. Ent. *103*, 712 (1971).
3 J.D. Castillo, G. Hoyle and X. Machne, J. Physiol. *121*, 539 (1953).
4 D.D. Shaw and M.G. Morgan, Can. Dept. For. Bi-Mon. Res. Notes *29*, 17 (1973).

Effect of B-chromosomes on the duration of mitotic cycle in pearl millet

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Summary. Effect of B-chromosomes on the duration of the mitotic cycle was studied by a colchicine shock method in the root-tip cells of pearl millet *(Pennisetum typhoides)*. 3 B-chromosomes were found to have very little effect, whereas 5 B-chromosomes resulted in an increase of the duration by about 39%.

Several aspects of cytogenetics of B-chromosomes of *Pennisetum typhoides* (S. & H.) have been reported[2-4]. The B-chromosomes at pachytene are largely heterochromatic; the short arm appears to be wholly heterochromatic, while the long arm consists of proximal heterochromatin followed by an euchromatic region with 8 chromomeres. This B-chromosome varies in number both in pollen mother cells (PMCs) and in somatic cells, between and within the plants. The B-chromosomes in small numbers (1-4) do not seem to influence the mean chiasma frequency of the normal (A) chromosomes, though 5 or more B's have a negative effect. Further, they increase the variance of the mean; this effect increases with the increase in the number of B-chromosomes per PMC. 5 or more B's per PMC also produce deleterious effects on the behaviour of A-chromosomes at meiosis and on exophenotypic characters[4].

B-chromosomes in general are known to have an influence on many different gene-controlled processes. They produce an extension of mitotic cycle time and reduction in cell number; these effects together with changes in cell size in the presence of B's provide a physiological basis for many effects of B-chromosomes like reduction in vigour, delay in germination and delay in flowering[5]. The present study was undertaken to investigate whether B-chromosomes affect the mitotic cycle in pearl millet.

Materials and methods. Seeds from stock without (0 B), with 3 (3 B), and with 5 (5 B) B's were germinated on moist filter papers at 30±2 °C. After 24 h germinating seedlings with 5-6 mm long roots were chosen. The roots were pretreated with 0.25% colchicine for 1 h and, after thorough washing in tap water, seedlings were replaced on the moist filter

Accumulation of metaphases expressed as percentage, in root tips of diploids without (0B) and with 3 or 5 (3B, 5B) B-chromosomes in pearl millet

Sampling time (h)	0B		3B		5B	
	2×	4×	2×	4×	2×	4×
1	10.9		9.0		5.5	
2	9.3		8.6		6.6	
3	10.0		16.3		8.0	
4	13.0		9.5		7.3	
5			13.7		1.6	
6			16.0			
7					0.08	
8						
9			5.0		2.5	
11					3.0	
12			0.03			
15			3.7		2.4	
16	0.3	0.8		2.0		4.0
17						
18		2.0				
19				0.03		5.3
20		9.0		0.0		
21						0.04
22		6.0		2.0		1.5
24		7.0		3.0		
25						5.0
26		8.0		14.6		
27						
28		0.0		0.0		3.0
29						2.7
30				3.4		2.3
31						3.3
32				4.4		8.8

paper. Root tips were sampled at intervals of either 1 or 2 h starting from the end of treatment with colchicine. The roots were sampled until 28 h for 0 B and up to 32 h for the 3 B and 5 B lines. Roots were fixed in 1:3 acetic alcohol for 24 h; following fixation roots were washed, hydrolyzed for 7–8 min in 1N HCl at 60 °C and stained in Feulgen solution. The numbers of diploid and tetraploid metaphases were scored from at least 1000 cells per root from squash preparations. Mean values from 3 replicates for each sampling time were expressed as percentages of metaphases (table).

Results and discussion. It was observed that the earlier samples contained only diploid metaphases, while tetraploid metaphases appeared 16 h after the end of colchicine treatment. The frequency of tetraploid metaphases increased gradually in later samples and decreased after reaching a peak. The time from the end of colchicine treatment to the sampling time of peak occurrence of the tetraploid metaphases was taken as the duration of the first mitotic cycle after 'labelling' a fraction of the cell population with colchicine. The duration of the mitotic cycle was found to be 23 h in the 0 B line, 26 h in the 3 B line and 32 in the 5 B line. Thus 3 B's increased the cycle duration by 13% while 5 B's resulted in a 39.1% increase of the duration. This result is consistent with the effect of B's in other plant species. In rye, for instance, mitotic cycle duration in plants with 4 B chromosomes was found to be 16.71 h which was 25% greater than that in plants without B's[6]. The increase in mitotic cycle duration in the presence of 3–4 B's in *Secale cereale*, 8 B's in *Zea mays* and 3 B's in *Lolium perenne* over controls was accounted for by the increase in the amount of DNA in the material containing B-chromosomes[7]. Duration of the mitotic cycle increases with increasing DNA amount, whether the increase in DNA is due to polyploidy and aneuploidy or to the amplification of chromosome segments within the diploid complement, or finally to the addition of B-chromosomes[8].

In *Pennisetum* 3 B's produced only a minor effect on the mitotic cycle time, while 5 B's caused a large increase. The reasons for this difference are not clear. A similar difference of effect between 3 and 5 B's was evident in changes of the meiotic behaviour of A chromosomes and also in the vigour and fertility of the B-carrying plants[4,9].

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2 J.V. Pantulu, Curr. Sci. *29*, 28 (1960).
3 J. Venkateswarlu and J.V. Pantulu, Cytologia *35*, 444 (1970).
4 J.V. Pantulu and V. Manga, Genetica *45*, 237 (1975).
5 R.N. Jones, Int. Rev. Cyt. *40*, 1 (1975).
6 U.W. Ayonoadu and H. Rees, Exp. Cell Res. *52*, 284 (1968).
7 H. Rees and J. Hutchinson, Cold Spring Harb. Symp. quant. Biol. *38*, 175 (1973).
8 H. Rees and R.N. Jones, Chromosome Genetics, p. 150. Ed. K.R. Lewis and B. John. Edward Arnold, London 1977.
9 J.V. Pantulu, Ph.D. thesis, Andhra University, Waltair (1961).

The chromosomes of *Passeromyia heterochaeta* Villeneuve (Muscidae: Diptera)

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Summary. The 2 n = 10 complement of *Passeromyia heterochaeta* Villeneuve consists of 4 pairs of metacentric chromosomes and 1 pair of dots. The evolutionary implications of 2 n = 10 in the tribe Phaoniini (Fam. Muscidae) are discussed.

Flies of the genus *Passeromyia*, which have ectoparasitic larvae that feed on the blood of nestling birds, belong to the tribe Phaoniini (S.F. Phaoniinae). The tribe is taxonomically very important, as it is possibly from its ancestors that subfamilies Fanniinae, Anthomyiinae and Muscinae have been derived[2]. The chromosomes of *P. heterochaeta*, the only species of the genus known to occur in the Indian region, are reported in the present communication.

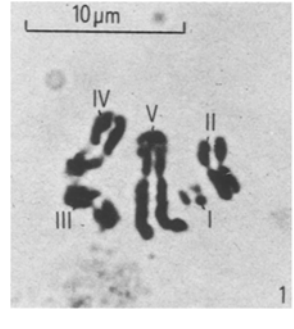
P. heterochaeta has a diploid chromosome number 2 n = 10 (figure 1). A summary of data from the analysis of 10 oogonial metaphases is presented in the table. The karyotype consists of 4 pairs of medium to very large, metacentric chromosomes (pairs II–V), and a pair of small dot-like chromosomes (pair I). The chromosome pairs II–V show close somatic pairing, while the dot-like chromosomes generally lie apart from each other. Details of male meiosis could not be analyzed in the material available, but first metaphases were extremely clear (figure 2). They invariably show 4 large and 1 small bivalent. None of the bivalents appears to be heteromorphic, therefore it has not been possible to distinguish the sex chromosomes from the autosomes. However, the dot-like chromosomes (pair I) are presumed to be the sex chromosomes.

While a vast majority of the calyptrate Diptera possess 2 n = 12 chromosome complements, a few species in the

A summary of data from analysis of 10 oogonial metaphase plates

Chromosome pair	Arm ratio	% TCL	Type of chromosome*
I	-	4.30	T
II	1.2	18.52	m
III	1.3	19.91	m
IV	1.2	23.30	m
V	1.5	33.95	m

* According to Levan et al.[4]



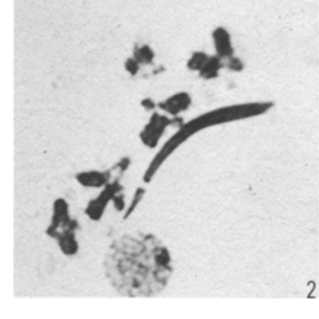


Fig. 1. Female mitotic metaphase.

Fig. 2. Male I meiotic metaphase.