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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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.

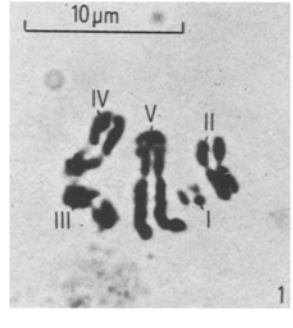
P. heterochaeta has a diploid chromosome number 2 n = 10 (figure 1). A summary of data from the analysis of 10 oogonial metaphases is presented in the table. The karyotype consists of 4 pairs of medium to very large, metacentric chromosomes (pairs II–V), and a pair of small dot-like chromosomes (pair 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]



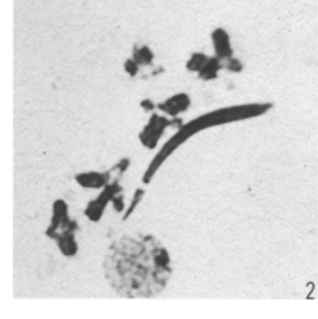


Fig. 1. Female mitotic metaphase.

Fig. 2. Male I meiotic metaphase.

family Muscidae have a diploid complement of 2 n = 10. 4 of the 7 species in the tribe Phaoniini that have been studied cytologically, have 2 n = 10 (Boyes and van Brink[3]) while the remaining have 2 n = 12. The 2 n = 10 complement of *P. heterochaeta,* however, does not resemble those of the other 2 n = 10 species. In *P. heterochaeta* 2 n = 10 complement has very short pair I chromosomes, and an apparently large pair V chromosome, whereas the other 3 species have medium sized, metacentric pair I and their pair V chromosomes are not large.

The presence of both 2 n = 12 and 10 complements in the tribe is rather interesting. It seems that as far as chromosome number and form is concerned the tribe has retained a flexibility and is not, as yet, completely fixed at 2 n = 12 level, but has produced karyotypes which may represent more specialized states.

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Studies on the late-pre-β-lipoprotein of human serum[1]

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Summary. Very low density lipoprotein (VLDL) isolated from 3 healthy normolipidaemic subjects had a raised VLDL cholesterol to triglyceride ratio. The VLDL fractions gave 2 pre-β-bands on agarose gel electrophoresis. Family study of the subjects appears to indicate sex linkage of this trait and a possible polygenic type of inheritance.

In a previous study[2,3] we demonstrated that VLDL composition (in terms of cholesterol to triglyceride ratio) is high in type III and type IIb hyperlipoproteinaemic subjects. During a population study[4], however, 3 healthy normolipidaemic subjects were observed to possess a raised VLDL cholesterol to triglyceride ratio (≥ 0.38). These 3 subjects were therefore studied in detail as regards lipid and lipoprotein concentration as well as family disposition to the trait.

Materials and methods. Subjects: The 3 probands M.R. (a 28-year-old mechanical engineer), F.P. (a 44-year-old plumber) and E.A. (a 59-year-old house-wife) were healthy and had normal lipid concentrations. None was taking any drug known to affect lipid metabolism.

Analysis. VLDL precipitation and measurement was done as reported previously[5]. Preparative ultracentrifugation was done according to the method described by Carlson[6]. Agarose gel electrophoresis was made according to Noble[7]. Blood was obtained after 12–14 h fast. Accessible first degree relatives (parents, siblings and children) of the probands were investigated for lipid and lipoprotein concentrations.

VLDL cholesterol: Triglyceride ratio in a normal population is 0.32 ± 0.06 (mean ± SD). *Results.* Lipoprotein and lipid concentration. The 3 probands had normal lipid concentrations in serum, VLDL, LDL and HDL. Their VLDL cholesterol to triglyceride ratios were however high.

Electrophoresis: Figure 1 shows the electrophoretic pat-

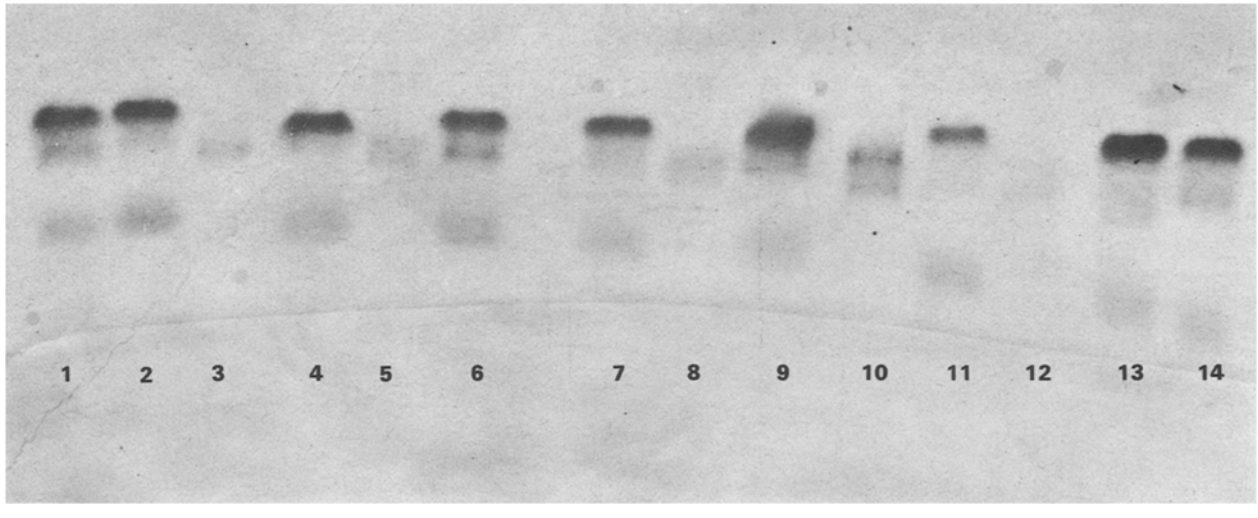

Fig. 1. Agarose gel electrophoresis showing the abnormal VLDL. Numbers 1, 2, 6, 11, 13 and 14 normal sera and numbers 3 and 12 are normal VLDL. Numbers 4, 7, 9, and 5, 8, 10 are sera and VLDL respectively of affected subjects, E.A., M.R., and F.P. respectively.