In addition, we looked for the pattern for frequency for the phenotypic variance. For this purpose, the variance values for the difference in esternopleural bristle number were grouped into three class intervals: 0-1, 1-2, and >2, for parental, F_1 and F_2 classes for each sex at each temperature. At each temperature the major part of the variance values in both the sexes occurred in the central class (1-2). The frequency in the case of the females grouped in the class greater than two was larger when compared with those of the males at either temperature. On comparing the class interval >2 between temperatures, a slight increase at 18° was observed than at 25°C for each sex. However, no specific pattern on this aspect could be noticed in the case of the crosses made between the two periods of collection. Comparison of the parental with F_1 's yielded almost homogeneity for the frequencies in each of the three classes of variance. Overall, F_2 's grouped in the central class, 1-2, were in larger number when compared with those of F_1 's for each sex at 18°C. No consistent pattern for such a comparison was observed at 25°C.

Likewise, the values of the variance for the difference in bristle number between the two sternites were also classified, into three classes: 2-6, 6-10, and >10, in order to search for pattern. At 25°, the majority of the phenotypic variance for the parental, F_1 's and F_2 's occurred in the central class (6-10) for each sex. While at 18°, such a frequency was spread into two classes (2-6 and 6-10), indicating a reduced number of phenotypic variances in the class greater than 10 at this temperature. No concludable pattern was observed for the comparison of F_1 's or F_2 's with their parental classes. The other aspects are under investigation.

This work was supported by Research Grants from CNPq (Proc. 40.0312/79 and 40.2525/81) and FUJB (UFRJ) awarded to Prof. Anand Prakash Gupta. We thank Stavna Uchoa for typing the manuscript.

Reference: Dobzhansky, Th. 1951, in:Genetics and the Origin of Species, 3d ed rev, Columbia Univ, New York.

Andrews, K. and C. Chihara. University of San Francisco, California, USNA. An overproducer of a third instar urea-soluble cuticle protein in Drosophila melanogaster.

Third instar larvae of **Drosophila melanogaster** show a standard electrophoretic pattern for the urea-soluble cuticular proteins (Fristrom et al. 1978; Chihara et al. 1982) (Figure 1, lanes 1 and 4). The bands are designated from slowest (top) to fastest (bottom) as L₃CP-1, 2, 2a, 3, 4, 5, 6, 7, 8, respectively.

L₃CP-1, 2, 2a, 3, 4, 5, 6, 7, 8, respectively. The overproducer variant of L₃CP-5 (named L₃CP5^{op}) was isolated from an Austin Species Center stock acquired from Kuala Lumpur, Malaysia. Several rounds of pair matings produced a stock which gave consistently dark bands at the position of protein 5, (125 samples). The intensity of the variant L₃CP-5 was checked against wild type using a gel scanner with integrator. The density of the L₃CP-5 band relative to the L₃CP-4 band of both stocks was compared and the following ratios were obtained (Figure 1):

5°P: Mean density ratio of Bands 5:4 = 1.95(
$$\pm$$
0.65):1;n = 67 +/+: " " " = 0.97(\pm 0.13):1;n = 7

The L₃CP5^{op} variant is at least partially dominant. When it was crossed to wild type the 5 band remained visibly darker than the wild type. This can also be seen in the crosses described below.

To make sure the darkened 5 band was due to overproduction of L₃CP-5 and not to the introduction of a new protein with the same electrophoretic mobility, the L₃CP5^{op} variant was crossed with, and then backcrossed to, a recessive mutant known as omega. Omega is a putative processing gene whose product, when inactive, results in the non-processing of L₃CP-5; as a result, L₃CP-5 migrates much more slowly than wild type L₃CP-5. This slow band is designated as the omega band (Figure 1, lanes 2 and 3).

Density comparisons between the L_3CP -omega band and L_3CP -4 were made as above (Fig. 2).

Omega/omega: Mean density ratio of omega:4 = 1.04:1, with a high value of 1.40 and a low of 0.84. This is comparable to the values for +/+, bands 5:4 shown above.

 5^{op} omega/ 5^+ omega: Mean density ratio of Omega:4 = 2.4:1, with a high of 3. and a low of 1.83 (Fig. 1, lane 5).

Wild type omega recombinant: Mean density ratio of Omega:4= 1.25:1, with a high of 1.67 and a low of 0.83.

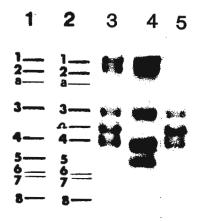


Figure 1. Lane 1: Schematic wild type banding pattern with numbers. Lane 2: Schematic omega homozygote pattern. Lane 3: Homozygous omega with wild type for gene 5. Lane 4: Typical wild pattern. Lane 5: $L_3\text{CP5}^{\text{Op}}$ heterozygote with homozygous omega, note dark omega band.

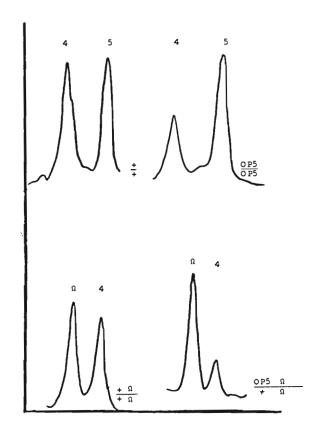


TABLE 1. Schema for the production of L₃CP5^{OP} - Omega recombinants with results of the cross.

	<u>5</u> op	x omega omega	>	<u>5</u> op	+	_ x +	omega
	-on			+	omega	+	omega
			5 ^{op} +		<u>pł</u>	nenotype 50p	_ #
	Parentals -	+ omega	/	>	5-1	20	
		a15 -	+ omega + omega		>	omega	19
	Crossovers-		5 ^{op} omega + omega		>	5 ^{op} omega	a 6
		ers-	+ + omega		>	+	1

Figure 2. Densitometer tracings as described in text.

While the numbers of recombinants are small they are consistent with an estimate of at least 15 map units between the omega and 5^{op} genes (Table 1). The gene for L₃CP-5 maps also maps at least 15 map units away from the Omega gene (Chihara & Kimbrell, in manuscript). The data are consistent with the L₃CP5 op locus being very close to the L₃CP5 gene.

This work was supported by NSF grant #PCM 8119181 to CJC.

References: Fristrom, Hall & Watt 1978, Biochem 19:3917; Chihara, Silvert & Fristrom 1982, Dev.Biol. 89:379.

Barker, J.S.F. and D.K. Fredline. University of New England, Armidale, Australia. Reproductive biology of Drosophila buzzatii.

Drosophila buzzatii and other cactophilic Drosophila provide a valuable model system for studies in population and evolutionary genetics (Barker & Starmer 1982), because they are specific to the cactus niche, feeding and breeding in rotting arms, fruits and cla-

dodes of various cactus species. Studies of **D.buzzatii** in Australia have concentrated on allozyme polymorphism and factors affecting genetic variation at the allozyme loci. As a basis for study of the fitness of genotypes at allozyme loci, three preliminary experiments were done to provide data on the reproductive biology of the species.

In the first experiment, time to copulation, copulation duration, time from copulation to first egg and female fecundity in the 6.5 days after copulation were recorded. The flies used derived from 100 females collected at Breeza, N.S.W., and were generation 3 of mass culture in the laboratory. The medium used for culture and in all experiments reported here was autoclaved cactus-yeast-sucrose-agar. Using previously collected and stored (at 25°C) virgin flies, 82 pairs were set up (without etherization) over a 2.5 hr period (1400-1630 hr) at 20°C in empty 7.5 x 2.5 cm vials. All females were 30-48 hr old at initiation of these pair meetings, while males in the first 48 were 9 days old and in the last 34, 5 days old. Thirty-four of the 82 pairs had copulated by 1705 hr, when observation ceased. Because of the longer average observation period for 9-day old males, male ages were compared for proportion copulating in 30 min or in 60 min. Neither difference was significant, and the overall proportions were 0.207 and 0.244, respectively. Copulation duration ranged from 44 to 236 seconds. Again age of males had no significant effect and the overall average was 138.2±47.2 seconds.