Although the B group species *(roseus, migueli* and *calcaratus)* have the same chromosomal number (2n=30), their fundamental numbers and telocentric pairs are different. For this reason the group B has been split into 2 sections. Section 1 only contains *E. migueli* (NF 44, 8 telocentric pairs) and in section 2 are *E. roseus* and *E. calcaratus* (NF 46, 7 telocentric pairs). If the number of telocentric chromosomes is considered to be a characteristic of karyological primitiveness[11] *E. migueli* should show the most primitive karyological form (8 telocentric pairs) and *E. vittatus* the most derived (no telocentric chromosomes are present).

Bogart[7] considered that the karyotype of *E. roseus* (here *E. migueli*) is very reminiscent of those encountered in some species of *Eleutherodactylus* and *Syrrophus marnocki* and that the genus *Eupsophus* is chromosomally more similar to the *Leptodactylus marmoratus* group than to Pleurodema[12]. On the other hand, Duellman and Veloso[13] consider that it is easiest to derive the chromosome complement of Pleurodema from a stock resembling *E. roseus.* If all the telocentric chromosomes of *E. migueli* are fused among themselves, the Pleurodema[14] karyotype could be reconstructed.

Summary of primary and secondary constrictions and length as a percentage of the largest chromosome of *Eupsophus calcaratus*

Chromosomes	r*	Type	%	C
1	1.1	m	100	
2	2.6	sm	73.6	sm
3	3.2	st	62.1	
4	∞	t	40.2	
5	1.3	m	39.3	
6	∞	t	34.3	
7	1.6	m	33.3	
8	1.3	m	32.8	
9	∞	t	31.3	
10	1.1	m	27.8	
11	∞	t	25.3	
12	∞	t	24.8	
13	1.0	m	21.8	
14	∞	t	19.9	
15	∞	t	19.4	

*r is the ratio of the short arm divided into the long arm. For a ratio of 1.0–1.7 the chromosome type is metacentric (m); 1.7–3.0 is submetacentric (sm); 3.0–7.0 and above is subtelocentric (st); 7.0 and above is telocentric (t). The positions of the secondary constrictions (C) are based on similar ratios. The chromosome lengths are expressed as a percentage of the longest chromosome in the karyotype.

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Esterase polymorphism in a population of *Zaprionus paravittiger*

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Summary. Esterase isozyme variation in *Zaprionus paravittiger* is controlled by multiple alleles at 2 autosomal loci (Est-1 and Est-3). Est-1 codes for dimeric esterases while Est-3 codes for monomeric esterases. The degree and pattern of esterase polymorphism have been described.

Hubby and Lewontin[1] pioneered the use of gel electrophoresis to reveal genetic variability at the level of proteins. Since proteins are primary gene products, electrophoretic variations (mobility differences between proteins) can be interpreted in terms of genetic variation. Such analysis has not been attempted to reveal the genetic architecture of fruit-fly populations in this region. The present studies have been undertaken to analyze the genetic control of esterase polymorphism in the most abundantly available species i.e. *Zaprionus paravittiger.*

Esterase polymorphism was studied by starch gel electrophoresis[2] using a discontinuous system of buffers[3]. The adult flies were individually homogenized, and the homogenates run electrophoretically in 12% starch gel for 3 h at 200 V and 25 mA. The gels were stained for esterases following Brewer[4]. Genetic control of esterase variation was studied from the zymograms of parents and progeny of single pair matings. The nomenclature of banding patterns proposed by Ayala et al.[5] has been followed in this study. Electrophoretic variants at any esterase zone have been indicated by letters A_1, A_2, A_3 etc. in an anodal to cathodal sequence. The phenotypes of homozygous and heterozygous banding patterns have been represented as A_1A_1 and A_1A_2 respectively.

Individuals of *Z. paravittiger* exhibit consistently 3 zones of esterase activity. The Est-1 zone is represented by 3 single bands and 3 triple-banded patterns (figure). The end bands of each triple-banded pattern have the same mobility value as that of 2 single variant bands; the middle band is of intermediate mobility. However there is no electrophoretic variation at the Est-2 zone. The Est-3 zone is represented by a single band in any of 2 different positions or by a 2-band pattern. In the latter case, the 2 bands occupy the same positions as those of 2 variant single bands (figure). The esterase genotypes of parents and progeny of single pair matings have been analyzed to reveal bands which are under the control of separate loci and those coded by allelic variants at a locus (table).

The segregating esterase genotypes/phenotypes at any Est zone appear in the expected 1:2:1 proportions. Thus, the

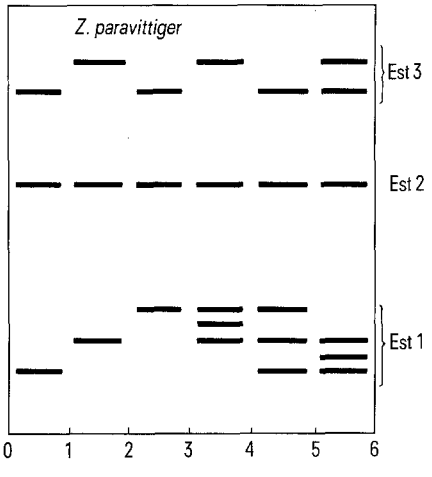
Genetic control, genotypic and allelic frequencies at polymorphic esterase zones in *Zaprionus paravittiger*

Esterase zone	Parental esterase phenotypes	Esterase phenotypes of progeny*						No. of individuals analyzed
		A_1A_1	A_2A_2	A_3A_3	A_1A_2	A_2A_3	A_1A_3	
Est-1	$A_1A_3 \times A_2A_3$	–	–	11	13	17	15	56
	$A_2A_2 \times A_1A_3$	–	–	–	22	19	–	41
	$A_1A_2 \times A_1A_2$	39	43	–	85	–	–	167
	$A_1A_3 \times A_1A_3$	37	–	31	–	–	67	135
	$A_2A_3 \times A_1A_2$	–	23	–	19	25	27	94
Est-3	$A_1A_2 \times A_1A_2$	17	21	–	45	–	–	83
		Esterase genotypes of wild caught individuals						
Est-1		18	10	28	24	35	28	143
Est-3		30	43	–	78			151
		Allelic frequencies						Heterozygosity
Est-1		$A_1 = 0.33$		$A_2 = 0.25$		$A_3 = 0.42$		0.60
Est-3		$A_1 = 0.46$		$A_2 = 0.54$				0.51

* χ^2-values insignificant at 5% level.

results of all the crosses are consistent with monogenic control. The presence of 2/3 distinct alternating single bands points to the diallelic/triallelic situation of the gene. The triple band variants in the Est-1 zone and the 2-band variants in the Est-3 zone represent heterozygous individuals. The banding patterns at the Est-1 and Est-3 loci are identical in both the sexes, indicating that these genes are autosomal. The occurrence of hybrid zones at Est-1 banding patterns suggest that the esterase variants are dimeric enzymes. The 2-band pattern in the Est-3 zone shows that esterases under the control of this locus are monomers.

The enzyme phenotypes being direct representatives of genotypes, the frequencies of different esterase alleles have been determined from the zymograms of wild caught individuals (table). The local population of *Z. paravittiger* showed a good fit to the Hardy-Weinberg equilibrium with respect to esterase variation at Est-1 and Est-3 loci, indicating that selection is not operating. The observed heterozygosities at Est-1 and Est-3 loci are 0.64 and 0.51 respectively. The present studies suggest that the high heterozygosity values at the esterase loci could contribute to considerable esterase polymorphism in this species.



Schematic representation of esterase banding patterns in *Zaprionus paravittiger*.

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Average dominance of interocellar bristle polygenes in *Drosophila melanogaster*

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Summary. The average dominance of interocellar bristle polygenes in *Drosophila melanogaster* was computed from the ratio of deviations from the base population mean of the F_1 and the selection lines. The alleles determining interocellar bristle number show recessiveness, more pronounced in 'low' lines than in 'high' lines.

The role and the possible consequences of dominance of alleles in the response to selection has been discussed by many authors[1-3], and it has been well established that the dominance of alleles is one of the parameters that must be specified in the studies about the nature of quantitative genetic variation[4]. There are a limited number of studies concerning the interocellar bristle polygenes in *Drosophila melanogaster*. In this investigation the average dominance of interocellar bristle polygenes and the contribution of maternally inherited factors to selection response was studied.

Material and methods. The selection lines used in this experiment were derived from 2 populations of *D. melanogaster* designated AR and BR, which have a common origin[5] and are described in detail by Marcos[5,6]. In each population, for simplicity here designated A, B, 5 lines were constructed: 2 high, 2 low and 1 control (A1H, A2H, A1L, A2L, AC, and B1H, B2H, B1L, B2L, BC). In all lines under selection the 20% of flies recorded of each sex, with the highest (or lowest) number of interocellar bristles were selected. Bristle number after selection ranged from 0.2 to 24; in wild populations the usual number is about 7.