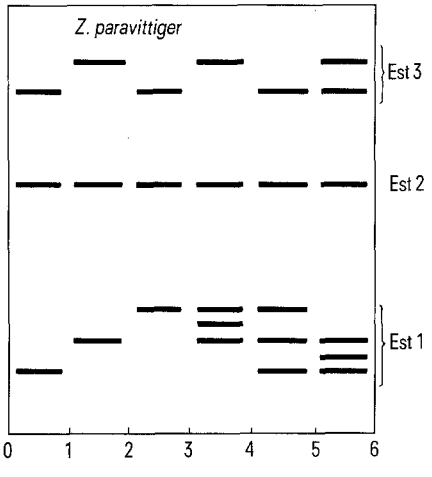
Genetic control, genotypic and allelic frequencies at polymorphic esterase zones in *Zaprionus paravittiger*

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.

Selection was practiced for 69 generations prior to this work. Reciprocal crosses were carried out between the selection lines and the base population. In order to reduce the environmental variance, samples of 100 eggs were seeded in bottles with 20 ml of food avoiding larval competition during development. For each cross four replications were set up, and 20 females were scored per bottle. All experiments were conducted at 19± 1 °C.

The average dominance was calculated from the ratio of deviations of the F_1 (selection line × basis population, and reciprocal cross) with respect to the mean value between the selection lines and the base populations.

Results and discussion. The means of interocellar bristle number for females from the selection lines, the base populations (control lines) and the reciprocal crosses between them are given in table 1. From the differences between the reciprocal crosses, we can determine the contribution of maternal components and cytoplasmic effects to response of selection. The values of average dominance are presented in table 2. The differences between the means of reciprocal crosses, except in B1H and B1L, are not significant. Therefore we can conclude that generally there was no significant directional contribution of maternally inherited factors.

The values of average dominance indicate that the alleles determining interocellar bristle number are recessive. The recessiveness, which is partial in alleles increasing the number of interocellar bristles, is practically absolute in alleles decreasing them. Consequently, in our populations the response to selection would be expected to be greater in high lines that in low lines. This is in agreement with the data obtained (see table 1). However it must be pointed out that the response in low lines is limited by the morphological threshold of 'zero bristles'.

So far, no other data are available about the average dominance of interocellar bristle polygenes. However, we can compare our results with those obtained by other authors for genes determining abdominal bristle number. For this trait, Frankham[4] also indicates recessive behaviour in the Canberra population, while other results suggest that alleles were additive or slightly dominant[7-10]. Consequently, it seems evident that the average dominance may differ considerably depending on the bristle system as much as on the population analyzed. Thus the results obtained with 1 specific experiment can never be generalized.

Table 1. Mean interocellar bristle number for females from the selection lines, the base populations (control lines) and the reciprocal crosses

Line	Mean	(A) F_1 Selection line* × control line	(B) F_1 Control line* × selection line
A1H	15.00±0.22	8.96±0.14	8.77±0.10
A2H	24.69±0.37	12.76±0.33	12.78±0.37
B1H	17.40±0.25	8.85±0.11	8.13±0.12
B2H	23.94±0.30	8.96±0.12	8.81±0.10
AC	7.10±0.07		
BC	6.16±0.09		
A1L	0.21±0.05	5.98±0.12	6.00±0.08
A2L	0.16±0.05	6.02±0.09	6.04±0.08
B1L	0.41±0.08	5.72±0.11	5.36±0.11
B2L	0.22±0.07	5.66±0.13	5.71±0.14

* Female parent.

Table 2. Average dominance from different lines

Line	d/a (1)	d/a (2)
A1H	0.52	0.57
A2H	0.35	0.35
B1H	0.52	0.64
B2H	0.68	0.70
A1L	0.79	0.80
A2L	0.78	0.78
B1L	1.13	1.00
B2L	0.97	0.99

(1) refers to cross (A) and (2) refers to cross (B), see table 1. d, genotypic values of the F_1; a, genotypic values of the selection lines.

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Effect of L-methionine-DL-sulphoximine on the photoproduction of hydrogen by *Rhodospirillum rubrum*[1]

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Summary. The repression of photoproduction of hydrogen by ammonia could be relieved by L-methionine-DL-sulfoximine. In the absence of ammonia, hydrogen evolution was inhibited by concentrations of L-methionine-DL-sulfoximine higher than 0.1 mM.

Apart from the reduction of several substrates, the photoproduction of hydrogen by cyanobacteria and photosynthetic bacteria also is catalyzed by nitrogenase. In whole cells of photosynthetic bacteria this enzyme is quickly inhibited by low concentrations of ammonium salts[2-5]. It has also been shown that glutamine synthetase activity decreases rapidly after addition of NH_4^+[6,7]. The glutamate analog L-methionine-DL-sulfoximine (MSO), a potent inhibitor of glutamine synthetase, is able to relieve the repression exerted by exogenous ammonia on nitrogenase activity[8-10]. Furthermore, studies on mutants of *Rhodospirillum rubrum*[11] and recently of *Rhodopseudomonas capsulata*[12] have also demonstrated that glutamine synthetase plays an important role in the regulation of nitrogenase activity.

The photoproduction of hydrogen by photosynthetic bacteria is under investigation as a potential source of fuel[5,13]. The efficient repression of nitrogenase by NH_4^+ poses severe restrictions when waste material containing com-