

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 Lewontin¹ 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 electrophoresis² using a discontinuous system of buffers³. 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 Brewer⁴. 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 A₁, A₂, A₃ etc. in an anodal to cathodal sequence. The phenotypes of homozygous and heterozygous banding patterns have been represented as A₁A₁ and A₁A₂ 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 parvittiger*

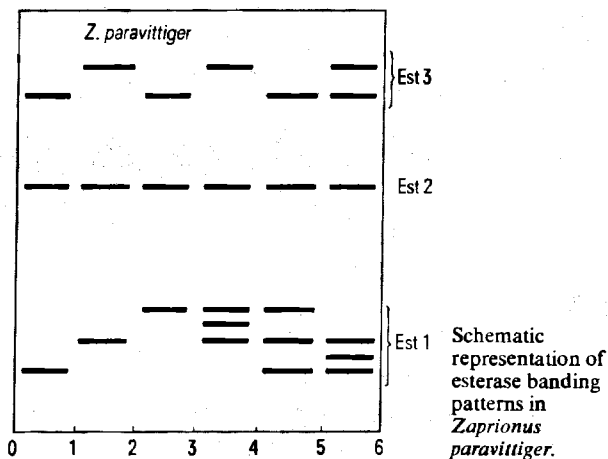
Esterase zone	Parental esterase phenotypes	Esterase phenotypes of progeny*						No. of individuals analyzed
		A ₁ A ₁	A ₂ A ₂	A ₃ A ₃	A ₁ A ₂	A ₂ A ₃	A ₁ A ₃	
Est-1	A ₁ A ₃ × A ₂ A ₃	-	-	11	13	17	15	56
	A ₂ A ₂ × A ₁ A ₃	-	-	-	22	19	-	41
	A ₁ A ₂ × A ₁ A ₂	39	43	-	85	-	-	167
	A ₁ A ₃ × A ₁ A ₃	37	-	31	-	-	67	135
	A ₂ A ₃ × A ₁ A ₂	-	23	-	19	25	27	94
Est-3	A ₁ A ₂ × A ₁ A 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								
Est-1		A ₁ = 0.33		A ₂ = 0.25		A ₃ = 0.42		Heterozygosity
Est-3		A ₁ = 0.46		A ₂ = 0.54				0.60
								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. parvittiger* 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.



- 1 J.L. Hubby and R.C. Lewontin, *Genetics* 54, 577 (1966).
- 2 O. Smithies, *Biochem. J.* 61, 629 (1955).
- 3 M.D. Poulik, *Nature* 180, 1470 (1957).
- 4 G.J. Brewer, *Introduction to Isozyme Techniques*. Academic Press, New York 1970.
- 5 F.J. Ayala, J.R. Powell, M.L. Tracey, C.A. Mourao and S. Perez-Salas, *Genetics* 70, 113 (1972).