

Table 1. Percentage (in moles) of free amino acids in Oregon-R larvae at different ages before and after 8 hours of food deprivation.

	36 hr*	36-44 hr H <sub>2</sub> O	56 hr*	56-64 hr H <sub>2</sub> O	85 hr*	85-93 hr H <sub>2</sub> O
Aspartic acid	3.6	1.6	3.4	2.1	2.0	2.4
Threonine	3.3	0.9	3.9	1.7	4.8	2.4
Serine	3.5	2.9	3.1	2.7	2.3	2.2
Asparagine & glutamine	32.9	32.2	30.1	37.1	25.6	27.5
Proline	2.5	3.1	7.6	5.4	12.2	14.2
Glutamic acid	11.5	12.6	8.9	7.8	7.2	9.8
Glycine	4.1	5.1	3.5	3.8	3.5	3.2
Alanine	16.6	5.9	13.3	6.2	10.9	5.6
Valine	1.3	0.8	1.0	0.8	1.0	1.2
Methionine	--	--	--	--	--	0.1
Isoleucine	0.5	0.3	0.3	0.4	0.7	0.7
Leucine	0.7	0.5	0.5	0.6	1.1	1.2
Tyrosine	0.9	0.9	3.4	4.6	7.7	13.3
Phenylalanine	--	0.2	--	0.4	0.6	0.9
β-alanine	3.1	2.3	4.7	3.4	4.6	2.4
Ethanolamine	2.1	5.0	2.3	5.0	0.6	0.3
Ammonia	2.9	11.0	2.2	1.2	2.6	1.6
Lysine	3.1	3.4	4.4	4.0	3.0	2.4
Histidine	4.2	5.3	3.6	6.7	4.6	4.0
Tryptophane	0.1	--	0.2	--	0.4	0.3
Arginine	3.2	6.0	3.6	6.2	4.7	4.2

\*removed from growth media and immediately prepared for analysis

References: Rapport and Sing 1971, Can. J. Genet. and Cytol. 13:822-833; Rapport and Yang 1974, Comp. Biochem. Physiol. 493:165-169.

Richmond, R.C. and M.E. Claerbout. Indiana University, Bloomington. Ratios in crosses segregating for Esterase 6<sup>0</sup> (Null) and Esterase 6<sup>S</sup> alleles.

The presence of a null allele at the esterase 6 locus in *D. melanogaster* was first described in these pages (Johnson et al. 1966). These investigators examined segregation ratios in crosses of Est 6<sup>S</sup>/Est 6<sup>0</sup> x Est 6<sup>0</sup>/Est 6<sup>0</sup> and Est 6<sup>S</sup>/Est 6<sup>0</sup> x Est 6<sup>S</sup>/Est 6<sup>0</sup>. In both cases

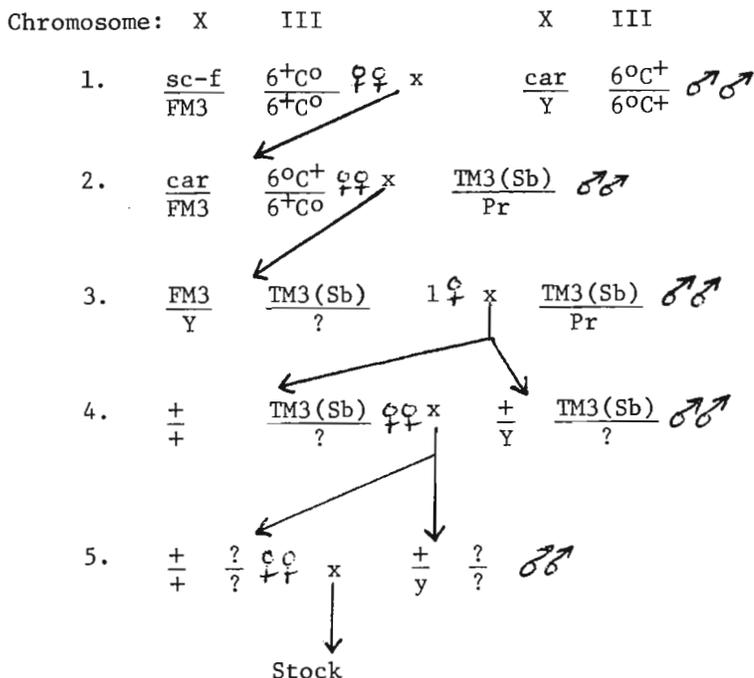
a significant deficiency of the Est 6<sup>0</sup>/Est 6<sup>0</sup> genotype was found. This result suggests that the Est 6 locus has an important function which is expressed during the development of flies. These data are suspect, however, since the stock homozygous for the Est 6<sup>0</sup> allele apparently also carried car. We repeated this analysis using esterase 6 stocks which do not carry morphological markers. Our data show no significant deviation from mendelian expectations.

Stocks homozygous for the Est 6<sup>S</sup> and Est 6<sup>0</sup> alleles were obtained by crossing a sc ec cv ct<sup>6</sup> v g<sup>2</sup> f/FM3 y<sup>3</sup>ld sc<sup>8</sup> dm B l strain which is also homozygous for a null allele of Esterase C to a car strain which is homozygous for Est 6<sup>0</sup>. F<sub>1</sub> females from this cross were mated to TM3(Sb)/Pr males to begin the series of crosses necessary to extract recombinant third chromosomes. This procedure is summarized on the following page and allowed us to produce four different types of strains each homozygous for the following combinations of alleles at the esterase 6 and esterase C loci: 6<sup>0</sup>C<sup>+</sup>, 6<sup>+</sup>C<sup>0</sup>, 6<sup>0</sup>C<sup>0</sup>, 6<sup>+</sup>C<sup>+</sup> (+ = active allele). These stocks contain no morphological markers.

Approximately 200 #3 crosses were made and strains that proved to have identical Est 6 and C genotypes were combined. Crosses made to determine segregation ratios utilized the 6<sup>0</sup>C<sup>+</sup> and 6<sup>+</sup>C<sup>+</sup> combined stocks.

? = 6<sup>0</sup>C<sup>+</sup> or 6<sup>+</sup>C<sup>0</sup> or 6<sup>0</sup>C<sup>0</sup> or 6<sup>+</sup>C<sup>+</sup>

$\frac{sc-f}{FM3} = sc\ ec\ cv\ ct^6\ v\ g^2/FM3\ y^{3ld}\ sc^8\ dm\ B\ L$



Segregation ratios were checked by first crossing 6<sup>0</sup>C<sup>+</sup> ♀♀ to 6<sup>+</sup>C<sup>+</sup> ♂♂. F<sub>1</sub> females and males from this cross were separately backcrossed to the 6<sup>0</sup>C<sup>+</sup> stock. Backcross progeny should exhibit a 1:1 ratio of Est 6<sup>0</sup>/Est 6<sup>+</sup> and Est 6<sup>0</sup>/Est 6<sup>+</sup> genotypes. Since females show low esterase 6 activity, only male progeny from the backcrosses were analyzed using standard starch gel procedures (Richmond 1972). In order to determine if larval density affected genotype ratios, the final crosses were completed under conditions which produce high larval density (10 pairs of adults allowed to lay eggs for 4 days at 25°C in a 1/2-pint bottle) or low larval density (2 pairs of adults allowed to lay for 2 days). Since there were no significant differences between the reciprocal backcrosses, they are combined in the data presented below.

Although there is an absolute deficiency of Est 6<sup>0</sup>/Est 6<sup>0</sup> genotypes at both densities

Density	N	6 <sup>0</sup> /6 <sup>0</sup>	6 <sup>0</sup> /6 <sup>+</sup>	X <sub>1</sub> <sup>2</sup>	P
High	174	81	93	0.83	>0.1
Low	143	63	80	2.02	>0.1

neither case approaches statistical significance as determined by chi-square. A chi-square test of homogeneity of the high and low density crosses is also insignificant (χ<sup>2</sup> = 0.2) indicating little effect of larval density on segregation ratios. The

discrepancy between our results and those of Johnson et al. can likely be traced to the inclusion of morphological markers in the earlier crosses or the presence of a gene affecting viability which was closely linked to the Est 6 locus but which was recombined away in our crosses. The present data demonstrate that the absence of the esterase 6 enzyme has little if any effect on viability.

Acknowledgments to Kathy Sheehan for technical assistance.

References: Johnson, F.M., B.B. Wallis and C.M. Denniston 1966, DIS 41:159; Richmond, R.C. 1972, Genetics 70:87-112.

Ruiz, A. and A. Fontdevila. Universidad de Santiago de Compostela, Spain. Two new chromosome arrangements in *D. buzzatii*.

*D. buzzatii* belongs to the mulleri subgroup of the repleta group of the genus *Drosophila*. Wasserman (1962) has proposed that the chromosomal arrangements of this species are derived from the most primitive chromosomal sequence

of the group by fixing three inversions in the second chromosome (2x<sup>3</sup>, 2k, 2w<sup>3</sup>) and one inversion in the fifth chromosome (5g). In addition, *D. buzzatii* has been reported heterozygous for inversion j, jz<sup>3</sup> and y<sup>3</sup> in the second chromosome (Wasserman 1962; Carson and Wasserman 1965).

We have studied the chromosomal polymorphism of 12 populations and two strains of *D. buzzatii* (Fontdevila et al. 1979) of the Old World. The majority of these samples showed the presence of two new inversions, one in the second and another in the fourth chromosome.