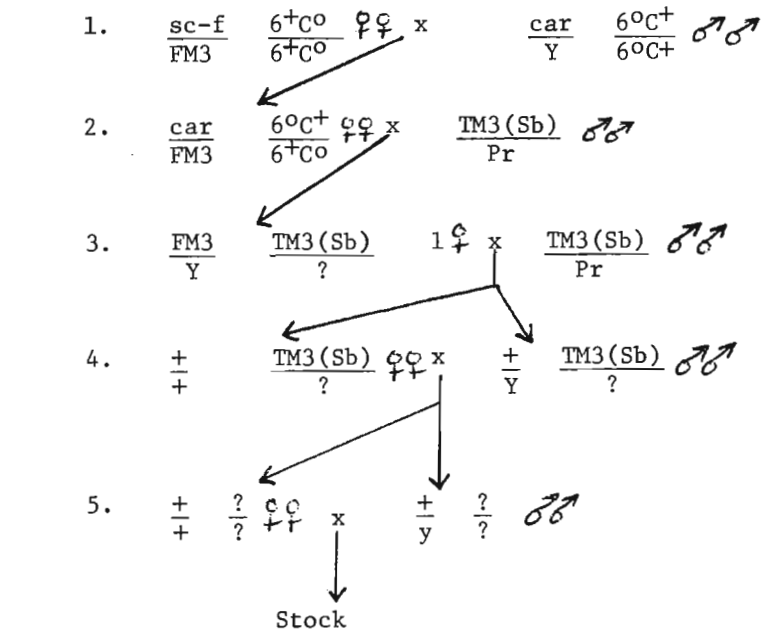
? = 6^oC^+ or 6^+C^o or 6^oC^o or 6^+C^+

$\frac{sc\text{-}f}{FM3}$ = sc ec cv ct^6 v g^2/FM3 y^{31d} sc^8 dm B L



Segregation ratios were checked by first crossing 6^oC^+ ♀♀ to 6^+C^+ ♂♂. F_1 females and males from this cross were separately backcrossed to the 6^oC^+ stock. Backcross progeny should exhibit a 1:1 ratio of Est 6°/Est 6° and Est 6°/Est 6^+ 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°/Est 6° genotypes at both densities 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 ($\chi^2 = 0.2$) 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.

Density	N	6°/6°	6°/6+	X^2_1	P
High	174	81	93	0.83	>0.1
Low	143	63	80	2.02	>0.1

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 ($2x^3$, 2k, $2w^3$) and one inversion in the fifth chromosome (5g). In addition, D. buzzatii has been reported heterzygous for inversion j, jz^3 and y^3 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.

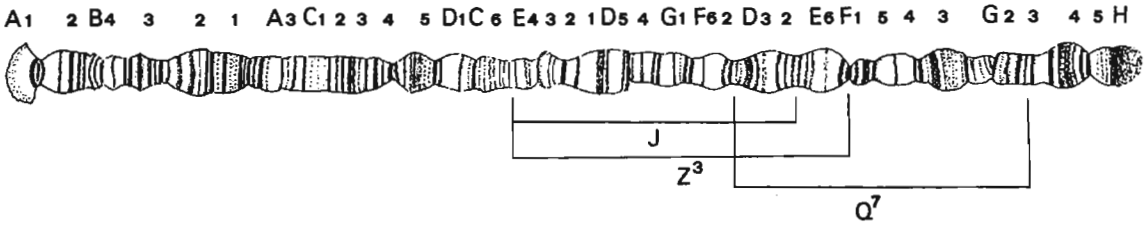

A1 2 B4 3 2 1 A3 C1 2 3 4 5 D1 C6 E4 3 2 1 D5 4 G1 F6 2 D3 2 E6 F1 5 4 3 G2 3 4 5 H
J
Z3
Q7

Fig. 1.

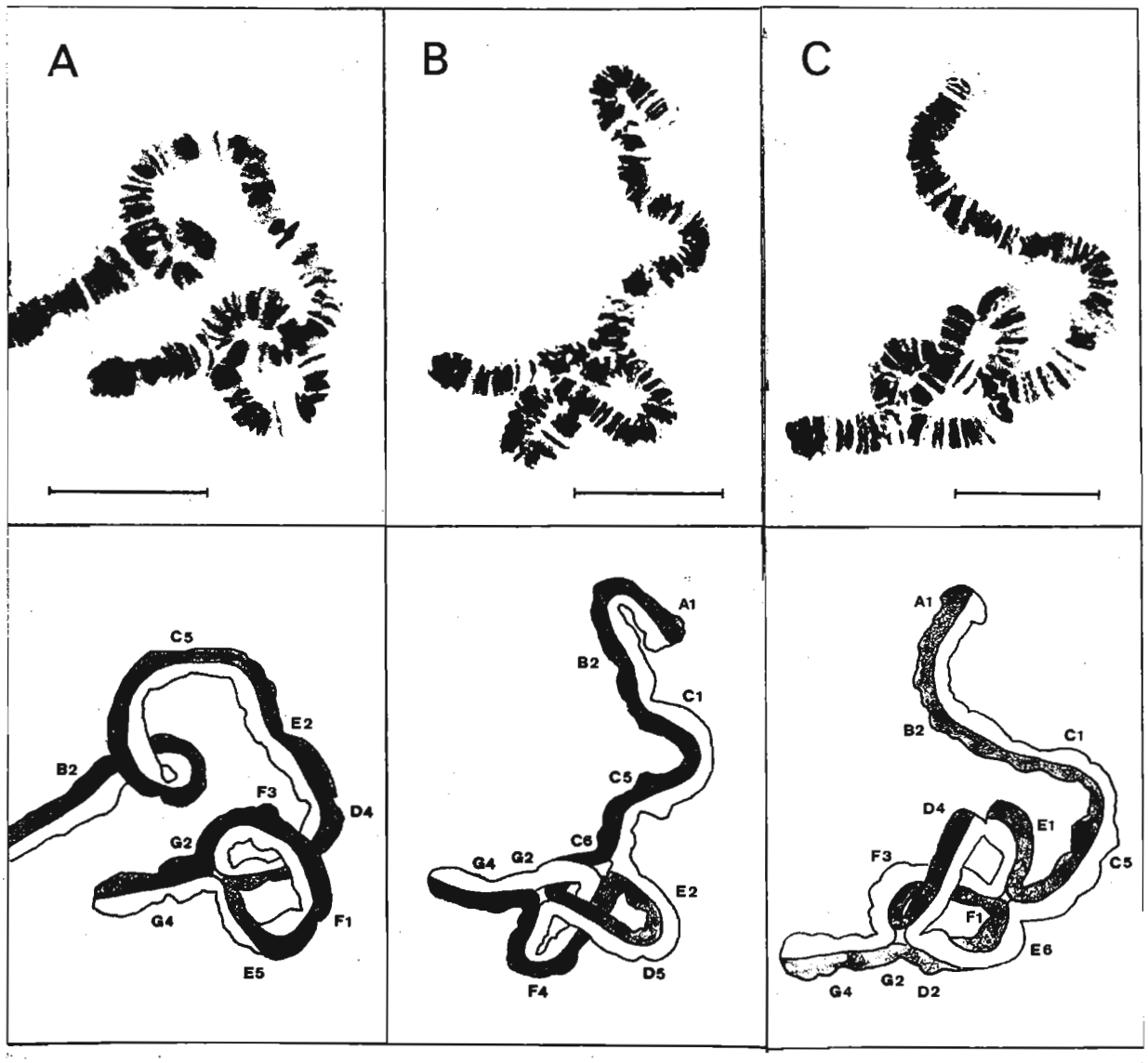

A
B
C
C5
E2
B2
F3
D4
G2
G4
F1
E5
A1
B2
C1
C5
G4
G2
C6
E2
F4
D5
A1
B2
C1
D4
E1
F3
C5
F1
E6
G4
G2
D2

Fig. 2.

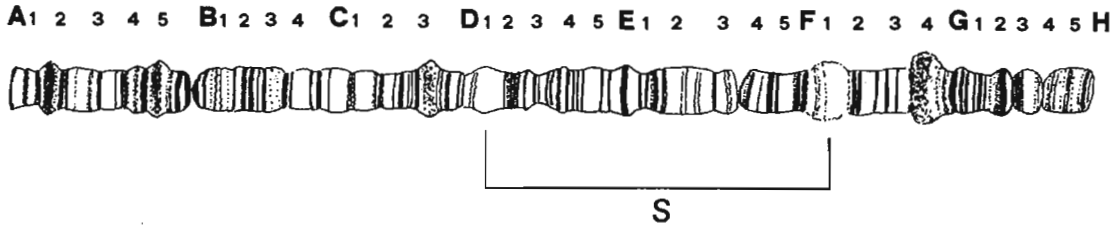


Fig. 3

The second chromosome has been found polymorphic for a new inversion which is always associated with j arrangement and it has been named tentatively jq^7. Its breakage points are D3b and G2f, the former included in inversion j region. In Fig. 1 is shown a scheme of both ends of inversion jq^7 in a chromosome j/j and also the ends of j and jz^3 already described (Wasserman 1962) for comparison.

Fig. 2 shows three microphotographs (A, B, C) of inversion loops formed in polytene chromosomes of three heterokaryotypes for the second chromosome ($2jq^7/j$, $2jq^7/st$ and $2jq^7/jz^3$, respectively), with the interpretative scheme. This inversion was found originally in Carboneras (Spain) and since then it has been found in the great majority of the studied populations of the Iberian Peninsula and Canary Islands. However, it is absent in the Balearic Island, the Madeira Island, Egypt and Dahomey populations. The frequency of jq^7 arrangement ranges from 0.13 to 0.04, which qualifies it as moderately frequent.

Most of the populations and strains studied by us have been found also polymorphic for the fourth chromosome. This chromosome shows two arrangements: the standard (st) which is the primitive fourth chromosome of the repleta group (Wasserman 1962), and another arrangement which bears the new inversion extending from D1d to F1c regions. The breakage points are diagrammed in Fig. 3. The s inversion had not been detected in all the previous analyses of natural populations (Carson and Wasserman 1965) or laboratory strains (Wasserman 1962, 1954; Mather 1957). Yet, the frequency of this inversion is rather high (between 0.1 and 0.3) in the great majority of populations and strains analyzed by us. Fig. 4 (D) shows a microphotograph of the inversion loop formed in salivary gland chromosome of one heterokaryotype for the fourth chromosome (4st/s), with the interpretive scheme.

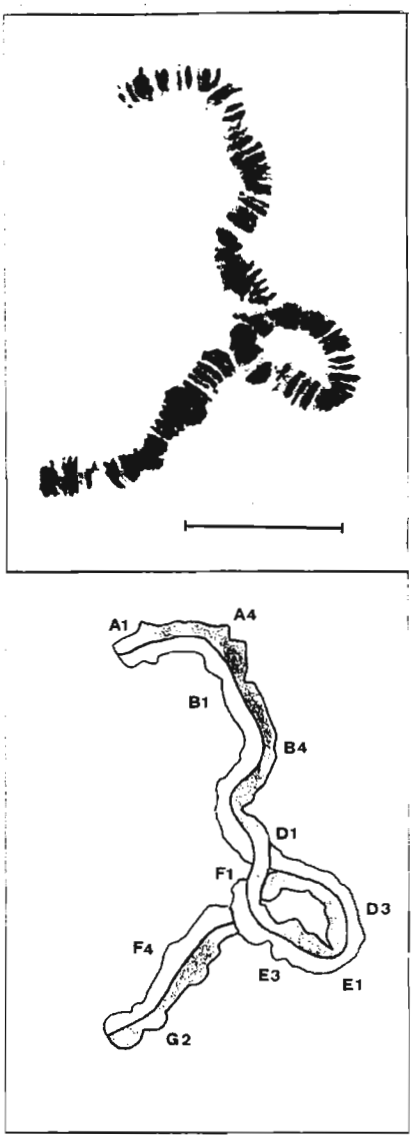


Fig. 4

The origin of these inversions is not known. The species has been given an Argentinian origin (Wasserman 1962; Carson and Wasserman 1965), on the basis of its high chromosomal polymorphism in the populations of S. Luis (Argentina). However, the polymorphism found by us in the Old World is the highest of all studied and poses the problem of its origin. D. buzzatii was introduced in the Old World following most probably the spread by man of its host plant Opuntia ficus-indica after the discovery of America. The evolutionary implications of this polymorphism, especially on the process of colonization, are discussed elsewhere (Fontdevila et al. 1979) and emphasize the interest for searching these new inversions in the endemic areas of the

New World in order to understand the colonizing strategy of this species. The presence of these new inversions in introduced populations of D. buzzatii suggests that colonization may not necessarily lead to loss of chromosomal polymorphism when the niche is narrow, although more information is needed from the original populations to further substantiate this point.

References: Carson, H.L. and M. Wasserman 1965, Amer. Natur. 905:111-115; Fontdevila, A., A. Ruiz, G. Alonso and J. Ocaña 1979, Evolution (submitted); Mather, W.B. 1957, Texas Univ. Publ. 5721:221-225; Wasserman, M. 1954, Texas Univ. Publ. 5422:130-152; Wasserman, M. 1962, Texas Univ. Publ. 6205:85-117.

Sampsell, B. Chicago State University, Chicago, Illinois. Survival differences between Drosophila with different ADH thermostability variants.

Temperature has been implicated as a potential selective agent in maintaining the polymorphism at the Alcohol dehydrogenase locus in D. melanogaster (Gibson 1970; Vigue and Johnson 1973; Clarke 1975). Two alleles, Adh^{Fm} and Adh^{Sm} (see Sampsell 1977 for an explanation of symbols) are found in most natural populations. Adh^{Sm} codes for an enzyme, ADH^{Sm}, that is generally less active, but more heat stable than the ADH^{Fm} form produced by Adh^{Fm}. Along the eastern coast of the United States, Adh^{Sm} increases in frequency from about 60% in Maine to nearly 90% in Florida (Vigue and Johnson 1973; Sampsell 1977). This allelic distribution may be the result of an increasing fitness of flies with ADH^{Sm} (or conversely a decreasing fitness of flies with ADH^{Fm}) with increasing mean temperature.

Numerous laboratory studies have shown that ADH is necessary for survival on various alcohol-supplemented media (the exception involves certain alcohols whose ketone metabolites are extremely toxic). If a significant portion of a fly's ADH enzyme were inactivated by high temperatures without killing the fly outright, the alcohol tolerance and thus survival would be reduced.

In an effort to test this hypothesis, larval viability was observed under various environmental conditions. Four strains have been constructed which are nearly isogenic except for a small region of the second chromosome containing the Adh locus. The relative thermostabilities of the allozymes of these strains is $ADH^{Fr} > ADH^{Sm} > ADH^{Fm} > ADH^{Fs}$ (Sampsell 1978). Three

Table 1. Survival of larvae under various combinations of temperature and ethanol.

Parental genotype	Temp °C	Ethanol conc.	Number of adults emerging FF	FS	SS	Total	X^2	Relative survival FF	FS	SS
$F^{r}S^{m}$	20	0%	201	422	179	802	3.31	.25	.53	.22
		5%	185	353	148	686	4.62	.27	.51	.22
		10%	13	17	2	32	7.69*	.41	.53	.06
	29	0%	209	413	171	793	5.01	.26	.52	.22
		5%	168	362	150	680	3.79	.25	.53	.22
		10%	24	50	9	83	8.81*	.29	.60	.11
$F^{m}S^{m}$	20	0%	234	411	186	831	5.69	.28	.49	.22
		5%	177	389	150	716	7.40*	.25	.54	.21
		10%	30	75	12	117	14.25**	.34	.56	.10
	29	0%	190	332	154	676	4.05	.28	.49	.23
		5%	210	406	185	801	1.72	.26	.51	.23
		10%	42	85	15	142	16.01**	.30	.60	.11
$F^{s}S^{m}$	20	0%	190	440	218	848	3.05	.22	.52	.26
		5%	193	405	190	788	0.64	.24	.51	.24
		10%	57	81	22	160	15.34**	.36	.51	.14
	29	0%	179	393	143	715	10.67**	.25	.55	.20
		5%	156	280	128	564	2.81	.28	.50	.23
		10%	32	37	7	76	16.50**	.42	.49	.09

* $p < 0.05$
** $p < 0.01$