for the evaluation of genotypical differences through the chromosomal polymorphisms, as had already been described by Dobzhansky (1950), da Cunha (1957), Cordeiro (1954) and others.

The progeny of each female captured in nature was analyzed in relation to the larval salivary gland chromosomal rearrangements, by the technique of Ashburner (1967); the same was applied to the progeny of females ecloded from "coquinho" fruits fecundated by males ecloded from the same fruit.

The analysis of 363 individuals showed that of the five chromosome arms, X L, X R and II R were homozygous. As for the left arm of the second chromosome (II L), the Kolmogorov-Smirnov test showed that the differences between the F_1 of females collected from banana and "coquinho" baits were significant ($P < 0.05$) for combined rearrangements (two to four inversions together). For the third chromosome (III) there were significant differences between the offspring of females captured with nets over the fruits of Arecastrum romanzoffianum and the offspring of females ecloded from these fruits in the laboratory, when combined rearrangements were considered (two to three inversions).

The results of the statistical test to the chromosomal rearrangements are summarized in Table 2. The total number of rearrangements observed for II L chromosome was 17, 6 of which were single rearragements (only one inversion) plus the homozygous; 11 were combined rearrangements (two to four inversions together), with a frequency different from those of each inversion separately, although most of these inversions being located far enough in the chromosome as to permit the occurrence of crossing over between them.

Four single rearrangements were found for the third chromosome, including the homozygous, as well as four complex rearrangements, representing two and three inversions. Among the combined rearrangements of II L, for example, whereas D, E, B/d, e, b reached a frequency of 54.1% in banan baits, it was not found in larvae of females ecloded in "coquinho" and attained 45.8% in larvae from females attracted by the fruit; F, D, E, B/f, d, e, b reached 77% in banana baits, 22% in the natural one as was not found in larvae of females ecloded from the native fruit.

Among the third chromosome complex rearrangements, J, B/j, b was 22.3% in larvae from females attracted by banana, 2.12% in larvae from flies ecloded from "coquinho" and 75.5% in larvae attracted by this same fruit; the B, C/b, c rearrangement reached 0%, 41.6% and 58.3%, respectively, in the offspring of the same samples and the J, B, C/j, b, c rearrangement was exclusive of larvae from flies ecloded from "coquinho" fruits. This indicates a clear association of certain types of rearrangements with the kind of explored trophic resource.

References: Ashburner, M. 1967, Chromosoma (Berl.) 21:289-428; Cordeiro, A.R. 1954, Bol. Instituto de Ciências Naturais 1:5-54; da Cunha, A.B. 1957, Bol. Fac. Fil. Ciên. e Letr. Univ. São Paulo #220, Biologia Geral 10:1-56; Dobzhansky, Th. 1950, J. Heredity 41:156-158.

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Selection against an Adh null allele.

Several null mutants of the alcohol dehydrogenase (Adh) locus in D. melanogaster are known. Homozygotes for these mutants, which lack detectable ADH activity, can be maintained as laboratory strains without culture problems when kept on regular food. On ethanol-supplemented medium, however, they lack detoxification ability and die quickly compared to ADH-positive flies. As we have found (van Delden et al. 1978) that selection occurs also on regular food in populations polymorphic for the naturally occurring Fast (F) and Slow (S) alleles we studied whether in populations polymorphic for a null mutant and either F or S alleles, selection would occur against the null allele. For this purpose the Adh^{nl} (0) mutant (Grell et al. 1968) was introduced into the background of the Groningen population, whereafter 0 x S and 0 x F crosses were made with S and F strains possessing the same background. The offspring of these crosses (F_1) were put in population cages at 25°C. The populations were continued in time and allele frequencies were determined at intervals beginning with the F_2 generation. Populations were started both on regular and ethanol-supplemented food. Table 1 lists the observed null allele frequencies, populations indicated as S0 and F0 are polymorphic for the null allele and S and F alleles respectively. To study the importance of strain effects, five S0 and five F0 populations were started, both on regular and ethanol-supplemented food. Populations numbered up to four inclusive each contained two S or F lines which differed from the lines used in the other three populations; populations numbered five contained all eight lines S or F lines used in the other four populations of the same type.

Table 1. Frequencies of null-alleles in the course of time (initial frequency: 0.50).

Populations	Regular food						Ethanol-supplemented food			
	F_2	Time (weeks)					F_2	Time (weeks)		
		8	14	26	38	52		8	14	26
SO 1	0.50	0.45	0.44	0.37	0.35	0.22	0.23	0.06	0.01	0
SO 2	0.49	0.45	0.46	0.40	0.37	-	0.20	0.05	0.02	0
SO 3	0.49	0.44	0.38	0.36	0.33	0.31	0.18	0.05	0.01	0
SO 4	0.48	0.42	0.43	0.31	0.34	0.28	0.18	0.05	0.01	0
SO 5	0.49	0.46	0.40	0.33	0.28	0.24	0.23	0.05	0.01	0
SO	0.49	0.44	0.42	0.35	0.34	0.26	0.22	0.06	0.01	0
FO 1	0.46	0.42	0.42	0.33	0.33	0.30	0.26	0.01	0	0
FO 2	0.44	0.41	0.40	0.33	0.28	0.27	0.24	0.02	0	0
FO 3	0.49	0.44	0.41	0.38	0.36	0.23	0.23	0.03	0	0
FO 4	0.50	0.43	0.38	0.35	0.32	0.22	0.20	0.03	0	0
FO 5	0.50	0.42	0.37	0.24	0.28	0.28	0.20	0.01	0	0
FO	0.48	0.42	0.39	0.32	0.31	0.26	0.23	0.02	0	0

From Table 1 it is clear that, as has been expected, a rapid decrease in frequency of the 0 allele has occurred on ethanol food: frequency of the 0 allele had dropped to 0.01 after 14 weeks (approximately 4 generations) in the SO populations and the 0 allele was even lost in the FO population. Also on regular food the frequency of the 0 allele decreased considerably: to 0.26 in 52 weeks (approximately 26 generations). It appears that the decline in 0 frequency is very similar in all populations of the same type: line effects are therefore small. We conclude that also on regular food the absence of ADH activity has detrimental effects and lowers the fitness of the homozygotes for the null allele; whether the fitness of the heterozygotes is also lowered is the object of further study.

References: Grell, E.H., K.B. Jacobson and J.B. Murphy 1968, Ann. New York Acad. Sci. 151:441-455; van Delden, W., A.C. Boerema and A. Kamping 1978, Genetics 90:161-191.

van Dijk, H. University of Groningen, The Netherlands. The relationship between ADH activity and body weight in D. melanogaster.

When measuring ADH-activity in larvae and flies of D. melanogaster it is important to take body weight into account. The parameter activity per mg is strongly positively correlated with body weight. The most likely explanation is the deposition of relatively large amounts of fat after reaching the critical weight. It is known (Ursprung et al. 1970) that fat bodies have a high ADH activity.

In this experiment done for the Groningen population (see Bijlsma-Meeles and Van Delden 1974) ADH activity was measured according to Van Delden et al. (1975) both in larvae showing the first signs of pupation and in 7-day-old male flies. Differences in individual weights were induced by varying the level of crowding. For ADH activity per mg ($\Delta E\ min^{-1}mg^{-1}$) = y and body weight (mg) = x, the following relationships were found (see figures on following page):

Larvae	ADH_{FF}	$y = 0.1144\ x - 0.0829$
"	ADH_{SS}	$y = 0.0355\ x - 0.0255$
Flies	ADH_{FF}	$y = 0.3765\ x + 0.0181$
"	ADH_{SS}	$y = 0.0776\ x + 0.0089$

All regression coefficients were significant ($P < 0.001$).

The larger ADH activities of larvae when ethanol is present in their food can be completely explained by this relation: body weights increase with increasing ethanol concentration. Selection experiments for increase of ADH activity will lead to selection for body weight when no precautions are made to keep body weight at a constant value.