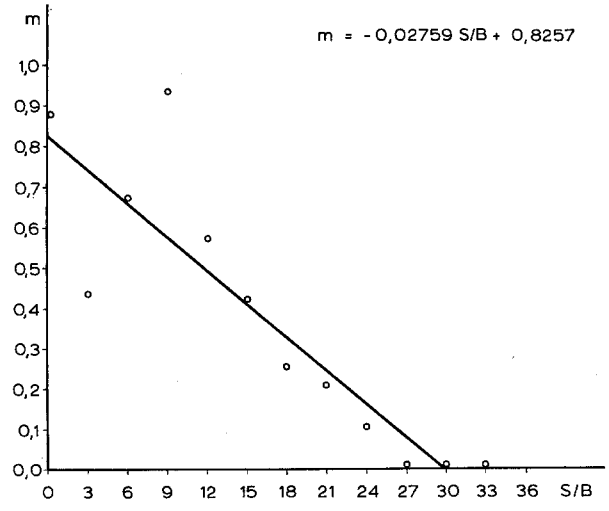

Fig. 4. Correlation between spine length (S/B) and the percentages of mictic and amictic females of Figure 3.

$$m = \frac{\text{mictic females \%}}{\text{mictic females \%} + \text{amictic females \%}}$$

of the adaptative values of a population genetics mechanism[10]: a kind of feed-back system takes place, before homozygosis grows too high, by means of the appearance of mictic females (which are expressions of the same homozygosis) and then of males, so that the subsequent cross-fertilization results in both recovering the original heterozygosis and producing resting eggs.

Riassunto. La correlazione fra un carattere morfologico (lunghezza delle spine postero-laterali) e la percentuale di femmine mittiche nella discendenza di una singola femmina partenogenetica di *Brachionus calyciflorus* (Rotatoria) dimostra l'esistenza di un meccanismo genetico comune ai due fenomeni. Dai risultati ottenuti emerge una interpretazione del ciclo eterogonico (comparsa di femmine mittiche e ciclomorfosi) in termini di valori adattativi di un meccanismo di genetica di popolazione.

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Adaptation Studies of Radiation-Induced Barley Mutants

It is commonly observed that the effects of genotype and environment are not independent and that the relative performance of different genotypes changes in different environments, i.e. there exists a genotype × environment interaction. The importance of this interaction reflects the necessity of evaluating genotypes in more than a single environment. The plant breeder must consider this interaction in the selection of superior genotypes. These genotypes can be selected on the basis of their stability of yield performance over a range of environments.

In the present work, a technique similar to that employed by FINLAY and WILKINSON[1] was used to estimate the stability parameters of barley mutants to elucidate the yield potential of the pertinent genotypes across different sites.

Material and methods. The material used in this project was comprised of *early* and *late* M_2 plants selected from the irradiated populations of Prior cultivar (a standard Australian commercial variety). The seeds of 10 M_3 plants of each of these M_2-derived *early* and *late* families were bulked and then were tested in the M_4 generation in field-plot experiments. 29 mutant families, along with 11 barley cultivars having different geographic origins, were grown in a two replicate randomized block layout at contrasting sites differing in annual rainfall pattern and soil type in cereal growing areas of South Australia in 1968, to assess their adaptation. These sites chosen were situated near towns of Monarto South (referred to herein as Bundaleer, the name of farm), Minlaton, Adelaide (at the Waite Institute) and Clinton.

The experimental plots, each of 3 rows, 17.5 cm apart and 3.10 m long, were sown 35 cm apart with pathways 1 m wide between blocks of plots. When plants were mature, 30 cm at each end of the plot was removed and remainder of plot (2.50 m) was harvested and weight of clean grain was recorded in g/plot.

Yield data were converted to $\log_{10}$ for statistical analysis. The 3 main parameters describing the performance of genotypes over a range of environments, i.e. mean yield (mean) and stability parameters viz. regression coefficient (b) and S.E. (b) were computed according to regression technique suggested and used by FINLAY and WILKINSON[1] and further extended by EBERHART and RUSSELL[2].

Results and discussion. The mean yield of all 40 genotypes at each site was used as an estimate of 'site mean yield' (environment mean). The sites used in 1968 provided a range of environments as shown in Table I. The site mean yields ranged from 236 g/plot at Bundaleer (low-yielding site) to 432 g/plot at Waite (high-yielding site). The mean yield of individual genotypes (averaged over 2 replicates) at each site is regressed upon the site means to provide stability parameters for each genotype.

In the calculation of means and regressions referred to in this paper, the basic yield data measured on a natural scale were transformed to a logarithmic scale because it induced 1. a reasonable degree of homogeneity of experimental error, and 2. a high degree of linearity in the regressions of individual yields on the site means. The mean yield over all environments (mean) and 2 measures of stability viz. regression coefficients (b) and S.E. (b) for each genotype are shown in Table II.

Table I. Site mean yields (g/plot) in the year 1968

Scale	Sites			
	Bundaleer (B)	Clinton (C)	Minlaton (M)	Waite (W)
Arithmetic (natural)	236	246	290	432
$\log_{10}$	2.346	2.358	2.444	2.622

[1] K. W. FINLAY and G. N. WILKINSON, Aust. J. agric. Res. *14*, 742 (1963).

[2] S. A. EBERHART and W. A. RUSSELL, Crop Sci. *6*, 36 (1966).

[3] A. GHAFOOR ARAIN, Ph. D. Thesis, University of Adelaide, Australia, 1973, p. 163.

FINLAY and WILKINSON[1] suggested that the regression coefficient (b) and genotype mean yield over all environments (mean) were the important measures of the performance of a genotype across environments, i.e. its adaptation. They classified a genotype with $b = 0.0$ as completely stable in performance across environments. A genotype producing above-average yields and with $b = 1.0$ was considered as generally adapted. Later EBERHART and RUSSELL[2] in their analysis extended the regression technique used by FINLAY and WILKINSON[1] by including a 3rd measure of stability, deviation mean squares (S^2d or standard error of b) in addition to 'mean' and b. They suggested that a genotype with $b = 1.0$ and $S^2d = 0$ should be classified as stable.

The regression coefficient (b) and S.E. (b) values for each genotype (Table II) reveal wide variation in performance across environments. It seems clear that many of the mutant families yielded similar or more than the average-yield of barley cultivars of diverse geographical origin (Nos. 30–40) that were included in the trial. Two mutant families, Nos. 8 and 11, gave the highest yields and the former family was the most desirable genotype according to EBERHART and RUSSELL's[2] terminology. Family No. 8 with high mean yield, is characterized by $b \leqslant 1.0$ and S^2d or S.E. (b) = 0.076. This indicates that this family produced above-average yields over all sites, and has general adaptation pattern. On the other hand, family No. 15, yielding less than average, had a regression coefficient more than 1.0 ($b = 1.295$) and relatively small deviations (S.E. (b) = 0.175). This genotype is sensitive to changes in the environment and is specifically adapted to high-yielding environment. Although other families, such as Nos. 7 (high yielding) and 28 (lowest yielding), had regression coefficients much greater than 1.0, these also showed large values of S.E. (b).

It is worth noting that family No. 22 producing similar to the average-yield, is characterized by having b less than 1.0 and second smallest S.E. (b). This family could be classified as the most stable in performance across sites when judged by both stability parameters. Mutant families (Nos. 24 and 28), the lowest yielding genotypes are characterized by $b > 1.0$ and large values of S.E. (b).

Table II. Mean yields (g/plot) and stability parameters for mutant families and other varieties of barley

Family/genotype No.	Family/genotype and origin	Arithmetic scale	Log_{10} scale		
		Mean	Mean	b	S.E. (b)
1	341 Prior 10 kR early	307	2.477	0.759	0.426
2	344 Prior 10 kR early	320	2.494	0.684	0.585
3	351 Prior 10 kR early	324	2.497	0.873	0.462
4	353 Prior 10 kR early	333	2.508	0.956	0.252
5	355 Prior 10 kR early	256	2.395	0.874	0.296
6	356 Prior 10 kR early	349	2.530	0.919	0.155
7	224 Prior 10 kR late	377	2.546	1.410	0.420
8	226 Prior 10 kR late	380	2.572	0.762	0.076
9	235 Prior 10 kR late	318	2.490	0.926	0.162
10	238 Prior 10 kR late	335	2.520	0.544	0.293
11	242 Prior 15 kR early	395	2.582	0.953	0.332
12	245 Prior 15 kR early	346	2.530	0.715	0.406
13	250 Prior 15 kR early	369	2.550	0.945	0.587
14	252 Prior 15 kR early	362	2.538	1.165	0.189
15	259 Prior 15 kR early	279	2.419	1.295	0.175
16	414 Prior 15 kR late	334	2.513	0.783	0.300
17	418 Prior 15 kR late	355	2.536	0.903	0.428
18	381 Prior 20 kR early	324	2.490	1.063	0.525
19	383 Prior 20 kR early	334	2.519	0.520	0.319
20	393 Prior 20 kR early	371	2.554	0.670	0.829
21	321 Prior 20 kR late	273	2.428	0.690	0.275
22	330 Prior 20 kR late	313	2.490	0.665	0.140
23	331 Prior 20 kR late	298	2.456	0.988	0.555
24	Prior 10 kR early 1	189	2.253	1.182	0.545
25	Prior 15 kR early 1	191	2.265	1.035	0.257
26	Prior 15 kR early 2	319	2.496	0.733	0.238
27	Prior 15 kR Fam. 66	234	2.351	0.999	0.486
28	Prior 20 kR early 1	173	2.154	2.350	0.449
29	Prior 20 kR Fam. 8	175	2.228	0.708	0.819
30	Calif. Feed	408	2.605	0.594	0.294
31	Trebi	278	2.384	1.671	1.487
32	Domen	216	2.303	1.262	0.836
33	Maraini	379	2.572	0.582	0.398
34	Nepal	117	2.037	1.173	1.018
35	Volga	365	2.535	1.326	0.187
36	Sahara 3765	156	2.131	1.941	0.727
37	C.I. 3576	331	2.495	1.246	0.420
38	Peruvian Seln.	269	2.354	1.960	1.320
39	Freja	325	2.499	0.878	0.430
40	Prior A	257	2.399	0.296	0.841
	Average yield	301	2.441		

These families were extremely early flowering when compared with other mutant families (i.e. Nos. 1–23). Thus, the extreme early mutants showed maximum genotype × environment inter-action in the present studies. Similar conclusions were also drawn by GHAFOOR ARAIN[3] where extreme early or late-flowering M_2-derived lines of EMS treated material of barley cultivars of diverse yields showed maximum genotype × environment inter-actions in M_4 and M_5 generations and these lines tended to possess specific adaptation pattern with respect to yield.

Zusammenfassung. Die Umweltstabilität von 29 strahleninduzierten Mutanten und 11 Kulturvarietäten wird anhand der Methode von EBERHART und RUSSELL[2] untersucht. Die Mutanten werden auf Grund der Versuchsergebnisse in stabile und angepasste klassiert.

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[5] This research work was conducted at the Waite Agricultural Research Institute, Glen Osmond, South Australia.

Adaptedness of the Carriers of Normal and Subvital Second Chromosomes of *Drosophila melanogaster*

Much research has been dedicated to the study of second chromosome genetic load of *Drosophila melanogaster*, for example, the extensive revision made by CRUMPACKER[1]. Nevertheless, there is relatively little information on the parameters, in particular on the adaptation, of the normal and subvital homozygous wild strains in experimental populations, in the specialized literature.

Adaptedness is defined as the ability of a genotype or group of genotypes to transform the available food into living matter, as well as the ability to survive and reproduce in a given environment[2,3]. It is necessary to quantify the 'adaptedness' for measuring the effect of natural selection or to compare different populations[4].

This paper is an attempt to investigate the adaptedness of wild homozygous second chromosomes strains of *D. melanogaster* with normal and subvital viability.

The homozygous 2nd chromosome strains were obtained by means of CyL/Pm technique[5], and their viabilities classified by the usual method[6]. With 10 homozygous strains (M6, M8, M10, M12, M17, M18, M19, M24, M27, and M32) for different wild normal 2nd chromosomes and 2 homozygous strains (M7 and M15) for different

[1] D. W. CRUMPACKER, in *Evolutionary Biology* (Appleton-Century-Crofts, New York 1967), vol. 1, p. 306.
[2] TH. DOBZHANSKY, *Genetics of the Evolutionary Process* (Columbia University Press, New York 1970).
[3] C. A. MOURÃO, F. J. AYALA and W. ANDERSON, Genetica *43*, 552 (1972).
[4] F. J. AYALA, Evolution *24*, 483 (1970).
[5] B. WALLACE, J. Genet. *54*, 280 (1956).
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Table I. Mean numbers and mean biomass of adults and young flies per week, with their standard errors, and the numbers of weekly census (N) utilized to computations, in 15 experimental populations of *Drosophila melanogaster*

Populations	*N*	Adults		Young	
		Number	Biomass (mg)	Number	Biomass (mg)
Heterozygous					
POL1	20	259 ± 12	210 ± 10	405 ± 26	294 ± 20
POL2	20	276 ± 11	217 ± 9	404 ± 28	281 ± 20
POL3	20	251 ± 11	202 ± 9	405 ± 31	297 ± 25
Means	20	262 ± 7	210 ± 5	405 ± 16	291 ± 13
Homozygous					
M 6	20	225 ± 16	188 ± 13	480 ± 41	362 ± 31
M 7	27	169 ± 11	142 ± 9	402 ± 24	306 ± 19
M 8	22	198 ± 16	153 ± 12	546 ± 37	375 ± 26
M10	24	227 ± 18	220 ± 18	514 ± 45	441 ± 36
M12	21	190 ± 12	160 ± 10	363 ± 27	282 ± 21
M15	21	145 ± 19	112 ± 15	530 ± 52	363 ± 34
M17	20	176 ± 17	131 ± 13	377 ± 30	270 ± 24
M18	21	158 ± 11	140 ± 10	482 ± 31	385 ± 21
M19	20	183 ± 22	146 ± 17	365 ± 40	257 ± 26
M24	23	209 ± 13	177 ± 11	377 ± 21	296 ± 15
M27	20	183 ± 11	145 ± 9	405 ± 23	300 ± 16
M32	20	171 ± 14	144 ± 11	360 ± 26	282 ± 20
Means	22	186 ± 4	155 ± 4	433 ± 10	327 ± 7