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Frequency of visible mutants in natural populations of D. subobscura.

The frequency of visible mutations in the offspring of ♀♀ of D. subobscura, captured in natural populations of Litochoron village at the foot of the mountain Olympus and on the isle of Samothrace in Greece has been established as a basic information for further studies on the genetical variability of Greek populations of this species.

In this first report we are giving the distribution of the number of visible mutant characters in the F_2 offspring of ♀♀ and ♂♂. In some cases we utilized for practical reasons also F_3 and F_4 cultures.

An aberrant phenotype has been considered as a mutant character when it occurred at least three times in one single F_2 culture. The table gives for each population on the first line the observed frequency of ♀♀ revealing in their offspring from 0 to 12 mutants; and on the second line the corresponding theoretical frequency, calculated on the basis of a Poisson distribution. The following populations are listed: A: Offspring of 47 single ♀ caught at Litochoron (Olympus). B: Offspring of 48 ♀ caught on the isle of Samothrace. C: Offspring of 32 groups of 5 to 10 ♀♀ in each vial, from Samothrace. D: Offspring of 55 ♂♂ captured on Samothrace and crossed with ♀♀ from the laboratory standard strain "Küssnacht", E: Analogous figures for the offspring of 218 ♀♀ of D. melanogaster, captured in a natural population of Banyuls, France, (Bösiger, 1962).

Table: Frequency of mutants in Greek populations of D. subobscura.

Population	n ♀	n mut.	m̄ per ♀	Frequency of ♀ revealing from 0 to 12 mutants											X^2	P
				0	1	2	3	4	5	6	7	8	9	10-12		
A Litochoron	47	217	4.6	0	2	8	15	3	4	2	4	3	0	4	15.2	< 0.01
				0.5	2.2	5	7.7	8.8	8.1	6.2	4	2.3	1.2	0.8		
B Samothrace	48	213	4.4	0	3	3	12	10	8	5	3	2	1	1	3.7	< 0.50
				0.6	2.6	5.7	8.4	9.2	8.1	5.9	3.7	2	1	0.6		
C Samothrace	32	89	2.7	1	5	10	8	5	1	1	0	0	1	0	1.6	< 0.50
				2.1	5.8	7.8	7	4.7	2.6	1.1	0.4	0.1	0.1	0		
D Samothrace	55	132	2.4	0	17	23	5	5	2	1	0	1	0	1	19.2	< 0.001
				5	12	14.4	11.5	6.9	3	1.3	0.5	0.1	0	0		
E Banyuls	218	971	4.5	5	7	20	30	55	41	27	21	9	2	1	14.2	< 0.05
				2.5	11	24.9	37.1	41	37	28	17.9	10	4.9	2.2		

The results presented in the table are leading to the following preliminary conclusions:

1. The heterogeneity observed in the offspring of single ♀ of D. subobscura, captured in the populations of Litochoron (A) and Samothrace (B) is as high as the heterogeneity observed in the offspring of single ♀ of D. melanogaster, caught in the population of Banyuls (E). The mean number of 4.4 to 4.6 mutants in the offspring of one ♀ is rather high and indicates an important degree of heterogeneity of the populations of D. subobscura. It is interesting to notice that the two species and the three populations are giving the same mean number of mutants.

2. The offspring of the 32 groups of ♀ (C) shows a lower number of mutants. The following two factors might be responsible for the lower mutation rate. Since several females had been placed together in each vial, the probability of the constitution of homozygote combinations for recessive mutations is smaller than in the offspring of single females with an obligatory brother-sister mating for the F_2. Modifiers may also partly be responsible for concealed genes in the population C. For these two reasons it seems plausible that the mutation rate is lower in population C, in spite of the presence of several ♀♀ in each vial, sharing together more mutants than the single ♀ per vial in populations A and B.

3. In the offspring of single males (D), crossed with females of another strain, we observe also a smaller number of mutants. The following three factors may be partially

responsible for the lower gene frequency in population D. The selection pressure against genes on the X-chromosome is much higher in ♂♂ than in ♀♀, since these genes are in a hemizygous state and always expressed in ♂♂, if there are no modifiers concealing them. In a natural population of D. melanogaster from Banyuls (Bösiger, 1962) the frequency of mutants is twice as high in ♀♀ than in ♂♂. The greater fragility of ♂♂ could add to the lower mutant gene frequency. The effect of modifier genes, introduced by the crossing of the Samothrace ♂♂ with the foreign Küssnacht ♀♀, may have prevented in some cases the phenotypical expression of present mutants.

4. The X^2 test shows, that the observed distribution of frequencies of mutant genes fits well with a Poisson distribution for the populations B and C, at the 1% level only for population A and not at all for population D.

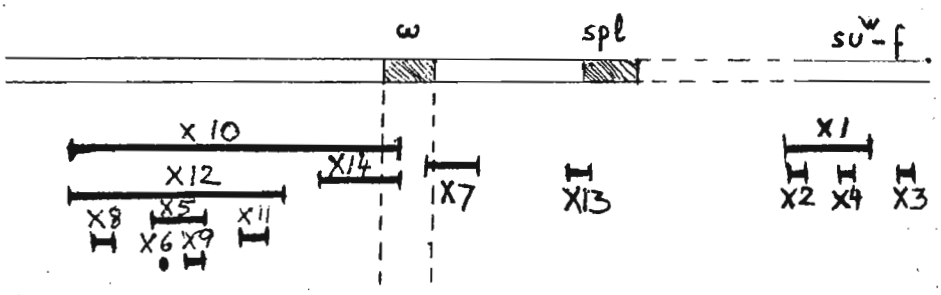
5. A preliminary morphological comparison of the mutant phenotypes found by Gordon, Spurway and Street (1939) in England, by Buzzati-Traverso (1941) in Italy and by Prevosti (1952) in Spain with those found in Greece shows that the great majority of the phenotypes are common in the four countries. The list and description of the mutants found in Greece will be given later.

Bösiger, E., 1962, Bull. Biol. France et Belgique, 96:3-122. Buzzati-Traverso, A., 1941, Scient. Genetica, II:1-34. Gordon, C., Spurway, H. and Street, P., 1939, J. Genetics, 38:37-90. Prevosti, A., 1952, Genetica Iberica, 4:95-128.

Lifschytz, Eliezer. Hebrew University, Jerusalem, Israel. Induced X-chromosome lethals covered by $Y \cdot w^+$.

7100 y ac sc chromosomes were irradiated with a 2000 r dose of X-rays. 363 chromosomes carried lethal mutations. 14 of these lethals (3.9%) were covered by a $Y \cdot w^+$ chromosome produced by Brosseau et al, (1961).

The lethals covered by the $Y \cdot w^+$ chromosome were crossed among themselves in all possible combinations in order to determine their allelism. Lethals that were suspected to be "point mutations" after the allelism test were checked further for crossing-over disturbance in the y-pn-w region. One group of lethals showed free recombination with the markers and proved to be proximal to f. They are also covered by $Y \cdot ma\text{-}1^+$ and by $Y \cdot B^S$. These lethals were thus located in the most proximal region of the X-chromosome, and are probably covered by su^W-f. All the lethals except one showed disturbances in the crossing over frequency in their immediate vicinity. The following "complementation map" is consistent with the data collected so far:



Since we selected for lethals covered by the $Y \cdot w^+$ compound, deficiencies extending beyond the region of the X-chromosome included in this compound were automatically excluded. This may explain the fact that only 3.9% of the lethals were found in a section comprising 10% of the cytological length of the X chromosome.

Most of these lethals do not disturb crossing-over between distant markers, such as y-sn, and would have been classified as "point mutations" by routine genetic procedures. These results suggest that many X-ray induced lethals that pass for "point mutations" are actually small aberrations.

Note that lethals X10, X14 and X7 are allelic to w, but X7 complements the lethal effect of both X10 and X14. This is in line with Lefevre's (1965) findings, and suggests that a deficiency for the w-locus is non-lethal.

We started to accumulate chemically induced lethals covered by $Y \cdot w^+$ in order to compare the "complementation map" of lethals induced by the various mutagenic agents.