2. Full-sib family selection for yield of ear corn in four populations.

A study was conducted in 1959 to compare the progress due to selection in four populations. The test included each cycle of selection (when available) of two varieties, Jarvis and Indian Chief, and two hybrid populations, (NC7 x CI21) F_2 and (NC34 x NC45) F_2. The results are given in Table 1 and show that selection seems to be more effective in the varieties than in the populations derived from crossing inbred lines. It is also apparent that the variety response is much closer to expectation than is the response of the hybrid populations. Since the test was conducted in only one location and year, the results are subject to errors due to genotype x environmental interaction. This material will be studied further over a wider range of environments, and results of additional cycles of selection will be included as they become available.

Table 1. Yield in pounds per plant for each cycle available for test.

Population	Cycle of Selection 0	1	2	3	4	Gain per cycle in percent of mean observed	predicted
Jarvis	.396	.369	.460	.469	---	6.1	6.7
Indian Chief	.399	---	.458	---	---	7.4	5.5
(NC7 x CI21)F_2	.362	---	.386	.400	.398	2.5	9.3
(NC34 x NC45)F_2	.267	---	---	.279	---	1.5	11.5

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1. Investigations on induced polygenic mutability in maize.

The experiments which were briefly described in Maize Genetics Cooperation News Letter 34 (p. 99-101) and which were intended to study the possibility of increasing through irradiation the genetic variability for quantitative traits in corn have been continued. Subject of this note are the measurements obtained on the R_3 generation grown in summer 1960 at the Agricultural Experiment Station in S. Angelo Lodigiano, in the Po Valley.

Nine different selfed lines were established in 1957 from seed of a single ear of a monoploid stock, HD 173 1375/11, kindly supplied by Professor G. F. Sprague. In the following year three groups of 5 plants (on average) were selfed within each line. The tassels of one group received an X-ray treatment of 1500 r two days before pollen shedding; a second group received a treatment of 3000 r and the third group did not receive any irradiation. Treatments were applied to the tassel cut from the original plant and maintained in tap water up to the time when pollen was collected to fertilize the proper plant. The X-ray machine was operated at 120 KV, 3 mA, 1 mm Al filter.

By selfing a sample of five plants on the average from each treated group within each line the R_2 generation was obtained and sublines started. By selfing a sample of 3 plants within each subline, the R_3 generation was obtained and subsublines established. In 1960 observations were made on about 10 plants per each subsubline of R_3 generation.

The analysis of variance was carried out independently for each treatment according to the hierarchical scheme given in table 1.

Table 1. Analysis of variance and expected components.

Source of variability	df	Variance	Composition
Total	nkmp-1		
between lines	n-1	V_L	$\sigma^2_E + \sigma^2_P + p\,\sigma^2_{SSL} + pm\,\sigma^2_{SL} + kpm\,\sigma^2_L$
between sublines within lines	n(k-1)	V_{SL}	$\sigma^2_E + \sigma^2_P + p\,\sigma^2_{SSL} + pm\,\sigma^2_{SL}$
between subsublines within sublines	(m-1)nk	V_{SSL}	$\sigma^2_E + \sigma^2_P + p\,\sigma^2_{SSL}$
between plants within subsublines	(p-1)nkm	V_P	$\sigma^2_E + \sigma^2_P$

In this table: n = number of lines, k = number of sublines per each line, m = number of subsublines per each subline, p = number of plants per each subsubline, and nkm = total number of plants in the experiment.

Estimates of the portion of variance due to different sources of variability may be obtained:

(1) from the variance due to differences between lines it is possible to identify a portion of variability (σ^2_L) which may be considered as due to differences between the seeds from the same parental ear with which the experiment was started. Since seeds from a monoploid plant were used as starting material this source of variability will give an estimate of variance due to random environmental influence only;

(2) from the variance due to differences between sublines it is possible to identify a portion of variability (σ^2_{SL}) due to the differences between the seeds produced by a single plant, which may be traced to random influences of the treatment on different pollen grains from the same treated tassel;

(3) the variance due to differences between subsublines within sublines enables us to identify a portion of variability (σ^2_{SSL}) traceable to segregation of mutants induced by the treatment and this gives us an estimate of its mutagenic effect. No significant estimate of variance from this source of variability is expected in the untreated material, except for the effects of segregation of spontaneous mutants;

(4) the variance due to differences between plants within subsublines is partly due to the effects of segregation of induced mutants in R_3 families (σ^2_P) and partly to the influence of environment (σ^2_E). In the untreated material the major fraction of the variance is to be attributed to environmental effect with possibly a limited portion due to segregation of spontaneous mutants.

It follows from the above considerations that in studying the effects of X-ray treatments on polygenic mutations in the R_3 generation, only the last two components (3 and 4) are of interest because they may give an estimate of the increase of variability as a consequence of polygenic mutants induced by the treatment. For the time being we will concentrate our attention on these two components only.

At present the analysis has been completed for the following characters:

1) number of internodes below the highest ear
2) total number of internodes in the plant
3) total length (in cm) of the internodes below the highest ear

and the results are given in table 2.

Table 2

Source of variability	control d.f.	control mean squares	1,500 r d.f.	1,500 r mean squares	3,000 r d.f.	3,000 r mean squares
1) Number of internodes below the highest ear						
Between subsublines within lines	59	2.7196	86	3.3728	48	3.0119
Between plants within subsublines	715	1.0477	1071	0.9003	537	1.1817
2) Total number of internodes in the plant						
Between subsublines within sublines	59	2.3873	86	6.1861	48	5.2927
Between plants within subsublines	715	1.4561	1071	1.2991	537	1.7467
3) Total length (in cm) of the internodes below the ear						
Between subsublines within sublines	59	453.1580	86	386.6124	48	563.0394
Between plants within subsublines	715	104.1533	1071	75.0160	537	80.1281

Table 3. Estimates of variance components and relative values

Character	treatment	σ^2_{SSL}*	$\sigma^2_E+\sigma^2_P$	total phenotypic variance	h^2_1	$h^2_2+e^2$
1) number of internodes below the higher ear	control	0.1851	1.0477	1.2328	0.15	0.85
	1500 r	0.3627	0.9003	1.2630	0.29	0.71
	3000 r	0.2163	1.1817	1.3980	0.16	0.84
2) total number of internodes in the plant	control	0.1031	1.4561	1.5592	0.07	0.93
	1500 r	0.5255	1.2991	1.8246	0.29	0.71
	3000 r	0.4191	1.7467	2.1628	0.19	0.81
3) total length of internodes below the ear	control	38.6495	104.1533	142.8028	0.27	0.73
	1500 r	33.5050	75.0160	108.5210	0.31	0.69
	3000 r	57.0817	80.1281	137.2098	0.42	0.58

* p weighted for disproportionate class numbers = 9.03.

The classification of the effects being hierarchical, makes it possible to isolate the genetic component σ^2_{SSL} (see paragraph 3) and to estimate from it the variance increase due to the treatment. In fact,

$$V_{SSL} - V_P = p\sigma^2_{SSL}$$

where σ^2_{SSL} is an estimate of the treated induced genetic variance. Hence the heritability, h^2_1, for each treatment may be computed from the ratio between this estimate and the total phenotypic variance:

$$h^2_1 = \frac{\sigma^2_{SSL}}{\sigma^2_E + \sigma^2_P + \sigma^2_{SSL}}$$

From this experiment it is not possible to estimate separately the environmental and the genetic fractions of variability which add to V_P, the variance between plants within subsublines. Such components would give us the relative estimates e^2 and h^2_2, respectively.

Both estimates of heritability are due partly to fixable effects (D, in terms of Mather notation) and partly to unfixable ones (H), their composition being:

$$h^2_1 = 1/2\ D + 1/16\ H$$

$$h^2_2 = 1/4\ D + 1/8\ H$$

The results of this analysis are given in table 3.

From table 3 it may be seen that h^2_1 values for the plants which received a treatment of 1500 r are in general higher than those for the plants which received no treatment. h^2_1 values for the 3000 r treatment, as obtained from the experiment described, are lower than those of the 1500 r treatment for characters 1 and 2.

This behaviour may be due to a high loss of chromosomes in the 3000 r dose as a consequence of genic and chromosomal lethal mutations. However, the trend is different for character 3 whose genetic variability steadily increases from the controls to the 3000 r group.

Measurements of other quantitative traits were also recorded and their analysis is in progress.

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