INHERITANCE OF QUANTITATIVE CHARACTERS IN ZEA MAYS.
I. ESTIMATION OF THE NUMBER OF GENES CONTROLLING THE TIME OF MATURITY

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THE estimation of the number of gene pairs controlling quantitative characters is a great challenge to geneticists. While the study of discontinuous variations is relatively simple, that of continuous variations is complicated, since such a study is concerned with multiple factors, heterosis, dominance and the nature of the interactions between the genes differentiating these quantitative characters.

The method suggested by ANDERSON (1938) using chromosomal interchanges as tools for detecting the number of gene pairs controlling quantitative characters, and applied by BURNHAM and CARTLEDGE (1939), SABOE and HAYES (1942), MILLER (1951), IBRAHIM (1954) and MOHAMED (1954, 1956), will not reveal the type of gene interactions. The chromosomal interchanges used in such studies were not in an isogenic background, which limits the final conclusions. Therefore, the methods given by EMERSON and EAST (1913) and POWERS (1950a) are very adequate if the genetic and environmental variabilities are following the same scale of measurement and the gene effects are additive on such a scale.

POWERS, LOCKE and GARRETT (1950) suggested and described a method for estimating the number of genes controlling quantitative characters. This method is based on partitioning the backcrosses and F_2 populations into their component genotypes. Also it involves the separation of environmental and genetic variances from the total variances with the purpose of determining the nature of all these variances. This can be accomplished from the three nonsegregating populations, namely, P_1, F_1, and P_2, and the three segregating populations, B_1 to P_1, F_2, and B_1 to P_2. The latter are essential in arriving at the entire genetic hypothesis.

The study in this paper will be limited to the estimation of the number of genes controlling the number of days from seeding to silking and pollen shedding. Also the number of gene pairs differentiating the two parents for the difference of days between silking and pollen shedding will be discussed. The time of maturity was used in these studies because of its importance in the production of hybrid corn, since differences between inbreds with respect to this character will affect the general output of the yield.

MATERIAL AND METHOD

The hybrid populations were obtained from a cross between E.G. 102 (P_1), and E.G. 205 (P_2) maize inbred lines, which were kindly furnished to the author by DR. M. A. IBRAHIM of the Ministry of Agriculture, Egypt, U.A.R. The genetic

study of the experiment included P_1, B_1 to P_1, F_1, F_2, B_1 to P_2, and P_2 populations. The field design of the experiment was a randomized complete block. Planting of the experiment started in the summer of 1955, at the University of Alexandria Experimental Farm. The above two inbreds were selected for this study because they are considered very promising in the Ministry of Agriculture program for producing hybrid corn for commercial use.

The dates of silking and pollen shedding were recorded once daily on the same plant. The means and the standard deviations were calculated to study the phenotypic dominance. The environmental and genetic variances were estimated according to the method suggested by POWERS (1942), and POWERS et al. (1950). In testing for the proper scale, the method discussed by POWERS et al. (1950) and POWERS (1951) was used.

EXPERIMENTAL RESULTS

1. Silking date

One of the essential steps in studying any continuous character is to determine the type of scale of measurement which fits better the biological processes causing the variability.

It can be seen from Table 1 that neither the arithmetic scale (on an additive base) nor the logarithmic scale agreed with the obtained means. The mean values for the number of days from seeding to silking date showed that E.G. 102 (P_1) had a mean of 65.73 days and E.G. 205 (P_2) a mean of 67.68 days. The difference between the two inbred lines was 1.95 days with a P value of 0.01. The mean of E.G. 102 (P_1) was slightly higher than that of the F_1 (64.95 days), but the difference was within the limits of variation expected due to the errors of random sampling. The mean of B_1 to P_1 (64.19 days) was less than the mean of P_1, with a difference of 1.54 days. This difference was significant. However, χ^2 test showed that the frequency distribution of B_1 to P_1 was not significantly different from that of P_1 and F_1, since χ^2 value was 13.0179 with a P value of .20–.10 (d.f. 8). Also "t" tests indicated that the mean of the F_1 did not differ significantly from the mean of B_1 to P_1. From the above analysis it was concluded that phenotypic dominance was complete for fewer days over more days.

TABLE 1

The obtained and the calculated means on the basis of both arithmetic and logarithmic scales for the number of days from seeding to silking

Generation	$\overline{X} \pm$ S.D.	Arithmetic mean	Logarithmic mean	Number of individuals
P_1	65.73 ± 3.05	65.73	65.73	40
B_1 to P_1	64.19 ± 2.47	65.34	65.34	122
F_1	64.95 ± 3.33	66.70	66.69	39
F_2	65.19 ± 3.12	64.09	64.09	154
B_1 to P_2	63.99 ± 3.04	66.31	66.29	147
P_2	67.68 ± 2.81	67.68	67.68	40

The fact that the genetic variance (Table 2) of B_1 to P_1 was not significant and was very small compared with that of F_2 and B_1 to P_2, indicated that genic dominance was also complete.

Number of major gene pairs differentiating parents: On the basis of the segregating generations, the assumption was made that the two parents were differentiated by three major gene pairs. The indication that three major gene pairs were involved was arrived at from the fact that only 1.95 percent of the individuals in the F_2 population fell in the class 65–69, whereas on a three-factor basis, 1.6 percent would be expected (Table 3). Also the indication was further supported by dividing 0.68 percent (class 72–75 of B_1 to P_2) by 7.70 percent (class 72–75 of F_1) which gave a value of 8.83 percent. On a three-factor basis, a ratio of 12.5 percent would be expected.

When the theoretical means of F_2 and B_1 to P_2 for one factor pair of genes, two pairs and three pairs were compared with the obtained means of these two populations (Table 4), it appeared that the calculations based on the hypothesis that the two inbred lines were differentiated by three major gene pairs was probably the best fit. Accordingly, the genotype of P_1 (E.G. 102) was symbolized as *AABBCC* and of the P_2 (E.G. 205) as *aabbcc*.

The B_1 to P_1 and B_1 to P_2 frequency distributions were partitioned into their component genotypes (Table 5). This partitioning will give the frequency distri-

TABLE 2

The means, standard deviations, variances and number of individuals in each population for the number of days from seeding to silking

Population	$\overline{X}$	S.D.	Total variance	Environmental variance	Genetic variance	Number of individuals
P_1	65.73	3.05	5.788	6.345	— .557	40
B_1 to P_1	64.19	2.47	4.581	6.580	−1.999	122
F_1	64.95	3.33	6.485	6.453	.033	39
F_2	65.19	3.12	9.538	6.430	3.108	154
B_1 to P_2	63.99	3.04	7.874	6.610	1.264	147
P_2	67.68	2.81	6.586	6.051	.535	40

TABLE 3

Condensed frequency distribution for the number of days from seeding to silking in percentages

Population	Classes in percentages					Number of individuals
	56–59	60–63	64–67	68–71	72–75	
P_1	2.50	17.50	55.00	22.50	2.50	40
B_1 to P_1	2.46	40.17	49.18	8.20	....	122
F_1	5.13	30.77	43.59	12.83	7.70	39
F_2	1.95	30.51	46.11	16.89	4.54	154
B_1 to P_2	5.44	38.78	45.58	9.52	.68	147
P_2	....	10.00	35.00	45.00	10.00	40

TABLE 4

Theoretical values for the number of days from seeding to silking based on hypothesis that indicated the number of gene pairs differentiating the two inbreds

Number of gene pairs	Mean for	
	F_2	B_1 to P_2
1	69.1	66.70
2	65.82	69.10
3	65.65	66.95
Actual	65.19 ± 3.12	63.99 ± 3.04

TABLE 5

Partitioning of B_1 to P_1 and B_1 to P_2 frequency distribution into their component genotypes for the number of days from seeding to silking

Population and genotype	Row no.	Classes in percentages					Theoretical percentage
		56–59	60–63	64–67	68–71	72–75	
B_1 to P_1	1	2.46	40.17	49.18	8.20	......	100.00
$F_1 + P_1$ (*AaBbCc* + *AABBCC*)	2	.95	6.03	12.32	1.28	4.42	25.00
Row 1 — row 2	3	1.51	34.14	36.86	6.92	—4.42	75.00
Row 3 on positive basis	4	1.51	34.14	36.86	2.50	......	75.00
Row 4 (100% basis)	5	2.01	45.52	49.15	3.33	......	100.00
F_1 (*AaBbCc*)	6	5.13	30.77	43.59	12.83	7.70	12.50
P_1 (*AABBCC*)	7	2.50	17.50	55.00	22.50	2.50	12.50
B_1 to P_2	8	5.44	38.78	45.58	9.52	.68	100.00
$F_1 + P_2$ (*AaBbCc* + *aabbcc*)	9	.64	5.10	9.82	7.23	2.21	25.00
Row 8 — row 9	10	4.80	33.68	35.76	2.29	—1.53	75.00
Row 10 on positive basis	11	4.80	33.68	35.76	.76	......	75.00
Row 11 (100% basis)	12	6.40	44.91	47.68	1.01	......	100.00
F_1 (*AaBbCc*)	13	5.13	30.77	43.59	12.83	7.70	12.50
P_2 (*aabbcc*)	14	......	10.00	35.00	45.00	10.00	12.50

bution for the different genotypes in the B_1 to P_1 and B_1 to P_2 populations. Following the partition, a theoretical frequency distribution for the F_2 genotypes could be calculated. Twenty-seven genotypes would be expected in the F_2 generation. However, the following genotypes of the F_2 do not occur in either of the two backcross populations.

Group I

AA	*BB*	*cc*		*Aa*	*BB*	*cc*
AA	*Bb*	*cc*		*Aa*	*bb*	*CC*
AA	*bb*	*CC*		*aa*	*BB*	*CC*
AA	*bb*	*Cc*		*aa*	*Bb*	*Cc*

Group II

$$AA \quad bb \quad cc \qquad\qquad AA \quad bb \quad cc$$
$$aa \quad BB \quad cc$$

It can be seen that group I had two nonallelic dominant genes, while group II had only one dominant gene. The frequency distribution of the group I genotypes could be calculated by taking 66.67 percent of the P_1 distribution and 33.33 percent of the P_2 distribution (SINGH 1949). The frequency distribution of group II could be calculated by adding both the distributions of group I and P_2, then dividing by two, since this group, i.e., group II, lies between both frequencies. This was based on the assumption that complete genic and phenotypic dominance exist. Table 6 gives the theoretical frequency distributions of the F_2 generation based on the above assumption.

TABLE 6

The F_2 generation frequency distribution partitioned into its component genotype on the basis of three-factor pairs for the number of days from seeding to silking

Population and genotype	Classes in percentages					Theoretical percentage
	56–59	60–63	64–67	68–71	72–75	
1. *AABBCC*	2.50	17.50	55.00	22.50	2.50	1.5625
2. *AABBCc*	2.01	45.52	49.15	3.33	......	28.1250
3. *AABbCC*						
4. *AABbCc*						
5. *AaBBCc*						
6. *AaBbCC*						
7. *AaBBCC*						
8. *AaBbCc*	5.13	30.77	43.59	12.83	7.70	12.5000
9. *Aabbcc*	6.40	44.91	47.68	1.01	......	28.1250
10. *AaBbcc*						
11. *Aabbcc*						
12. *aabbCc*						
13. *aaBbcc*						
14. *aaBbCc*						
15. *AaBBcc*	1.67	15.00	48.34	30.00	5.00	23.4375
16. *AAbbCC*						
17. *AAbbCc*						
18. *AABBcc*						
19. *AABbcc*						
20. *aaBBCC*						
21. *aaBBCc*						
22. *aaBbCC*						
23. *AabbCC*						
24. *aabbCC*	.84	12.50	41.67	37.50	7.50	4.6875
25. *aaBBcc*						
26. *AAbbcc*						
27. *aabbcc*	......	10.00	35.00	45.00	10.00	1.5625
F_2 population	3.48	33.82	47.38	12.67	2.68	

The χ^2 test for goodness of fit between the obtained and the theoretical F_2 frequency distributions gave a χ^2 value of 5.2938 with a P value lying between 0.20 and 0.10 (Table 7), indicating a good fit and supporting the hypothesis that the two parents were differentiated by three major gene pairs with respect to silking date.

2. Pollen shedding

The mean values for the number of days from seeding to pollen shedding showed that P_1 (E.G. 102) and P_2 (E.G. 205) had mean values of 62.68 and 66.57 days respectively (Table 8).

The F_1 cross between the two parents gave a mean value of 62.20 days, which was somewhat lower than that of P_1, but the difference was insignificant. This fact indicated a complete phenotypic dominance of fewer days over more days. If this were true, then the B_1 to P_1 mean should not differ significantly from the means of either P_1 or F_1. This was found to be true with respect to F_1 *vs.* B_1 to P_1, but not with P_1 *vs.* B_1 to P_1. However, since B_1 to P_1 gave a mean value less than B_1 to P_2, then the conclusion would be justified as to the presence of complete

TABLE 7

Chi-square for goodness of fit between the obtained and the theoretical frequency distributions of the F_2 population for the number of days from seeding to silking based on the assumption that the parents were differentiated by three gene pairs

Population	Classes					Number of individuals
	56–59	60–63	64–67	68–71	72–75	
	In percentages					
Obtained	1.95	30.51	46.11	16.89	4.54	154
Calculated	3.48	33.82	47.38	12.67	2.68	154
	In numbers					
Obtained	3	47	71	26	7	154
Calculated	5.36	52.08	72.97	19.51	4.13	154
$\chi^2 = 5.2938$	d.f. $= 3$ (the last two classes on the left					
P .20–.10	were grouped in one)					

TABLE 8

The means, standard deviations, variances and number of individuals in each population for the number of days from seeding to pollen shedding

Population	$\overline{X} \pm$ S.D.	Total variance	Environmental variance	Genetic variance	Number of individuals
P_1	62.68 ± 2.08	3.4067	3.1679	.2388	38
B_1 to P_1	61.61 ± 2.05	3.6264	2.7932	.8332	126
F_1	62.20 ± 1.80	3.1142	2.9998	.1144	35
F_2	62.88 ± 2.53	6.2577	3.2380	3.0197	139
B_1 to P_2	63.18 ± 2.60	6.3635	3.3430	3.0205	132
P_2	66.57 ± 2.43	4.1771	4.5302	—.3531	46

phenotypic dominance. The justification was arrived at by comparing the frequency distributions of the three populations, namely P_1, F_1, and B_1 to P_1. χ^2 test gave a value of 1.6177 with a P value of .50–.30 (d.f. 2).

By studying both the total variances and the genetic variances for P_1, F_1 and B_1 to P_1, it can be seen that the total variances did not differ significantly from each other and were less than those of F_2 and B_1 to P_2. This supported the assumption of the occurrence of phenotypic dominance. By studying the genetic variances for the six populations it can be seen that the genetic variances of both F_2 and B_1 to P_2 were much higher than B_1 to P_1, which indicated complete genic dominance.

Number of major gene pairs differentiating parents: On the basis of the segregating generations, Table 9, it was suggested that the parents were differentiated by two major gene pairs. This was arrived at from the fact that dividing 18.19 percent (class 66–74 of B_1 to P_2) by 77.14 percent (class 61–65 of F_1) gave a value of 23.58 percent, whereas on a two-factor basis a ratio of 25 percent would be expected. Also the indication was arrived at from the fact that only 10.88 percent of the individuals in the F_2 population fell in the class 66–74, whereas 6.25 percent would be expected on the basis of two factors. When the theoretical means of F_2 and B_1 to P_2 for one factor gene pair, two and three pairs were compared with the obtained means of these two populations (Table 10), it appeared that the calculation based on the hypothesis that the two inbreds were differentiated by two major gene pairs was the fit.

TABLE 9

Condensed frequency distribution for the number of days from seeding to pollen shedding in percentage

| Population | Classes in percentages | | | Number of individuals |
	56–60	61–65	66–74	
P_1	21.05	78.95	......	38
B_1 to P_1	30.16	69.84	......	126
F_1	22.86	77.14	......	35
F_2	20.83	68.28	10.88	139
B_1 to P_2	16.67	65.15	18.19	132
P_2	......	34.78	65.22	46

TABLE 10

Theoretical values for the number of days from seeding to pollen shedding based on hypothesis that indicated the number of gene pairs differentiating the two inbreds

| Number of gene pairs | Mean for | |
	F_2	B_1 to P_2
1	63.65	64.63
2	62.91	63.53
3	62.80	63.17
Actual	62.88 ± 2.53	63.18 ± 2.60

Following this, the backcrosses were partitioned into their component geno-types, Table 11.

Following this partition, a theoretical frequency distribution could be calculated for the F_2 population, Table 12. The χ^2 test for goodness of fit between the theoretical and the obtained F_2 frequency distributions gave a χ^2 value of .5469 with a P value of .80–.70 (d.f. 2) indicating a good fit and supporting the hypothesis that the two parents were differentiated by two major gene pairs, Table 13.

3. The difference in days between silking and pollen shedding

From the mean values given in Table 14, it can be seen that inbred E.G. 102 (P_1) started shedding pollen 2.48 days, on the average, before silking. Mean-

TABLE 11

Partitioning of B_1 to P_1 and B_1 to P_2 frequency distributions into their component genotypes for the number of days from seeding to pollen shedding

Population and genotype	Row	Classes in percentages				Theoretical percentage
		56–60	61–65	66–70	71–74	
B_1 to P_1	1	30.16	69.84	....	....	100.00
$F_1 + P_1$ ($AaBb + AABB$)	2	10.98	39.03	....	....	50.00
Row 1 — row 2	3	19.18	30.81	....	....	50.00
Row 3 (100% basis)	4	38.37	61.63	....	....	100.00
F_1 ($AaBb$)	5	22.86	77.14	....	....	25.00
P_1 ($AABB$)	6	21.05	78.95	....	....	25.00
B_1 to P_2	7	16.67	65.15	16.67	1.52	100.00
$F_1 + P_2$ ($AaBb + aabb$)	8	5.72	27.99	14.68	1.63	50.00
Row 7 — row 8	9	10.95	37.16	1.99	—.11	50.00
Row 9 on a positive basis	10	10.95	37.16	1.88	....	50.00
Row 10 (100% basis)	11	21.90	74.32	3.76	....	100.00
F_1 ($AaBb$)	12	22.86	77.14	....	....	25.00
P_2 ($aabb$)	13	....	34.78	58.70	6.52	25.00

TABLE 12

The F_2 frequency distribution partitioned into its component genotypes on the basis of two-factor pairs for the number of days from seeding to pollen shedding

Population and genotype	Classes in percentages				Theoretical percentage
	56–60	61–65	66–70	71–74	
$AABB$	21.05	78.95	....	....	6.25
$AaBB$	30.16	69.84	....	....	25.00
$AABb$					
$AaBb$	22.86	77.14	....	....	25.00
$AAbb$	16.67	65.15	16.67	1.52	12.50
$aaBB$					
$Aabb$	16.67	65.15	16.67	1.52	25.00
$aaBb$					
$aabb$	....	34.78	58.70	6.52	6.25
F_2	20.83	68.28	9.91	.97	

while, in the inbred E.G. 205 (P_2), the differences were 1.50 days. The magnitude of the difference between the two parents was .98 days. This difference was shown to be highly significant.

The means of P_1, F_1 and B_1 to P_1 were approximately the same. These means indicated complete phenotypic dominance of longer duration between silking and pollen shedding. The total variances of the three populations, P_1, F_1, and B_1 to P_1 were approximately the same, indicating complete genic dominance.

Number of gene pairs differentiating the two parents: The assumption was made that the two parents were differentiated by one major gene pair. This assumption was reached from the fact that only 28.29 percent of the individuals in the F_2 population fell in the class 0–1, whereas, on a one gene pair, 25 percent would be expected (Table 15). The assumption was also arrived at by dividing 48.97 percent (class 2 or more of B_1 to P_2) by 76.46 percent (the same class for F_1) which gave a value of 64.05 percent. On the basis of one pair of genes, a 50 percent value would be expected.

On the assumption that one gene pair was responsible for the difference between silking and pollen shedding in the two parents, where P_1 was the dominant one, it would be expected that the frequency distributions of the three

TABLE 13

Chi-square test for goodness of fit between the obtained and theoretical F_2 frequency distributions for the number of days from seeding to pollen shedding based on the assumption that the two inbreds are differentiated by two gene pairs

Population	Classes				Number of individuals
	56–60	61–65	66–70	71–74	
	In percentages				
Obtained	26	96	17	......	139
Calculated	20.83	68.28	19.91	.97	139
	In numbers				
Obtained	26	96	17	......	139
Calculated	28.95	94.91	13.77	1.35	139

$\chi^2 = .5469$ d.f. $= 2$ P $= .80-.70$ (last two classes on left were grouped in one)

TABLE 14

The means, standard deviations, the variances and the number of individuals in each population for the difference in days between silking and pollen shedding

Population	$\overline{X} \pm$ S.D.	Total variance	Environmental variance	Genetic variance	Number of individuals
P_1	2.48 ± 1.12	1.2707	1.1598	.1109	33
B_1 to P_1	2.46 ± 1.25	1.4349	1.1628	.2721	113
F_1	2.41 ± 1.13	1.3450	1.1704	.1746	34
F_2	2.55 ± 1.58	2.5258	1.1492	1.3766	152
B_1 to P_2	1.54 ± 1.25	1.4522	1.3020	.1502	145
P_2	1.50 ± 1.06	1.0226	1.3081	—.2855	36

TABLE 15

*Condensed frequency distribution, in percentage, for the differences in days
between silking and pollen shedding*

Population	Classes in percentages		Number of individuals
	0–1	2-more	
P_1	9.09	90.90	33
B_1 to P_1	21.24	78.75	113
F_1	23.52	76.46	34
F_2	28.29	71.71	152
B_1 to P_2	51.03	48.97	145
P_2	52.78	47.22	36

populations, P_1, F_1, and B_1 to P_1, would be the same or differ within the limits of random sampling. This was found to be the case, since χ^2 value was 2.8532 which gave a P value of .30–.20 (d.f. 2). χ^2 tests for goodness of fit for the ratio 3:1 in the F_2 population gave a P value of .50–.30. Also the χ^2 test for the ratio 1:1 in the B_1 to P_2 population gave a P value of .90–.80. All these supported the hypothesis that the difference between the two parents was governed by a major gene pair.

DISCUSSION AND CONCLUSION

The development of an organ or an organism involves an organized system of interrelated and interdependent physiological processes, the end result of which is the manifestation of the phenotypic character. In this system the effects of most genes are integral parts (WRIGHT 1934). In such studies it was necessary to recognize both phenotypic and genic dominance. Phenotypic dominance was determined by studying the means of the two parents and the mean of the F_1 generation. This relation could be checked by studying the mean of the backcross to the dominant parent. Genic dominance was determined from studying the means, variances and phenotypes of the different genotypes. However, it should be realized that dominance is a relative phenomenon and its manifestation differs according to the genic background of the different gene combinations (FISHER 1931; WRIGHT 1934; DOBZHANSKY and HOLZ 1943).

"Fewer" days from seeding to silking and to pollen shedding showed complete phenotypic dominance over "more" days. The genetic variance indicated also complete genic dominance. SINGH (1949) found complete phenotypic and genic dominance for fewer days in the squash from seeding to opening of the first male and the first female flower. The same thing was reported by POWERS (1941) in tomatoes. It was found from these studies that silking date was determined by at least three major gene pairs by which the two inbred lines were differentiated. The number of days from seeding to pollen shedding was found to be governed by at least two major gene pairs. The difference in days between pollen shedding and silking indicated complete phenotypic and genic dominance for longer duration with at least one major gene pair controlling the difference.

The author, in 1954, by using chromosomal interchanges in maize, reported at

least two gene pairs responsible for the number of days from seeding to silking and at least three gene pairs for the number of days from seeding to pollen shedding. He concluded that since his observations were made on the same plants, and since only two of the genes indicated by the associations in pollen shedding studies were in the same arm as those for silking date, it appeared that not all the genes controlling pollen shedding and silking dates were the same.

Later the author, in 1956, in his studies on the effect of environment on gene segregation, using the same material used in 1954, reported that at least two major gene pairs controlled silking date and that one major gene pair controlled pollen shedding date under Alexandria, Egypt, conditions. The author concluded that the gene controlling pollen shedding date could be the same as that controlling silking date but the other gene which was found to be present in silking date could act as a differential one.

In the present studies, it can be stated that in the early stages of development, two major gene pairs would be responsible for pollen shedding and silking dates. However, a third gene probably interacts with the other two genes on the female side, i.e., silking date, and causes the silk appearance to be delayed more than that of pollen shedding. This conclusion can support that reported earlier by the author, i.e., the two characters are not the same but some genes are common to both. This can by no means be considered conclusive until more linkage data are available.

This finding should be of considerable importance to maize breeders who are breeding for earliness. If we consider what the author reported in 1954 and 1956, we could assume that the three genes are independent. Therefore, the breeder can combine earliness in his varieties since it is somewhat simply inherited. This earliness is essential in the northern parts of Egypt where the corn borer is abundant in August. Thus, earlier varieties will have a better chance to escape the damage done by this pest.

SUMMARY

1. The maize inbred line (E.G. 102) was crossed to the inbred (E.G. 205) raised by the Ministry of Agriculture, Egypt, in its program for producing hybrid corn.

2. By using the partitioning method suggested by POWERS (1942) and POWERS et al. (1950) it was possible to estimate the number of gene pairs controlling the number of days from seeding to silking and pollen shedding.

3. The number of days from seeding to silking and the number of days from seeding to pollen shedding were differentiated by three and two major gene pairs, respectively.

4. The differences in days between silking and pollen shedding was found to be governed by one major gene pair.

5. There was complete phenotypic and genic dominance for fewer days from seeding to silking and from seeding to pollen shedding, as well as for the longer duration of the difference in days between silking and pollen shedding.

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