GENETIC CONTROL OF VARIETAL TRAITS IN WATERMELON
Citrullus vulgaris Schrad.

by

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A MASTER'S THESIS

submitted in partial fulfillment of the

requirements for the degree

MASTER OF SCIENCE

Department of Horticulture

KANSAS STATE UNIVERSITY
Manhattan, Kansas

1967

Approved by:

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INTRODUCTION

Although all watermelon varieties are generally considered to belong to Citrullus vulgaris Schrad., a great variation occurs within this species. The range includes small, bitter, edible and inedible fruits as well as large, sweet fruits which make watermelons one of the first ten commercial truck crops in this country.

With the increased emphasis on development of new varieties of watermelon, additional basic genetic information is needed for certain quantitative and qualitative characters. In spite of the long time and wide spread cultivation, the watermelon has not been thoroughly analyzed genetically. This is probably because of the relatively large land requirement to mature fruits in sufficient quantity to provide an adequate population for genetic analysis.

It is evident that most of the genetic research and breeding has been designed to determine the inheritance of fruit and seed characters, and to develop varieties resistant to fusarium wilt (Fusarium oxysporum f. niveum). The main characters by which melon fruits are distinguished are size, shape, rind color, rind toughness and thickness, flesh color, texture, sugar content, seed size, seed coat color, and the number of seeds.

In order to facilitate further breeding operations the mode of inheritance and the linkage relationships for a number of these characters were studied using the varieties, Crimson

Sweet and Sugar Baby.

REVIEW OF LITERATURE

Porter (10) found that a dark green rind background color was dominant over yellowish white but incompletely dominant over yellowish green. The F_2 data indicated a single-gene difference. Like Porter, Weetman (18) reported that dark green rind was dominant over light green by a single factor difference, although other genes appeared to determine minor variations in the light color.

Mohr (6) verified that the inheritance of rind background color in the bush type was identical to that of the vining varieties. When the yellow rind colored Bush Desert King was crossed with dark green Black Diamond the F_2 generation segregated 3 plants with green rinded fruits and 1 with yellow rind.

From crosses among several cultivars, Weetman (18) found that striping of a certain cultivar was dominant in crosses with one cultivar, but recessive in crosses with another cultivar. It was assumed that the genes for striping and rind color were either allelomorphic or very closely linked. These characters of different cultivars are inherited in a more complex manner, and no satisfactory interpretation was proposed. Shimotsuma (15) demonstrated that out of 73 fruits in the F_2 generation, 49 had striped exocarp and the remaining 24 were whole-colored (non-striped). Consequently, a single gene difference between striped and whole-colored indicates that

striped is simply dominant over whole-colored.

Porter (10) has shown that a tough rind is dominant over the tender rind by a single-factor difference since a 3:1 segregation ratio was observed in the F_2.

Sugar content in watermelon is very important. The higher quality melons will range between ten and twelve per cent total soluble solids (7). The trends for total soluble solids and total sugars are essentially alike, and approximately 85 per cent of the total soluble solids is sugar (11). Porter and others (12) assured that the total sugar content of watermelon varieties was governed entirely by hereditary factors. There is some evidence that the total sugar content of a variety differs under varying environmental conditions, but this effect is meager (11). There have been no published references of genetic analysis of sugar content in watermelon.

Sax (14) in a study with beans clearly demonstrated that differences in fruit size is dependent on genetic factors. Size differences have generally been attributed to multiple factors, but some investigators have questioned the Mendelian interpretation of size inheritance. Weetman (18) assumed that small size of mature watermelon fruit was dominant over large fruit with probably several genes involved, if data for fruit were plotted arithmetically, but if they were plotted logarithmetically the genes for size seemed to lack dominance and had proportional effects with cumulative factors. The number of genes segregating for weight inheritance in the cross between

Northern Sweet (3.2 kilos) and Dove (8.0 kilos) was estimated at 25 genes from the F_2 population and at 12 genes from the backcross to Northern Sweet by Poole and Grimball (9).

There is a wide range in the size of watermelon seed. Weetman (18) approximated seed-length factor studies in populations derived from a cross between races wherein weight samples of 25 seeds were light (1.22 g) and heavy (2.60 g). In the F_2 backcross generations to both parents the lighter weight parent approached monogeneic dominance over the heavier fruit, but chi-square analysis failed to establish and acceptable fit between his observed and calculated ratios. Poole and others (8) reported that watermelon seed length can range from 5.5 to 15.5 mm. Three seed-length phenotypes were studied, short (av. 6 mm), medium (av. 10 mm), and long (av. 13 mm). Segregation was similar to that a di-hybrid F_2 population of nine medium (LS), three long (lS), and four short (Ls and ls), demonstrating that medium length was dominant over both long and short. From the cross short X long, the F_2 populations segregated into the three classes. It was suggested that Weetman's light vs heavy seeds corresponded to their medium vs long seeds.

Konslar and Barham (4) reported that the medium seed size of a breeding line, N.C. 9-2, averaging 7.4 mm in length, was found to be simply dominant over the long seed of Charleston Gray, averaging 12.7 mm. The results obtained from the progeny of the cross between them corresponded to those of Poole's

medium and large seeded varieties. Shimotsuma (15) used two lines, large-seed V. No. 3 (12.9 mm) and medium-seed line, V. No. 1 (8.8 mm). All seed in the F_1 and backcross to V. No. 1 fall in the medium seed size group. The F_2 and backcross to V. No. 3 can be divided in medium and large size groups. Therefore it is indicated that there is completely dominant single gene difference between medium and large seeds.

Environmental influences are said to determine the number of seeds produced in watermelon, but experimental evidence is lacking (7). According to Marx (5), in an extensive study of a number of pea (Pisum) inbred lines, Teräsvouri observed that individual lines exhibited a characteristic number of ovules per fruit, that for a given plant there was little variation from fruit to fruit, and that ovule number was less subject to environmental variation than seed number.

In the study of ovule number (all visibly identifiable ovules present in a given fruit whether developed to maturity or not) Marx (5) found that there was monogenic segregation for the high ovule number, and that dominance for the low number was incomplete.

MATERIALS AND METHODS

The eight traits evaluated in this study were melon size, melon rind background color, fruit stripes, rind toughness, rind thickness, total soluble solid content, seed weight, and ovule number. The parent lines used were Crimson Sweet, Sugar

Baby, and a mutant male sterile line which originated from irradiated Sugar Baby seed (17).

Table 1. Description of traits of the parent lines.

Traits	Crimson Sweet (P_1)	Sugar Baby (P_2)	Mutant (P_3)
Rind background color	yellowish green	dark green	dark green
Stripe	striped	non-striped	non-striped
Rind toughness (lbs.)	23.25	21.82	21.86
Rind thickness (inches)	0.65	0.67	0.66
Total soluble solid content (%)	10.64	7.19	8.51
Fruit weight (lbs)	28.6	6.2	6.4
Seed weight (g/100 seeds)	4.16	7.44	6.37
Total ovule number	1081.45	626.29	466.07
Fertilized seed number	823.80	571.17	281.20

The morphological difference between the male-sterile mutant line and normal Sugar Baby was a completely glabrous condition of vine and no functional male flowers on the latter.

The genetic lines and crosses included were P_1, P_2, and P_3, the F_1 (P_3 X P_1), and the F_2.

Appropriate crosses for producing the desired combinations were made in greenhouse in the winter of 1965. They were seeded

in peat pots and transplanted to the field at the Ashland Horticultural Farm in 1966. Transplanting was made with a spacing of 5 feet within the row, 10 feet between the rows and 5 hills per row. The total numbers of individuals were as follow: 20 plants for each parent and F_1, 80 plants for F_2 line. Randomized block design with four replications was used. Fertilization, irrigation, and other cultural practices in the field were uniform except for the transplanting of the F_2 population which was delayed a week. Two or three melons were left on each plant. At maturity one fruit was picked from each plant, cut, and evaluated for the characters concerned.

The data obtained for individual melons were sorted into the following categories: weight of mature fruits, rind color and stripe, per cent total solids, the number of aborted and matured ovules were counted separately, one-hundred seed weight, rind thickness and toughness.

A hand refractometer was used to determine the total soluble solid content of juice taken from the heart of each fruit. Its scale is calibrated directly in the per cent soluble solids. According to results reported by Porter and others (12), two or three drops of juice taken from the center of one-half of a fully mature fruit gave approximately the same refractometric reading as a composite sample of edible tissue from the seed zone of the same half. A standard fruit pressure tester with a 3/16 inch plunger tip was used to measure rind toughness.

After three to four days fermentation, all ovules, mature

and immature, were separated carefully from the pulp. The white aborted ovules were counted then, but the matured dark seeds were counted after drying.

Since there could be difference in the coefficient of correlation between seed length and width in the F_2 population, 100 seeds were weighed as a criterion for seed size. The seed samples were placed in packets and left until they had equalized in moisture content.

The per cent total soluble solids of each fruit was transformed to arcsin. Analyses of variance were made for all different traits. A contingency chi-square test was used to detect independence between two monogenic characters. Difference between mean values of the P_2 and P_3 were measured by the t-test for these characters. Fertility levels of the three parent lines (P_1, P_2, and P_3) were compared by an L.S.D. value.

The minimum number of gene pairs involved in each character was estimated with the assumption that all such genes had equal effect and that there was no dominance or epistasis. The following formula suggested by Wright (19) was used:

$$n = \frac{D^2}{8(\sigma^2_{F_2} - \sigma^2_{F_1})}$$

where n denotes the number of gene pairs involved and D is the mean difference between the two parental lines.

For some other characters which were assumed to be controlled by completely dominant genes, the following formula (13) was used:

$$n = \frac{D^2}{4(\sigma^2_{F_2} - \sigma^2_{F_1})}$$

In this case the genetic range should be:

$$D = 2(\bar{F}_1 - \frac{\bar{P}_1 + \bar{P}_2}{2}) .$$

EXPERIMENTAL RESULTS

Inheritance of Rind Background Color and Stripe Pattern

Watermelon rind color consisted of a general background color often broken by various types of striping. The F_2 progeny of $P_3 \times P_1$ segregated into 42 dark green, 23 yellowish green, and 15 medium green fruits in background color. When the dark green and medium green fruits were grouped the frequencies would be dark and medium green 57, and yellowish green 23. This approaches a 3:1 ratio closely enough to give a probability of 0.50. These results indicate that one dominant gene is responsible for the difference between dark and yellowish green background color. The variations in shade from yellowish to dark green are apparently brought about by other undetermined modifier genes.

In contrast to Sugar Baby, which has no stripe, fruits of Crimson Sweet have a peculiar type of broad dark green stripe. Fruits from the F_1 of these two varieties were all striped. In the F_2 there were 61 striped and 19 non-striped. This is almost a perfect 3:1 ratio. According to the chi-square test this frequency approaches 3:1 ratio with a probability of 0.75.

This indicates that striping is controlled by a single dominant gene.

Inheritance of Rind Thickness and Rind Toughness

An attempt was made to estimate the inheritance of rind thickness and toughness. But as revealed by the analysis of variance (Tables 2 and 3) there is no significant difference among the lines in either of these characters. The mean rind thickness of Crimson Sweet and Sugar Baby was 0.65 and 0.66 inch respectively. The mean rind toughness was 23.25 and 21.86 pounds for fruits of the two parents.

Table 2. Analysis of variance of rind thickness.

Source	DF	SS	MS	F
Blocks	3	0.01	0.003	1.00
Lines	3	0.00	0.000	0.00
Error	9	0.03	0.003	
Total	15	0.04		

F .05 = 3.86

Table 3. Analysis of variance of rind toughness.

Source	DF	SS	MS	F
Blocks	3	7.17	2.39	0.33
Lines	3	6.42	2.14	0.29
Error	9	6.58	7.31	
Total	15	20.17		

F .05 = 3.86

Inheritance of Total Soluble Solid Content

Analysis of variance of the data (Table 4) shows significant differences in varieties at the 1 per cent level. In Crimson Sweet the mean of solid content was 10.64 per cent, whereas that of Sugar Baby was 8.51. Frequency distribution for total solid content of parents, F_1 and the F_2 are shown in Fig. 1. The mean of the F_1 is 10.75 per cent and the F_2 distribution is skewed in the direction of high total solid content. From these data it is evident that the high total solid content is governed by completely dominant genes. The F_1 variance is smaller than for the parents. The F_2 variance is high and individuals in the population cover the entire range of the parents which indicates a segregation of genes governing total soluble solid content.

Table 4. Analysis of variance of total soluble solid content.

Source	DF	SS	MS	F
Blocks	3	1.13	0.38	0.27
Lines	3	12.83	4.28	30.57**
Error	9	1.22	0.14	
Total	15	15.18		

**Indicates significance at 1 per cent level. F .01 = 6.99

The estimated number of gene pairs is 1.38 or one pair of genes. Since the data show monogenic inheritance, an attempt was made to verify the segregating 3:1 ratio by chi-square test.

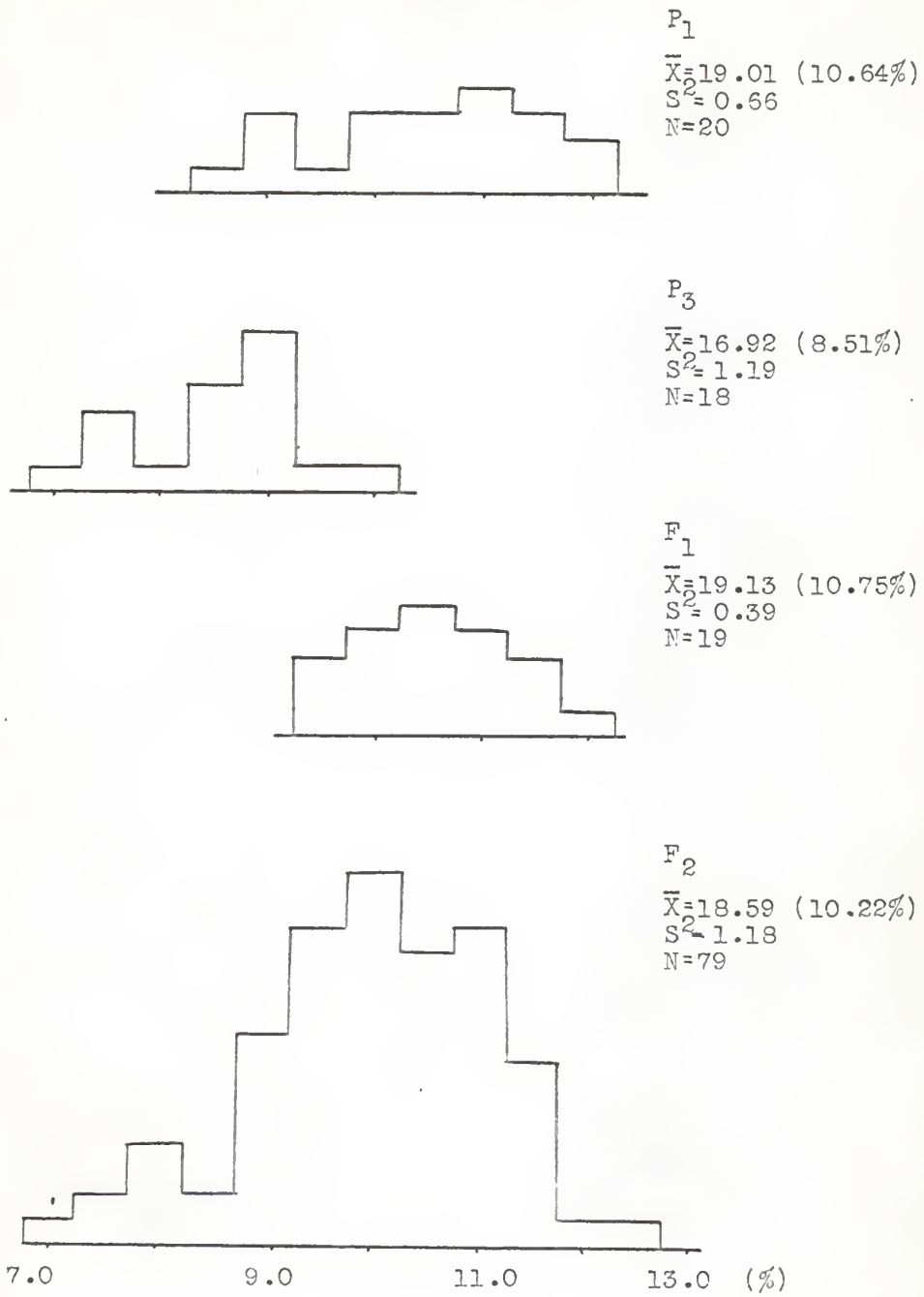

Fig. 1. Frequency distribution of total soluble solid content in Parents, F_1, and F_2.

Following Parris (7), total solid content from 6.5 per cent to 9.5 was considered as low, from 9.6 to 12.5 per cent as high. The frequencies were high 54 and low 22 with results approached a 3:1 ratio sufficiently close to give a probability of 0.50.

Inheritance of Fruit Weight

Analysis of variance of the data in Table 5 reveals that differences due to lines are significant at the 1 per cent level and that those among blocks are not significant. Frequency distribution of fruit weight data is shown in Fig. 2. The mean weight of Crimson Sweet fruits is 28.61 pounds, while that of Sugar Baby is only 6.37 pounds. The F_1 mean is 16.16 which is about intermediate between the parents. The F_2 mean is also contiguous to the expected mean. The P_1 variance is much higher than for any of the other lines, presumably because of the larger fruit weights.

The estimated number of the incompletely dominant gene pairs for fruit weight is 4.45 or for all practical purposes 4.

Table 5. Analysis of variance of fruit weight.

Source	DF	SS	MS	F
Blocks	3	1.44	0.48	0.17
Lines	3	1002.44	333.15	116.84**
Error	9	25.76	2.86	
Total	15	1029.64		

**Indicates significance at 1 per cent level. F .01 = 6.99

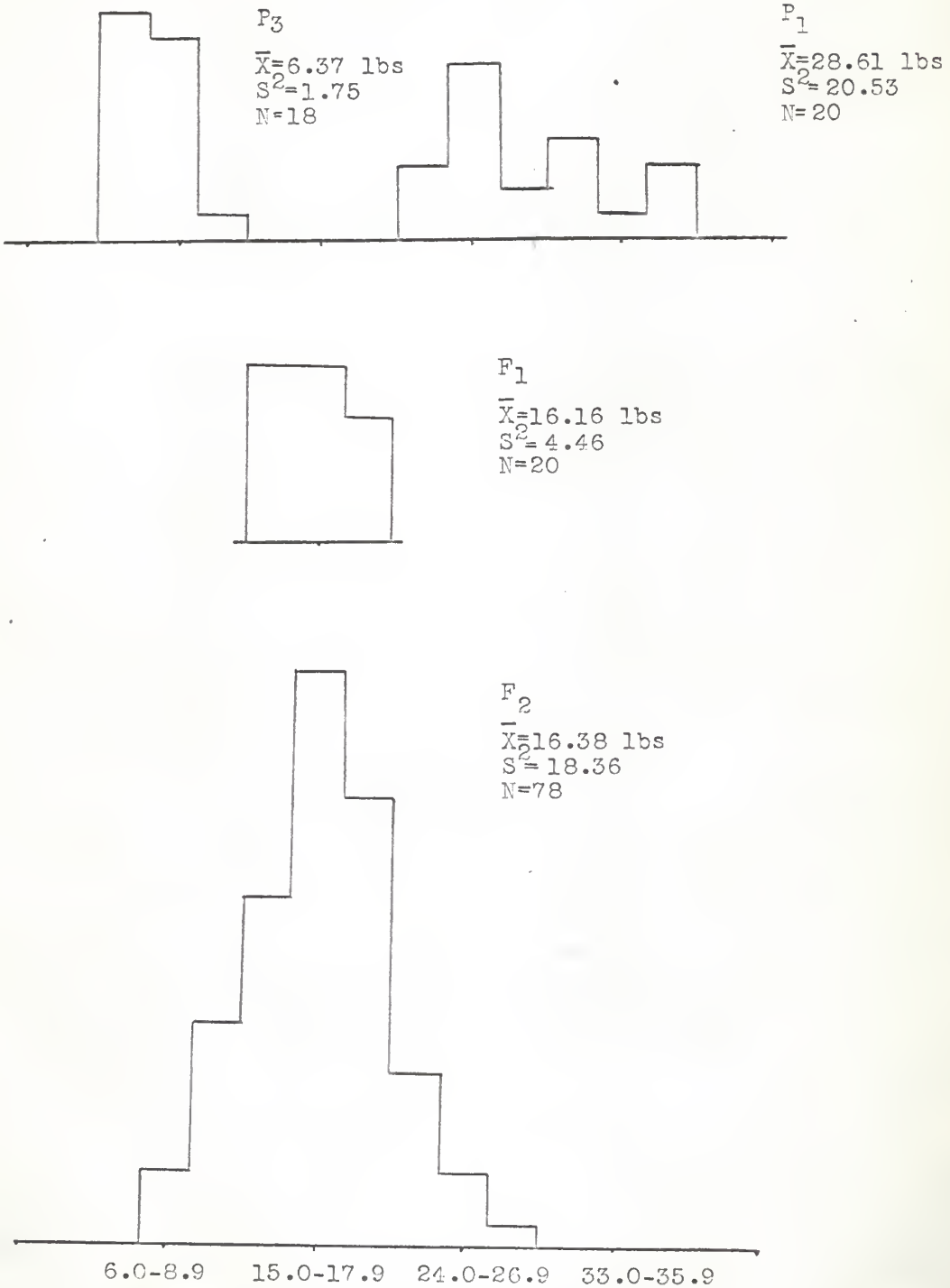

Fig. 2. Frequency distribution of fruit weight in Parents, F_1, and F_2.

Inheritance of Seed Weight

The analysis of variance of seed weight data is presented in Table 6. Differences among lines are highly significant. In the Crimson Sweet parent the mean seed weight from twenty melons is 4.15 g per 100 seed, whereas the mean seed weight from fourteen samples of Sugar Baby seed is 6.37 g per 100 seed. Histograms showing the distribution of seed weights from parents F_1 and F_2 progenies are shown in Fig. 3. Seed from the F_1 fruits were light (mean 4.38 g) and fall in light seeded parent group. This fact indicates complete dominance for light weight seeds. The F_2 distribution is bimodal, with segregation into a large class of small seeds and much smaller class of large seeds. This distribution suggests a 3:1 ratio, or that one major gene could be responsible for small vs large seed size. The estimated number of gene pairs is one which conforms to the above population segregation. Nevertheless, the classes into which the F_2 population is divided into a 3:1 ratio do not correspond to those of the two parents (Fig. 3). Moreover, the variation mode of the F_2 extends beyond that of the heavier seed parent (Sugar Baby), suggesting more than one gene pair must be involved. According to the seed weight mean, the F_2 population can be divided into three seed weight groups. The three seed weight phenotypes resemble a di-hybrid F_2 segregating population of light (av. 4.15 g), medium (av. 6.37 g), and heavy (av. 9.08 g). By this classification, the two parent varieties, P_1 and P_3 would be considered as small and medium seeded.

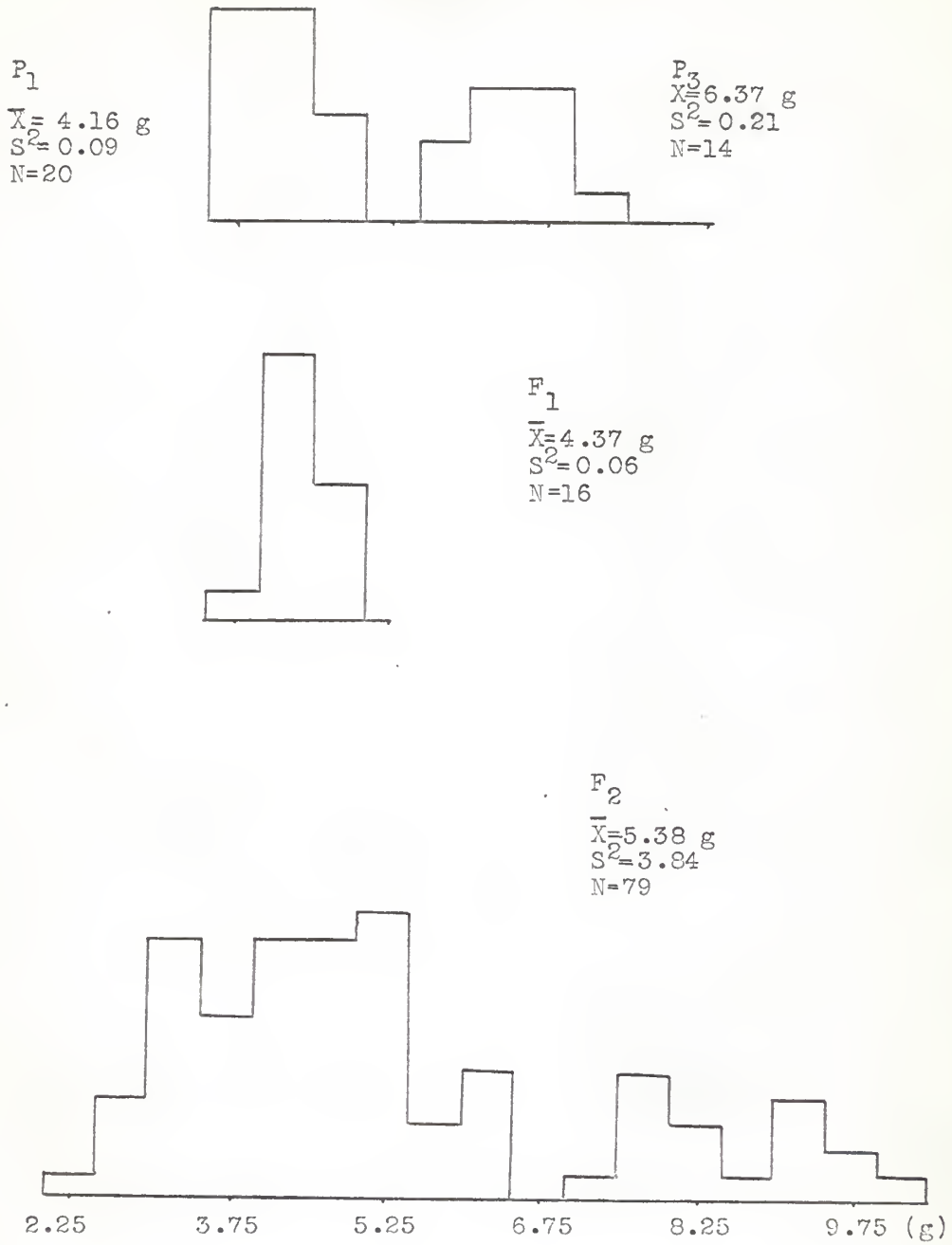

Fig. 3. Frequency distribution of seed weight in Parents, F_1, and F_2 (per 100 seeds).

Table 6. Analysis of variance of seed weight.

Source	DF	SS	MS	F
Blocks	3	0.61	0.20	3.33
Lines	3	13.07	4.36	72.66**
Error	9	0.52	0.06	
Total	15			

**Indicates significance at 1 per cent level. F .01 = 6.99

The presence of the 2 pairs of genes is confirmed by the satisfactory fit to a ratio 9 light to 4 medium to 3 heavy in the F_2 population (Table 7).

Table 7. Chi-square analysis of three classes os seed weight.

Phenotypes	Observed segregation	Expected segregation	X^2
Light	42	43.8	2.45
Medium	25	19.6	
Heavy	11	14.6	

X^2 .05 = 5.99

Inheritance of Ovule Number

Total ovule number. The term "total ovule" is used to designate all the visibly identifiable primordia and matured dark seeds in a given fruit. In Table 8, analysis of variance of the data shows significant differences in total ovule numbers among the genetic lines. Frequency distributions for total ovule number per fruit for the lines are shown in Fig. 4.

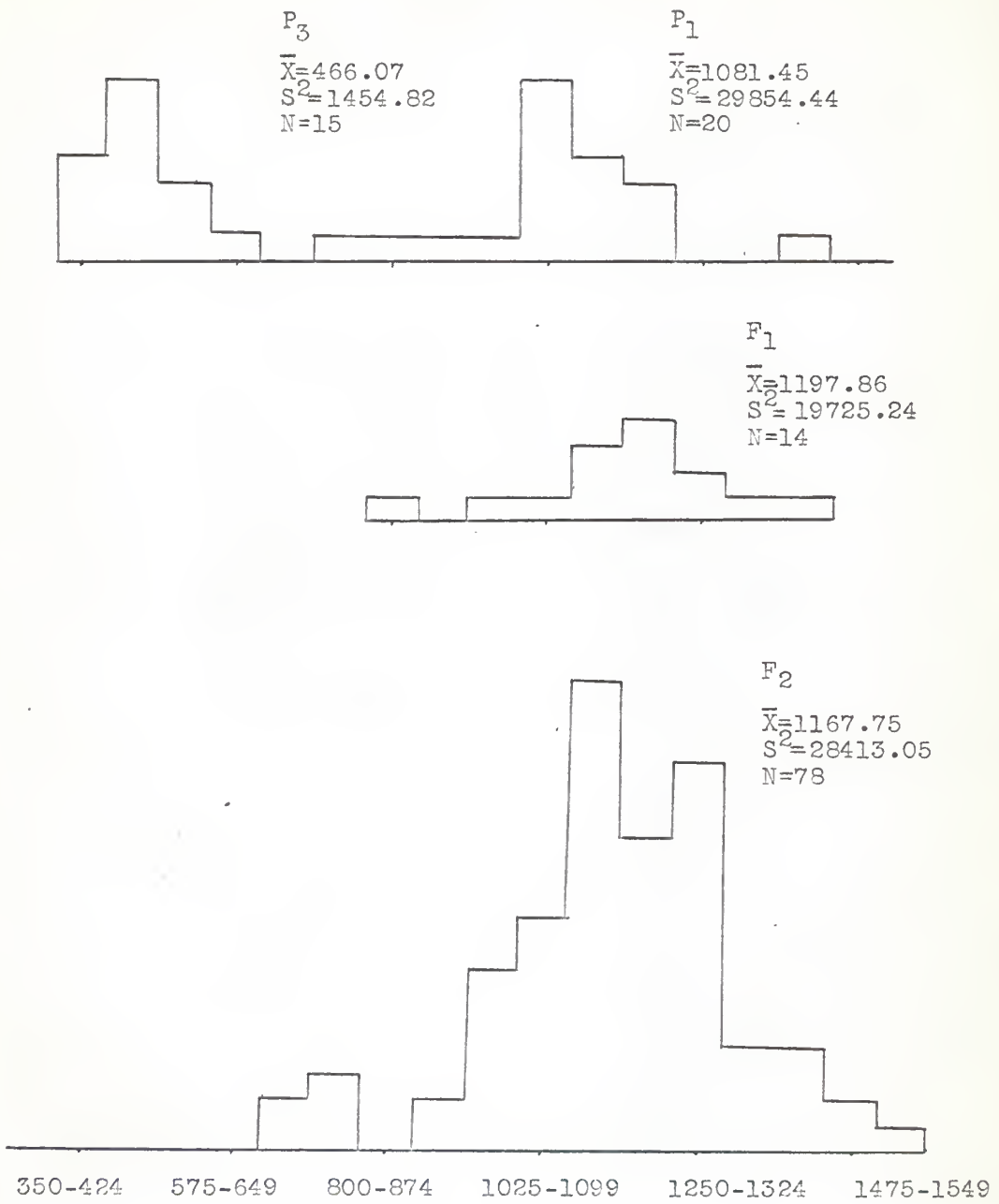

Fig. 4. Frequency distribution of total ovule number in Parents, F_1, and F_2.

Table 8. Analysis of variance of total ovule number.

Source	DF	SS	MS	F
Blocks	3	13417.53	4472.51	0.78
Lines	3	1394290.42	464763.47	80.64**
Error	9	51867.88	5763.09	
Total	15	1458575.83		

**Indicates significance at 1 per cent level. F .01 = 6.99

The mean number of total ovules per fruit of Crimson Sweet is 1081, whereas that of the Sugar Baby mutant line is only 466. The F_1 mean 1197 shows overdominance toward the larger number of total ovules. The F_2 population shows a slightly lower mean number of total ovules per fruit (1167) than in F_1 population, but it is still larger than Crimson Sweet. The F_2 variance did not fully overlap the whole range for the parents. It is rather skewed also toward the parent which had the larger mean number of total ovules.

The estimated number of gene pairs for total ovules is 10.89 or 11.

Fertilized seed number. The fertilized mature seed number has more importance than the aborted white seed number in watermelon. Analysis of variance of data shows significant differences among lines (Table 9). The mean Crimson Sweet seed number is 823, and that of Sugar Baby mutant is only 281. As in case of the total ovule number, F_1 exceeds both parents and the larger number shows dominance over the lower number.

It is not logical to separate the fertilized black seeds from the total ovule number and estimate the mode of inheritance of each separately, however some information about gene control of fertilization is useful.

The estimated number of gene pairs is 6.

Table 9. Analysis of variance of fertilized seed number.

Source	DF	SS	MS	F
Blocks	3	6746.64	2248.88	0.55
Lines	3	1426869.34	475623.11	115.64**
Error	9	37017.64	4113.07	
Total	15	1470633.62		

**Indicates significance at 1 per cent level. F .01 = 6.99

Tests of Independence

Striping and fruit rind background color. Since striping and rind background color are due to single factor differences when considered separately, if they are inherited independently the F_2 population should show an agreement between expectation number and observation number in these two characters (Table 10).

It is found that the observed chi-square gives a value of P between .30 and .50. These data indicate, therefore, that there was no association between striping and fruit rind background color in this segregating population.

Table 10. Test for independence of striping and fruit rind background color.

Total plants	Striping	Fruit rind	Background color	X^2	P-value
80		Dark green	Yellowish green	.757	.30-.50
	Striped	42(43.5)	19(17.5)		
	Non-striped	15(13.5)	4(5.5)		

Theoretical numbers appear in ( ).

Striping and total soluble solid content. Data in Table 11 show that the observed F_2 segregation approximated the expected value. The chi-square value is not significant. This makes it probable that linkage of the factors controlling striping and total soluble solid content do not exist.

Table 11. Test for independence of striping and total soluble solid content.

Total plants	Striping	Total soluble solid content		X^2	P-value
74		High	Low		
	Striped	44(42.4)	13(14.6)	1.02	.30-.50
	Non-striped	11(12.6)	6(4.4)		

Theoretical numbers appear in ( ).

Rind background color and total soluble solid content. According to data in Table 12, segregation among the four classes is very close to the theoretical frequencies. The chi-square value failed to show a significant difference among the classes, indicating that the factors that govern rind background

color and total soluble solid content are not linked but are independently inherited.

Table 12. Test for independence of rind background color and total soluble solid content.

Total plants	Rind color	Total soluble solid content		X^2	P-value
		High	Low		
74	Dark green	36(36.1)	15(14.9)	.00	.95-1.00
	Yellowish green	15(14.9)	6(6.1)		

Theoretical numbers appear in ( ).

Fertility Differences among the Three Parent Lines

For comparison of the fertility among the three parental lines, arcsin transformation was used for the ratio data;

$$\frac{\text{number of fertilized seeds}}{\text{number of total ovules}} \times 100.$$

Analysis of variance shows a significant difference among the three lines (Table 13).

Table 13. Analysis of variance of fertility in P_1, P_2, and P_3.

Source	DF	SS	MS	F
Blocks	3	6931.76	2310.59	2.90
Lines	2	38203.77	19101.89	23.99**
Error	6	4776.36	796.06	
Total	11	49911.89		

**Indicates significance at 1 per cent level. F .05 = 4.76
F .01 = 10.92

There is no difference in fertility between Crimson Sweet and normal Sugar Baby but a highly significant difference is present for the Sugar Baby mutant line (Table 14). In other words the male-sterile mutant line of Sugar Baby has a lower fertility than normal line and Crimson Sweet.

Table 14. Comparison of the fertility mean values of the parent lines.

Lines	Means	Differences
P_1	307.13	$P_2 - P_1 = 9.60$
P_2	316.73	$P_1 - P_3 = 114.61^{**}$
P_3	192.52	$P_2 - P_3 = 124.21^{**}$

**Indicates significance at 1 per cent level.
L.S.D. (.05) = 48.88
L.S.D. (.01) = 74.01

Differences in the Genetic Traits of Normal and Mutant Lines of Sugar Baby

Rind background color and striping. None of the fruits of these two lines showed striping and all had the identical dark green rind background color.

Fruit weight.

	Mean	t		
P_2	6.23 lbs.	0.37	2.02	(.05)
P_3	6.37			

Fruit weights of the two lines are the same.

Total soluble solid content.

	Mean	t		
P_2	7.19%	4.89**	2.70	(.01)
P_3	8.51			

The mutant line has a higher total soluble solid content than the normal line.

Seed weight.

	Mean	t		
P_2	7.44 g	7.13**	2.75	(.01)
P_3	6.37			

Seeds of mutant line are lighter than for the normal line.

Seed number.

1. Total ovule number

	Mean	t		
P_2	626.29	42.37**	2.75	(.01)
P_3	466.07			

2. Fertilized seed number

	Mean	t		
P_2	571.17	8.33**	2.75	(.01)
P_3	281.20			

**Indicates the significance at 1 per cent level.

The mutant line has a lower number of total ovules and mature

seeds than those of the normal line.

DISCUSSION

In general, quantitatively inherited characters are not assumed to be controlled by one pair of factors. Data for rind background color present evidence which suggests that it might be polygenically controlled. While a single gene pair has major control of dark green and yellowish green color, there are apparently some modifying genes to the major gene pair which produce intermediate color between dark green and yellowish green. This agrees with the report of Weetman (18). However, since Porter (10) reported that dark green was incompletely dominant over yellowish green, the modifier gene is assumed to act differently on different varieties. Weetman (18) assumed that the genes for striping and background color were either allelomorphic or very closely linked, but it is clear that these two characters are controlled by completely independent genes and segregate independently.

The frequency distribution chart for melon fruit weight (Fig. 2) shows the typical mode of inheritance of quantitative characters. The estimated number of gene pairs for fruit weight was only 4, whereas Poole and Grimball (9) estimated 25 pairs from the F_2 generation and 12 from backcross generation. As a result, it was admitted that one parent was undoubtedly heterozygous for weight genes. Moreover they estimated the gene number by an extension of the binomial formula.

The estimated gene pairs by Wright's formula was verified as the same as from Burton's formula (1), that is:

$$n = \frac{0.25(0.75 - h + h^2)\, D^2}{\sigma^2_{F_2} - \sigma^2_{F_1}}$$

$$\text{where } h = \frac{\bar{F}_1 - \bar{P}_1}{\bar{P}_2 - \bar{P}_1}, \quad D = \bar{P}_2 - \bar{P}_1.$$

Since the two parent lines did not show differences in rind thickness and rind toughness, the mode of inheritance could not be determined in this experiment.

Evidence has been presented to show that a single pair of genes control total solid content. This agrees with the general classification suggested by Parris for total solid content (7). Parent 1 had mean of 10.64 per cent and P_3 was as low as 8.51. The simplicity of the manner of inheritance in the F_2 population is verified by the chi-square test.

Seed weight is estimated to be controlled by one gene pair. Considering the fact that the F_2 population variation extends widely beyond that of the heavier seed parent and that the two seed weight classes of the F_2 do not correspond with the classes of the both parents (Fig. 3), it is hard to accept simply as a monogenic trait without admitting probable environmental effects on the variation. It might be possibly assumed that more than two gene pairs are involved along with transgressive variation, or it might be caused by di-hybrid segregation. Under this assumption, it was confirmed that the

inheritance of seed weight is similar to a typical di-hybrid F_2 segregation of a 9 light to 4 medium to 3 heavy. In the study of Weetman (18), 25 seeds from each watermelon fruit were sampled and weighed for a seed size sample. It was reported that in the F_2 the lighter weight parent approached monogenic dominance over the heavier, but the chi-square test failed to confirm the 3:1 ratio. Weetman's light (1.22 g per 25 seed) and heavy (2.60 g) classes correspond to those of the present study. If Weetman had grouped them into three weight classes, the result would have agreed with the ratio 9:4:3 of this study.

Environmental variation, doubtless, exerts an influence on the ovule number and fertilization. But a genetic potential for seed number in effect extends the limit on which the environment can exert its influence. In other words the genetically higher number should persist under diverse conditions. Therefore it is sound to estimate the mode of inheritance on ovule number. Although seed number is more subject to environmental variation than is ovule number (5), estimation of the inheritance of the fertilized seed number shows some information on gene behavior. In both cases, for the total ovule and seed number, the F_1's exceed their parents. This indicates either over dominance or linkage of all the genes.

In comparison between normal and mutant line of Sugar Baby, it was found that there was no difference in rind background color, striping and fruit weight, but differences were

significant for total solids, seed weight, total ovule number and fertilized seed numbers. It is obscure whether the difference in total soluble solid contents, seed weight, total ovule number and fertilized seed numbers were from linkage of these genes with the mutant glabrous vine and male-sterility genes or from physiological effects of less and light seeds on higher total soluble solid contents.

SUMMARY

The mode of inheritance of following watermelon traits were studied by comparing Crimson Sweet and Sugar Baby with the F_2 progeny: rind background color, striping, rind thickness, rind toughness, fruit weight, total solid content, seed weight, and ovule number.

The study was conducted at the Ashland Horticultural Farm at Kansas State University in 1966.

This study showed that one dominant gene was mainly responsible for the dominance of dark green rind background color over yellowish green with an unknown modifier gene for the intermediate color. Striping was controlled by single dominant gene over the non-stripe. The total soluble solid content also showed a monogenic inheritance with the higher content dominant over low. Quantitative inheritance was observed for fruit weight. The estimated number of incompletely dominant gene pairs were 4. The three seed weight phenotypes in the F_2 population - light, medium and heavy - showed a

di-hybrid segregation of 9 light, 4 medium and 3 heavy. Total ovule number (aborted and fertilized) also showed quantitative inheritance. The estimated number of gene pairs was 11 with over dominance toward the larger total ovule number. Gene behavior for fertilized seed was the same as for total ovule number, but the estimated gene number was 6.

There was no evidence of linkage between rind background color, striping, and total soluble solid content.

ACKNOWLEDGMENTS

The author wishes to acknowledge gratitude to Dr. Charles V. Hall, his major professor, for the kind guidance and encouragement throughout this investigation.

Sincere appreciations are due to my colleague Mr. Y. Suzuki for his valuable suggestions and assistance during the period of this research. Thanks are conveyed to Dr. George H. L. Liang, Assistant Professor of Agronomy, for his valuable suggestions in statistical analysis.

To others who have aided in this study, but are not mentioned, the author also wishes to express his thanks.

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GENETIC CONTROL OF VARIETAL TRAITS IN WATERMELON
Citrullus vulgaris Schrad.

by

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B. S., Seoul National University, Seoul, Korea, 1959

AN ABSTRACT OF A MASTER'S THESIS

submitted in partial fulfillment of the

requirements for the degree

MASTER OF SCIENCE

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KANSAS STATE UNIVERSITY
Manhattan, Kansas

1967

With the increased emphasis on development of new varieties of watermelon, Citrullus vulgaris, Schrad., additional basic genetic information is needed concerning certain quantitative and qualitative traits. The watermelon has not been thoroughly analyzed genetically, although a number of varieties have been developed.

In 1966 the mode of inheritance of the following traits were studied in the cross of Crimson Sweet and Sugar Baby with the F_1 and F_2 generations: rind background color, striping, rind thickness, rind toughness, fruit weight, total soluble solid content, seed weight, and ovule number.

Information obtained showed that one dominant gene was mainly responsible for the dominance of dark green rind background color over yellowish green with an unknown modifier gene for the intermediate color. Striping was controlled by a single dominant gene over the non-striped. The total soluble solid content also showed a monogenic inheritance with the higher content dominant over low. Quantitative inheritance was observed for fruit weight. The estimated number of incompletely dominant gene pairs was 4. Three seed weight phenotypes in the F_2 population - light, medium, and heavy - were assumed to be from a di-hybrid segregation of 9 light, 4 medium and 3 heavy. Total ovule number (aborted and fertilized) also showed quantitative inheritance. The estimated number of gene pairs was 11 with over-dominance toward the larger total ovule number. Gene behavior for fertilized seed was the same

as for total ovule number, but the estimated gene number was 6.

An attempt was made to detect a linkage relationship between the simply inherited traits. There was no evidence of linkage between rind background color, striping, and total soluble solid content. Further study is needed to clarify the inheritance of rind background color and seed weight.