STUDIES ON THE QUANTITATIVE INHERITANCE
OF *ORYZA SATIVA*, L.

II. A Diallel Analysis for Panicle Number, Tiller Number, Panicle Length, Spikelet Number and the Number of Primary Branch in F₁ Progeny[1]

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(Received May 25, 1968)

Interoduction

This is a continuation of my previous work in which the method of diallel analysis was employed to study the basic nature of some quantitative characters of rice. In this paper five characters, panicle number per plant, tiller number, panicle length, spikelet number per panicle and number of primary branch per panicle are investigated, and some basic genetic parameters such as additive, dominance effect, reciprocal difference, degree and size of dominance, allele frequency, number of gene groups, heterosis and heritability of the above five characters are derived. It is hoped that, in combination with my previous work, the information obtained in these papers might be utilized as references for future plant breeding purposes of rice.

Materials and Methods

The experimental materials consist of five parental varieties, Yen-no, Wu-no-tao, Mang-hua-chu, Chih-chueh-chu and Warisanmochi 2, which differ significantly from one another in one or more of the following characters, plant height, heading date, panicle number per plant, tiller number, panicle length, spikelet number per panicle and the number of primary branch per panicle. In 1965, crosses were made between these five varieties in accordance with a diallel scheme, including reciprocals and selfings. The five parental varieties and 20 groups of F₁ hybrids were then grown in a completely

randomized design, during the first cropping season of 1966 at Nankang, Taipei.

All plants were recorded on an individual plant basis, and the scaling procedure for evaluating the quantitative character were as follows:

Panicle number per plant—counted as the number of panicle-bearing tillers at the time before harvested.

Tiller number—culm or tiller includes both panicle-bearing and non-bearing tillers. The observed single value was transformed to the common logarithm.

Panicle length—measured to the centimeter from the panicle base to the tip at the time after harvested.

Spikelet number per panicle—counted as the number of spikelets of a panicle at the time after harvested.

Number of primary branch per panicle—counted as the number of primary branch of the panicle at the time after harvested.

For each of these characters the following genetic parameters were estimated by adopting the conventional method of diallel crosses as given in Hayman (1954):

1. An overall measure of the degree of dominance.

2. The mean value of the product of gene frequencies of dominance and recessive alleles.

3. The ratio of the total numbers of dominance to recessive genes in all parents.

4. An estimate of the number of gene groups which control the character and exhibit dominance to some degree.

5. The order of dominance of the parents.

6. The heterosis of F_1 hybrids.

7. The heritability of five metrical characters.

For the basic notations of this paper, I shall follow my first report (Wu, 1968).

Results and Discussion

1. *Additive, dominance and maternal effects of parents on F_1 hybrids*

The mean values of parents and their F_1 hybrids together with the analysis of variance of the diallel table are given respectively in tables 1 and 2, it is revealed that there are highly significant differences among parents with respect to each of the five meterial characters. One may infer further from table 2 that there are significant genetical variation amongst the parental varieties in all five characters; and also, all the characters seemed to show some degree of dominance at some of the loci and further that the dominance

Table 1. *Mean values of parents (underlined) and F_1 hybrids in a 5×5 diallel cross*

Character	Female array	Male array				
		Yen-no	Wu-no-tao	Mang-hua-chu	Chih-chueh-chu	Warisan-mochi 2
Panicle number per plant	Yen-no	11.4	18.6	15.2	14.6	9.4
	Wu-no-tao	17.8	15.8	19.4	19.8	16.2
	Mang-hua-chu	13.0	18.8	14.4	17.2	12.6
	Chih-chueh-chu	14.8	15.4	18.6	10.8	12.0
	Warisanmochi 2	4.8	10.2	10.2	11.8	6.0
Tiller number	Yen-no	11.8	19.0	16.0	15.6	9.4
	Wu-no-tao	18.2	17.4	20.2	21.4	16.2
	Mang-hua-chu	13.4	20.0	15.2	17.8	13.0
	Chih-chueh-chu	15.6	16.4	19.2	11.8	12.6
	Warisanmochi 2	6.0	11.0	14.4	14.4	6.0
Panicle length	Yen-no	18.3	19.8	21.1	20.1	23.5
	Wu-no-tao	20.0	15.2	18.6	16.8	23.1
	Mang-hua-chu	21.0	17.4	17.7	18.1	23.3
	Chih-chueh-chu	19.5	17.0	18.3	15.7	21.9
	Warisanmochi 2	24.7	22.0	22.7	21.6	26.2
Spikelet number per panicle	Yen-no	83.2	78.8	97.3	86.6	115.6
	Wu-no-tao	76.1	47.4	82.8	67.7	104.1
	Mang-hua-chu	80.8	65.1	58.7	69.1	81.6
	Chih-chueh-chu	67.5	60.5	67.3	51.3	83.1
	Warisanmochi 2	122.3	85.1	86.0	83.5	83.7
Number of Primary branch per panicle	Yen-no	8.8	7.4	7.9	7.5	10.2
	Wu-no-tao	7.6	6.1	7.9	7.1	8.9
	Mang-hua-chu	7.8	7.4	7.2	7.9	8.3
	Chih-chueh-chu	7.1	6.5	7.9	6.2	8.0
	Warisanmochi 2	11.1	9.4	8.2	8.0	8.7

might be largely unidirected. Moreover, the results of item (b_2) in table 2 suggested asymmetry of the gene distribution in the characters of panicle length and number of primary branch per panicle, and those of items (c) and (d) in table 2 tended to imply that some maternal effect might exist in the characters of panicle number per plant and spikelet number per panicle.

2. *Genetic components of variation in F_1 plants*

The values of the various statistics estimated by the mean values of parental varieties and their progenies are shown in 3. (The values of V_r and W_r of each parental variety were omitted.)

Table 2. *Analysis of variance* (*M. S. values*)

Source of variation	df	Panicle number per plant	Tiller number	Panicle length	Spikelet num. per panicle	Number of primary branch per panicle
Treatment	24	81.8547**	0.1147**	41.3081**	1,592.2448**	6.5167**
(a)	4	342.6760**	0.4754**	218.9521**	5,918.8757**	25.0292**
(b₁)	1	161.3120**	0.2429**	73.6512**	6,621.8883**	10.1388**
(b₂)	4	30.5240	0.0203	5.4288*	288.0763	1.7815*
(b₃)	5	17.0000	0.0447*	1.4370	635.4595**	6.8415**
(b)	10	36.8408*	0.0548**	10.2551**	1,095.1491**	5.1472**
(c)	4	42.8800*	0.0421	0.9125	612.8483*	0.4539
(d)	6	8.9800	0.0226	1.5642	189.2481	0.4994
Error	100	16.2720	0.0184	1.9553	196.3332	0.6770
Total	124					

* and **: Significant at 5% and 1% level, respectively.

From table 3, it is observed that the progeny mean ($\bar{F}_1$) is larger than the parental mean ($\bar{P}$) in all five characters. Thus, it seemed that the high tiller number, long panicle length, high spikelet number and high number of primary branch were dominant to their respective alternatives.

Table 3. *Estimates of the second degree statistics, mean values and heterosis, obtained from a diallel cross of* ***O. sativa*** *experiment*

Statistics	Panicle number per plant	Tiller number	Panicle length	Spikelet num. per panicle	Number of primary branch per paincle
V_p	14.3720	0.0349	19.7972	305.1799	1.7071
$\bar{V}_r$	10.5376	0.0150	5.4045	221.7998	1.0149
$V_{\bar{r}}$	6.8538	0.0095	4.3790	118.3775	0.4997
$\bar{W}_r$	9.5308	0.0176	9.1655	186.0302	0.8737
$\bar{P}$	11.68	1.0487	18.6132	64.8560	7.4000
$\bar{F}_1$	14.52	1.1589	20.5322	83.0520	8.1120
$\frac{1}{2}\delta = (\bar{F}_1 - \bar{P})$	+ 2.84	+ 0.1102	+ 1.9190	+ 18.1960	+ 0.7120
Heterosis	+ 24.3%	+ 10.5%	+ 10.3%	+ 28.1%	+ 9.6%

The results of the homogeneous test of ($W_r - V_r$) seems to indicate that the Hayman's assumptions (1954b) are adequate for all five characters. Therefore, it is permissible to adopt Hayman's method to draw the (V_r, W_r) graph (fig. 1, A to E), and to make estimation of the various genetical components, D, F, H_1, H_2, δ^2, E, and ($D - H_1$) for each of the five characters. The results are given in table 4.

From the value of ($D - H_1$) of each character, we observe that the additive genetic variance are greater than the dominance genetic variance for the characters of panicle number per plant, tiller number and panicle length.
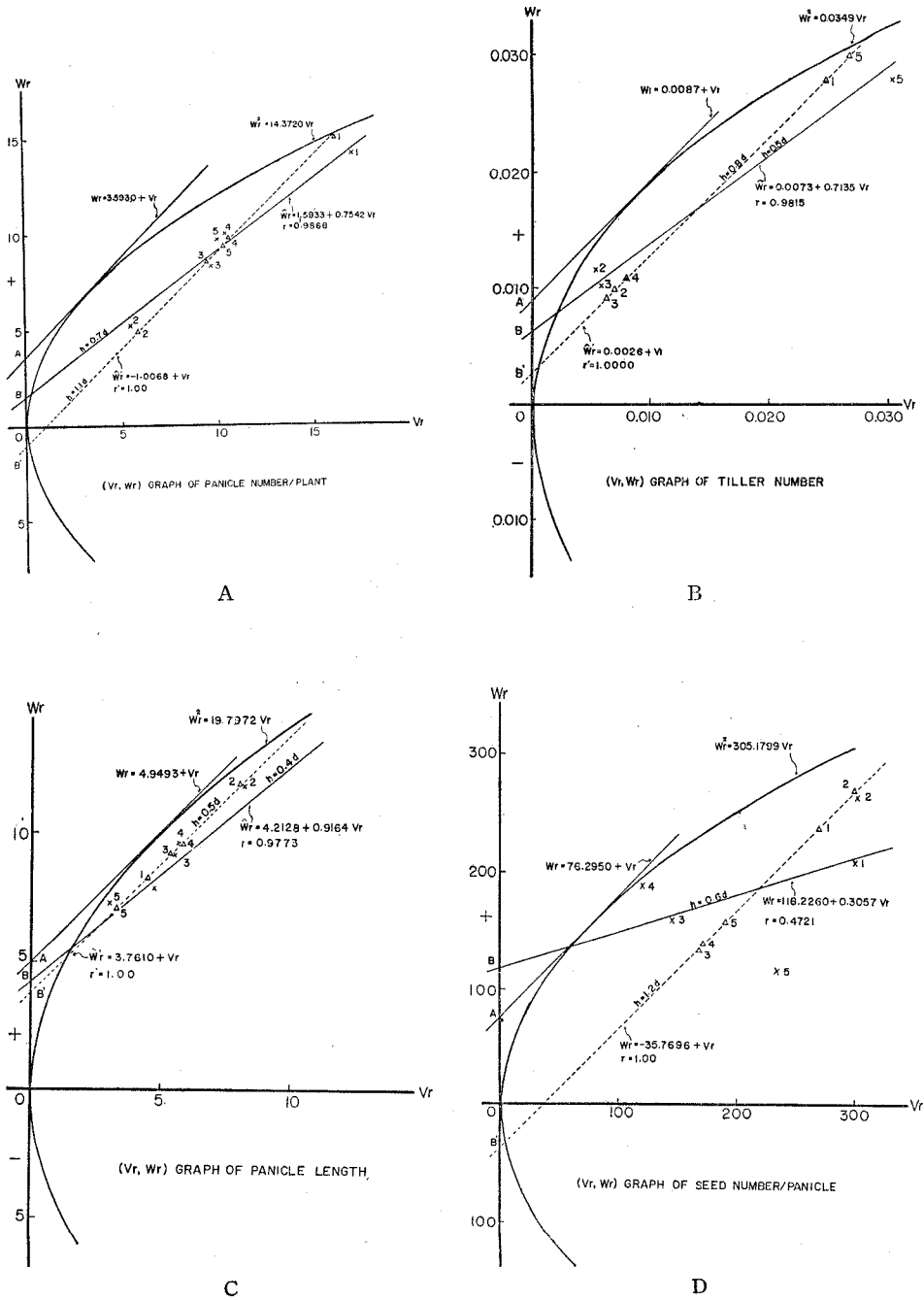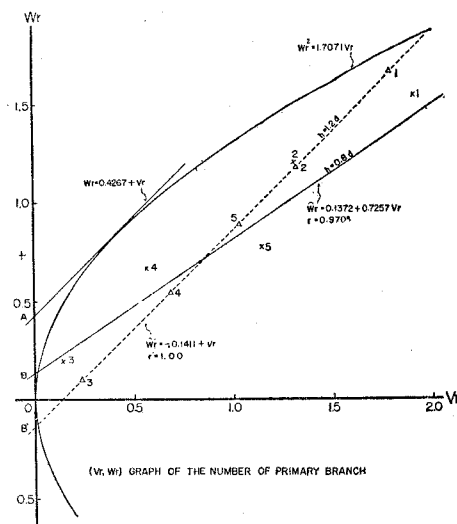
A

B

C

D

Fig. 1A. Relationship between V_r and W_r of five quantitative characters in a 5×5 diallel cross of *O. sativa*. A: panicle number/plant, B: tiller number, C: panicle length, D: spikelet number per panicle. The five parental varieties are: 1: Yen-no, 2: Wu-no-tao, 3: Mang-hua-chu, 4: Chih-chueh-chu, 5: Warisanmonchi 2.

E

Fig. 1. Relationship between V_r and W_r of five quantitative characters in a 5×5 diallel
cross of *O. sativa*. E: number of primary branch per panicle. The five parental
varieties are: 1: Yen-no, 2: Wu-no-tao, 3: Mang-hua-chu, 4: Chih-chueh-chu, 5:
Warisanmochi 2.

Table 4. *The estimated values of genetical components and their
standard error of the five quantitative characters
based on Hayman's method*

Genetical component	Panicle number per plant	Tiller number	Panicle length	Spikelet number per panicle	Number of primary branch per panicle
D	11.1176±0.8920	0.0312±0.0026	19.4061±0.3118	265.9133± 59.1498	1.5717±0.1736
F	-13.2845±2.2281	-0.0050±0.0064	2.4631±0.7788	-180.8809±147.7560	-0.2431±0.4335
H_1	9.9378±2.4089	0.0149±0.0069	3.7363±0.8420	346.1651±159.7410	1.9199±0.4687
H_2	8.2276±2.1849	0.0146±0.0063	3.3198±0.7637	335.1560±144.8860	1.7960±0.4251
δ^2	9.2772±1.4751	0.0462±0.0042	14.4799±0.5156	1299.2471± 97.8195	1.9411+0.2870
E	3.2544±0.3641	0.0037±0.0010	0.3911±0.1273	39.2666± 24.1478	0.1354±0.0709
$(D-H_1)$	1.1798±2.1407	0.0163±0.0061	15.6698±0.7482	- 80.2518±141.9590	-0.3482±0.4165

3. *Regression analysis*

    The linear regression lines of W_r on V_r for the five characters are shown
in fig. 1 (—A to—E). As depicted in fig. 1—A,—B and—E for the characters
of panicle number per plant, tiller number, and number of primary branch
per panicle, the W_r's are significantly regressed to V_r value, giving a signifi-
cant slope (compare with slope zero), b=0.7542±0.0715 (p<0.01) for panicle
number per plant, b=0.7637±0.0861 (p<0.01) for tiller number and b=0.7257±

0.1043 ($p<0.01$) for number of primary branch per panicle, but these slopes are significantly different from the unit slope ($p=0.020\sim0.021$ for panicle number per plant, $p=0.034\sim0.037$ for tiller number and $p=0.037\sim0.040$ for number of primary branch per panicle). This might be interpreted as indicating the presence of non-allelic interaction, particularly complementary gene action between parental gene combination. For the character of panicle length (fig. 1—C), the regression line of W_r on V_r gave a slope $b=0.9164\pm0.1148$ ($p<0.01$), which is not significantly different from the unit slope ($p=0.241\sim0.267$). This would indicate that the existence of additive and partially dominant genes among the parental gene combinations; but there was no genic interaction. As regards of the character of spikelet number per panicle (fig. 1—D), the slope of the regression line of W_r on V_r was $b=0.3057\pm0.4984$ ($p>0.05$), which is not significantly difference from zero.

4. Distribution of alleles

A summary of the results of the genetic analysis for each of the five characters are given in table 5.

Table 5. *Genetic analysis of five quantitative characters*

Statistics	Panicle number per plant	Tiller number	Panicle length	Spikelet num. per panicle	Number of primary branch per panicle
$\overline{uv}$	0.21	0.25	0.22	0.24	0.23
K_d/K_r	0.23	0.79	1.34	0.54	0.87
n	3.92	3.16	4.43	3.88	1.08
h^2	1.5439 ± 0.0793	1.0190 ± 0.1987	0.8766 ± 0.0782	1.3645 ± 0.2261	0.4770 ± 0.3246

In the analysis of diallel crosses, it is well-known that the mean value of the product of gene frequencies of dominance and recessive alleles is presented by $\overline{uv}=H_2/4H_1$. If $\overline{uv}=0.25$ and $H_1=H_2$, then $\overline{u}=\overline{v}=0.5$, which indicate that the positive and negative alleles at these loci are in equal proportions in the presents. For the character of tiller number, we notice that $\overline{uv}=0.25$. Since $H_1\simeq H_2$ from table 2, so $\overline{u}\simeq\overline{v}\simeq0.5$. For the characters of panicle number per plant and spikelet number per panicle, the respective $\overline{uv}$ values are 0.21 and 0.24; but by virture of $H_1\simeq H_2$ as derived from the results of the analysis of variance, $\overline{u}\simeq\overline{v}\simeq0.5$ theoretically, to compare with the observed values $\overline{u}\simeq\overline{v}\simeq0.46$ for panicle number per plant, and $\overline{u}\simeq\overline{v}\simeq0.49$ for spikelet number per panicle. The difference between the theoretical and the observed values may be attributed to the high error variances as shown in table 2. For the characters of panicle length and the number of primary branch per panicle, the values of $\overline{uv}$ were were estimated as 0.22 and 0.23 respectively. But from tables 2 and 4, $H_1>H_2$, since $F>0$ for panicle length and $F<0$ for the number of primary branch per

panicle, we otained that $\bar{u}=0.33$, $\bar{v}=0.67$ and $\bar{u}=0.64$, $\bar{v}=0.36$ for panicle length and the number of primary branch per panicle respectively. Thus, as regards in these two quantitative characters, the positive and the negative alleles at these loci do not seem to be in equal proportions in the parental lines.

5. *The degree of dominance*

The degrees of dominance (table 6) were estimated by $(H_1/D)^{1/2}$, $(\overline{AB}/\overline{AO})^{1/2}$ and $(\overline{AB'}/\overline{AO})^{1/2}$, with the latter two $(\overline{AB}/\overline{AO})^{1/2}$ and $(\overline{AB'}/\overline{AO})^{1/2}$ being derived from the regression analysis (fig. 1—A to—E). The difference between $(\overline{AB}/\overline{AO})^{1/2}$ and $(\overline{AB'}/\overline{AO})^{1/2}$ lies in the fact that the environmental variation has been eliminated in $(\overline{AB'}/\overline{AO})^{1/2}$.

As the character of panicle number per plant which is concerned fig. 1—A, shows that the actual regression line cuts the ordinate above the origin (as B), whereas the theoretical regression line below the origin. This would indicate the presence of over-dominance in some of the crosses after the environmental variation being eliminated; but from the results of table 6, the estimated value of $(H_1/D)^{1/2}$ is 0.9, implying partial-dominance of panicle mumber per plant.

Table 6. *Estimates of the degree of dominance*

Formula	Panicle num. per plant	Tiller number	Panicle length	Spikelet num. per panicle	Number of primary branch per panicle
$\sqrt{(H_1/D)}$	0.9	0.7	0.4	1.1	1.1
$\sqrt{(\overline{AB}/\overline{AO})}$	0.7	0.5	0.4	0.6	0.8
$\sqrt{(\overline{AB'}/\overline{AO})}$	1.1	0.8	0.5	1.2	1.2
Degree of dominance	partial-dominance	partial-dominance	partial-dominance	over-dominance	over-dominance

For each of the characters of tiller number and panicle length (fig. 1—B and 1—C), both actual and the theoretical regressioin lines cut the ordinate above the origin (as B and B'), indicating the presence of partial-dominance in some of the crosses. We observe that these three estimation methods have the same results as shown in table 6. From the comparisions between $(\overline{AB}/\overline{AO})^{1/2}$ and $(H_1/D)^{1/2}$ or $(\overline{AB'}/\overline{AO})^{1/2}$, it seemed that these two characters were less influenced by environmental factors.

For each of the characters of spikelet number and primary branch number per panicle (fig. 1—D and 1—E), the actual regression line cuts the ordinate above the origin (as B) while the theoretical regression line below the origin (as B'), indicating the presence of over-dominance in some of the crosses after the evironmental variation was eliminated. But from the results of table 6, the value of $(H_1/D)^{1/2}$ of each character was estimated as 1.1; hence, both these two characters seemed to show over-dominance.

6. *Direction and size of dominance*

By utilizing the covariance analysis, it is observed that the parents Wu-no-tao and Mang-hua-chu seem to contain a large number of dominant alleles for high count of panicle number per plant. But the opposite is true for the parent Yen-no, that is, it carries a large number of recessives for low count of panicles. As for the parents Warisanmochi 2 and Chih-chueh-chu, it seems that there are only small numbers of alleles involving in them; and Warisanmochi 2 seems to contain a small numbers of dominant alleles for low count of panicles whereas Chih-chueh-chu a small number of recessive alleles for low count of panicles (fig. 2—A).

For the character tiller number per plant, the mean values of Wu-no-tao and Mang-hua-chu are estimated as 17 and 15; next come Yen-no and Chih-chueh-chu each with 12 tillers per plant and Warisanmochi 2 with a mean of 6 tillers per plant. It is revealed by utilizing the covariance analysis (fig. 2—B), that the parents Wu-no-tao, Mang-hua-chu and Chih-chueh-chu seem to contain a large number of dominant alleles for high tillers, whereas Yen-no and Warisanmochi 2 only a small number of recessive alleles for high tillers. Therefore, it appears that the characters high panicle number and high tiller number are largely controlled by dominant alleles.

By utilizing the covariance analysis, the five parents seems to differ in dominance effect on the arrays of F_1 hybride for the character of panicle length (fig. 2—C). Thus, in accordance with the degree of dominances, the parents may be classified into two groups: (a) dominance of the long panicle's parents, Warisanmochi 2 and Yen-no; and (b) recessiveness of the short panicle's parents, Mang-hua-chu, Chih-chueh-chu and Wu-no-tao. This results seem to comply with the results of Section 2. That is long panicle length is dominant, that of the variety Warisamochi 2 being the longest whereas carrying most of the dominant genes.

From the covariance analysis of the spikelet number and the number of primary branch per panicle (fig. 2—D and 2--E), it seems that there is no relationship between the value of (W_r+V_r) and standardized deviations of the mean value, $(\bar{X})$.

7. *Number of gene groups*

The ratio δ^2/H_2 was utilizing to estimate the number of gene group, that was involving in the five characters in question to exhibit some degree of dominance. As given in table 5, the value of $n(=\sigma^2/H_2)$ was approximated by 4.0 for the characters of panicle number per plant, panicle length and spikelet number per panicle; from this, it may be inferred that there seem to involve at least four gene groups for these three characters. By adopting the same argument we are led to conclude that there are at least three gene
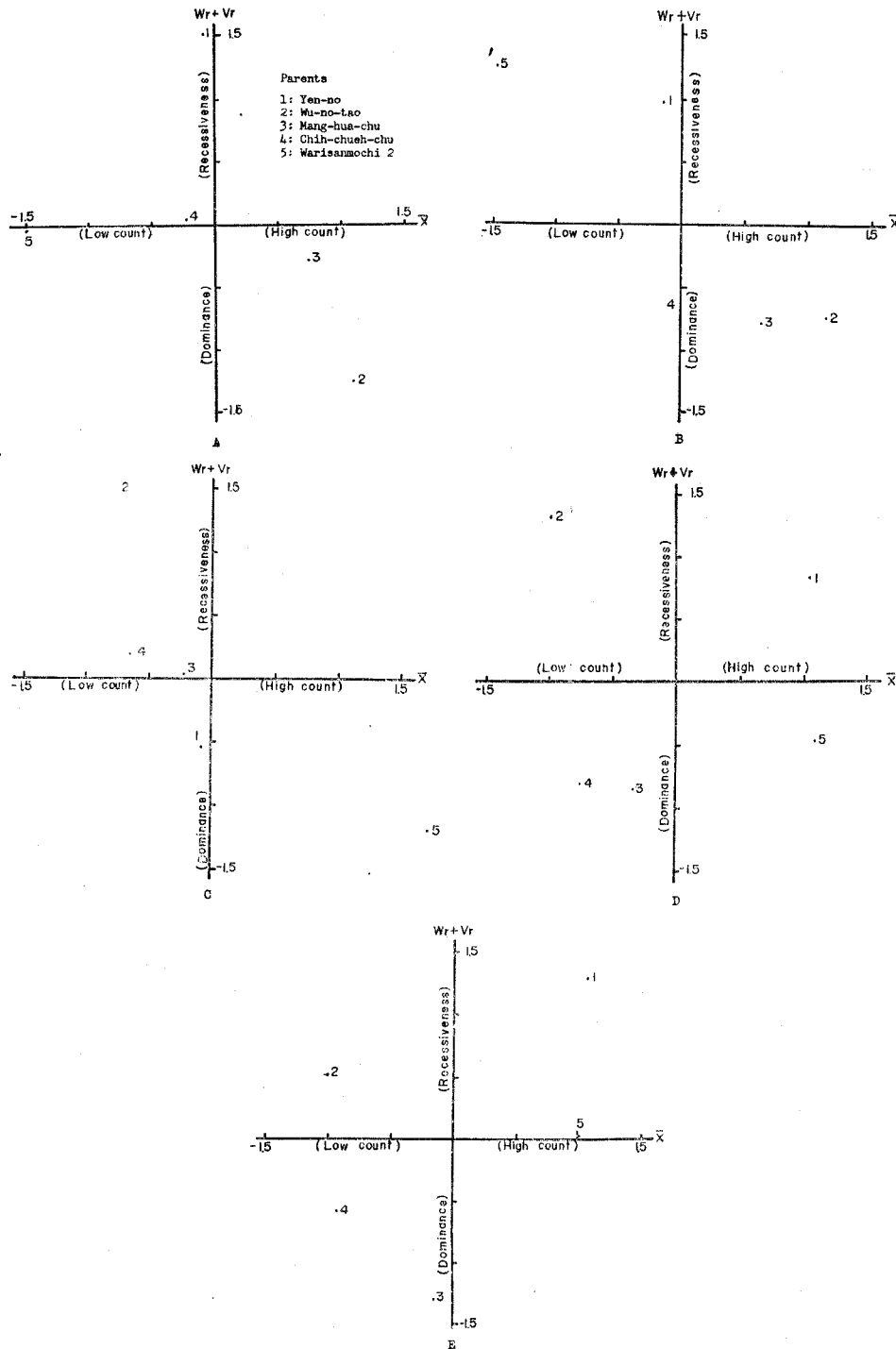
Fig. 2.   Showing the distribution of standardized deviations of parental measurements ($\overline{X}$) and the parental order of dominance ($W_r + V_r$), in the 5×5 diallel cross of *O. sativa*, A: panicle number per plant, B: tiller number C: panicle length, D: spikelet number per panicle. E: number of primary branch per panicle.

group controlling tiller number, and one gene group controlling the number of primary branch per panicle.

8. *The ratio of the total number of dominent to recessive genes*

The value of K_d/K_r over all the parents were estimated by 0.79, 1.34 and 0.87 for the characters tiller number, panicle length and number of primary branch per panicle, respectively (table 5). We notice that all the above values are close to unity to imply proximity between the numbers of dominant and recessive alleles in the parents. But for the characters of panicle number per plant and spikelet number per panicle, the value of K_r/K_d ratio were approximately by 4.4 and 1.9, respectively. This would indicate that the total numbers of recessive genes might be about four times greater than that of dominant genes in the character of panicle number per plant; and the number of recessive allels is about two times greater than that of dominant alleles in the character of spikelet number per panicle.

9. *Heritability*

The heritability (h^2) was estimated by the method of regression of the mean values of F_1 hybrids on the value of mid-parent. The result are also given in table 5. From these results, it is apparent that a major portion of the total phenotypic variation is genetically controlled.

From the above results, we may conclude that:

(1) The genetic mechanism of these charactes seems rather complex as compared to that of plant height (Wu, 1968). They are also less stable in their response to environmental variations except the character of panicle length. Therefore, in practicing breeding procedure one should try to increase the selection intensity for panicle length and do best to eliminate environmental variations for the other four characters, panible number per plant, tiller number, spikelet number per panicle and number of primary branch per panicle, so as to increase the rate of selection response in the early generations.

(2) High panicle number and high tiller number seems to be largely controlled by dominant alleles.

(3) Negative genetical correlation seems to exist between the number of panicle and the length of panicle; that is, if the variety would contain the dominant genes for high panicle number, it should be companied by the recessive genes for short panicle and *vice versa*.

(4) The characters of plant height and the panicle length are probably positively correlated genetically. Thus, one would expect that the tall plant should be always companied by the long panicle and the short status by the short panicle.

Summary

In this paper, a study of basic nature on the quantitative inheritance of *O. sativa* were carried out by means of 5×5 diallel cross with a view to estimating genetic parameters, additivety, dominance, maternal effect, heterosis, distribution of alleles, number of gene groups, degree of dominance, direction and size of dominance of each variety and the heritability for five metrical characters in F_1 hybrids.

The five parental varieties were Yen-no, Wu-no-tao, Mang-hua-chu, Chih-chueh-chu, and Warisanmochi 2. The parents differed significantly in one or more of the following characters, panicle number per plant, tiller number, panicle length, spikelet number per panicle, and number of primary branch per panicle. The chief features of the results are as follows:

1. The genetical variation among these five parents were highly significant for each of the two genetical components, additive effect and dominance eeffect; but between the reciprocal crosses, maternal effect might be in existence in the characters of panicle number per plant and spikelet number per panicle.

2. Long panicle length was dominant to short length. High panicle number, high tiller number, high spikelet number and high number of primary branch per panicle also showed dominance over their alternative low count.

3. Regression analysis of the data of W_r/V_r for each character of panicle number per plant, tiller number, and number of primary branch per panicle indicated the presence of non-allelic interaction, particularly complementary gene action, between parental gene combination. But in the character of panicle length, we observed only additive and partially dominant genes effect existing between the parental gene combinations, but there was no genic interaction. For the analysis of spikelet number per panicle, no relationship was found between V_r and W_r.

4. The gene frequencies of dominance ($\bar{u}$) and recessive ($\bar{v}$) might be equal in the characters of tiller number, panicle number per plant and spikelet number per panicle. For the characters of panicle length and the number of primary branch per panicle, the values of ($\bar{u}$, $\bar{v}$) were estimated by (0.33, 0.67) and (0.64, 0.36), respectively.

5. The degree of domiance for the characters of panicle number per plant, tiller number and panicle length appeared to be partially dominanted; but, for the character of spikelet number per panicle and number of primary branch per panicle, we observed over-dominance.

6. The parents, Wu-no-tao and Mang-hua-chu seem to contain a large number of dominant alleles for high count of panicles, whereas, the parents

Warisanmochi 2 and Chih-chueh-chu only a small number of dominant and recessive allels, and Yen-no a large number of recessive alleles. In the same manner we conclude that the parents Wu-no-tao, Mang-hua-chu and Chih-chueh-chu, seem to contain a large number of dominant alleles for high tiller numbers, whereas the parents Yen-no and Warisanmochi 2, with only a small number of recessive alleles.

In accordance with the degree of dominance of panicle length, it seems that the pareantal varieties may be classified into two groups: (a) dominance of the long panicle's parents, Warisanmoci 2 and Yen-no; and (b) recessiveness of the short panicle parents, Mang-hua-chu, Chih-chueh-chu and Wu-no-tao.

7. High panicle number and high tiller number seem to be controlled mostly by dominant alleles, whereas the low count of tillering number by recessive alleles.

8. It seemed that there were at least four gene groups effecting the characters of panicle number per plant, panicle length and spikelet number per panicle. By adopting the some argument, there seemed to involve at least three gene groups effecting the character of tiller number and one gene group effecting the number of primary branch per panicle.

9. The total number of dominant and recessive alleles are approximately equal for the characters of tiller number, panicle length and number of primary branch per panicle. The total number of recessive genes was about four times greater than that of dominant genes in the character of panicle number per plant; but in the character of spikelet number per panicle, the total number of recessive alleles was about two times greater than that of dominant alleles.

10. Form the calculation of the heritabilities for all the five characters, we observe that a major protion of the phenotypic variation is genetically controlled.

11. The genetic mechanism of four metrical characters, panicle number per plant, tiller numbe, spikelet number per panicle and the number of primary branch per panicle are rather complex as compared to that of plant height; they are however more stable in their response to enviromental variations.

12. In practicing rice hybridization breeding procedures, it is difficult to select the high panicle number together with the long panicle, or short status together with the long panicle individuals.

水 稻 數 量 性 狀 之 遺 傳 研 究

II. 雜種第一代穗長，穗數，每穗粒數，分蘗數及穗上第一枝梗數之全互交分析

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　　本研究係利用五種水稻品種：岩糯，烏糯稻，尖仔朮，赤脚朮及哇喱薩恩糯2號等爲試驗材料，進行全互交（包括正逆什交及自交）以研究水稻重要數量性狀之遺傳現象。本報告爲利用什種第一代及親本自交後代爲資料，依據全互交法之統計分析原理及方法，分析水稻之穗長，穗數，每穗粒數，分蘗數及第一枝梗數等五數量性狀之遺傳，其主要結果有：

　　1.　在此五性狀中，由品種間平均效果所引起之遺傳變異甚大，累加性遺傳變異及顯性效應等亦存在。細胞質效應則只存在於穗數及每穗粒數等二性狀。

　　2.　長穗爲顯性，短穗爲隱性。其他性狀則以數多者爲顯性，少者爲隱性。

　　3.　從廻歸分析之結果知，穗數，分蘗數及穗上第一枝梗數等三性狀具有非相對因子間之交感作用，特別是因子的輔助作用存在於親本什交後的因子組成內。在穗長方面，只發現有部分顯性，因子間之交感作用不顯著存在。分析第一枝梗數結果知 V_r 與 W_r 間無任何關係存在。

　　4.　分蘗數，穗數及每穗粒數之平均顯性因子頻度 $(\bar{u})$ 與平均隱性因子頻度 $(\bar{v})$ 略爲相等在穗長方面，$\bar{u}$ 爲 0.33 $\bar{v}$ 爲 0.66。而在第一枝梗數方面，則 $\bar{u}$ 爲 0.64 $\bar{v}$ 爲 0.36。

　　5.　穗數，分蘗數及穗長等性狀爲部份顯性，而第一枝梗數與每穗粒數爲超顯性。

　　6.　烏糯稻及芒花朮等二品種具有大量顯性因子之多穗數性狀，而哇喱薩恩糯2號具有少量的顯性因子，赤脚朮則有少量之隱性因子，而岩糯則有大量之隱性因子，因此其穗數亦最少。另一方面，烏糯稻，芒花朮及赤脚朮等三品種，據有大量顯性因子之多分蘗性性狀，而岩糯及哇喱薩恩糯2號等則具有少量之隱性因子，其分蘗數亦較少。在穗長方面，五親本品種可分爲二組：一爲具有顯性因子的長穗親本，如哇喱薩恩糯2號及岩糯，而具有隱性因子的短穗親本爲芒花朮，赤脚朮及烏糯稻等。

　　7.　穗數及分蘗數多者同被顯性因子控制，而少者則同被隱性因子控制，這些因子可能具有多效性作用。

　　8.　穗數，穗長及每穗粒數等性狀至少各被四羣因子數控制着，而分蘗數及第一枝梗數則各被三羣及一羣因子數控制。

　　9.　綜觀此五親本知，分蘗數，穗數及第一枝梗數等各性狀之顯性因子總數與隱性因子數略爲相等，在穗數方面，則隱性因子總數較顯性因子總數大四倍，而在每穗粒數方面，隱性因子總數較顯性因子總數大二倍左右。

　　10.　從遺傳力的分析結果知，此五性狀之外表型變異大部份來自遺傳性。

　　11.　穗數，分蘗數，每穗粒數及第一枝梗數等四性狀之遺傳現象較株高或穗長爲複雜，且此等性狀對生長環境之反應亦較不穩定。

　　12.　從雜交組合中，很難選拔出穗數多而又長穗或矮株而又長穗之後裔。

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