6 X 6 F₂ DIALLEL ANALYSIS IN FINE GRAINED RICE (Oryza sativa L.)

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6 X 6 F₂ DIALLEL ANALYSIS IN FINE GRAINED RICE (Oryza sativa L.)

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CERTIFICATE

This is to certify that the thesis entitled "6 x 6 F_2 DIALLEL ANALYSIS IN FINE GRAINED RICE (Oryza sativa L.)" submitted by Mr. SAI MURALI RAJ, in partial fulfilment of the requirements for the degree of MASTER OF SCIENCE (AGRICULTURE) in PLANT BREEDING AND GENETICS to the University of Agricultural Sciences, Bangalore is a record of research work carried out by him under my guidance and supervision and that no part of the thesis has been submitted for the award of any other degree, diploma, associateship, fellowship or other similar titles.

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INTRODUCTION

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I. INTRODUCTION

Rice (Oryza sativa L.) is the most important of the three cereals - rice, wheat and maize - which feed the world. Rice is used exclusively for direct human consumption, unlike wheat and maize. It is the staple food of 40 percent of the world population and for another 20 percent, a major item of diet. More than 90 percent of the rice is produced and consumed in Asia which happens to be the most densely populated region of the world (Khush, 1990). In 1990, it was planted to 145.86 million hectares of land all over the world with a production of 518.82 million tonnes. In an area of about 41.8 million hectares, India produces 109.5 million tonnes of rice, of which, 3.56 million tonnes are produced in Karnataka on 1.18 million hectares. (IRRI, 1991)

Selection of parents for simply inherited characters controlled by major genes, is easy and does not require any special technique. But selection of parents for improving quantitative characters such as yield and quality which are controlled by polygenes with small effects coupled with high genotype x environment interaction has been rather difficult. This necessitates the separation of genetic variability from total variability to make selection effective and the genetics of such yield components, their

heritabilities and combining ability need to be studied. Hence a knowledge of genetic architecture of various quantitative traits contributing to yield would be helpful to plan crosses to maximise the frequency of superior genotypes in segregating populations.

the fifties, analysis of diallel orosses described In Hayman (1954), Jinks (1954, 1956) and Griffing (1956) by attracted the attention of several workers and a large number of studies in different crops have been conducted to determine the value of diallel cross analysis to predict the performance of parents and to identify promising crosses. Griffing (1956) presented a model to show variance for GCA that involves mostly additive gene effects where as SCA involves the dominance and epistatic component of genetic Thus the knowledge of the relative magnitude variance. of additive, dominance and epistatic gene effects would help in breeding methodology. the choice of appropriate The diallel analysis technique provides among others, an elegant method for estimation of the genetic parameters in terms of total variance as well as for assessing combining ability effects which ultimately reflects on heterosis. Gilbert (1958) made a critical appraisal of the value of diallel crosses in plant breeding and concluded that diallel cross gives information that cannot be obtained from the parents as such.

In the present study, six fine grained genotypes of rice namely Ambrose, HP-32, Pak-Basumathi, HP-33, HP-5 and HP-20, were intercrossed in a diallel fashion.

The present investigation was envisaged to understand the genetic architecture of grain yield and its components through F_2 diallel analysis. The objectives of the study are:

- i. to estimate genetic variability for grain yield and its
 components,
- ii. to evaluate potential crosses which could profitably
 be used for exploiting heterosis,
- iii. to assess the combining ability and the components of gene action,
 - iv. to estimate the direct and indirect effects of characters through correlation and path coefficient analysis, and,
 - v. to formulate selection indices for grain yield.

REVIEW OF LITERATURE

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II. REVIEW OF LITERATURE

Rice is a strictly self pollinated crop. Hence improvement in this crop has been largely through introduction, selection, mutation and hybridization. Recently, with the discovery of male sterility greater importance is being placed on the possibility of developing hybrids for commercial cultivation. In the subsequent pages an attempt has been made to review the pertinent literature in consonance with the objectives of the present investigation under the following headings:

- 1. Methods of biometrical analysis
- 2. Heterosis
- 3. Combining ability
- 4. Gene action
- 5. Character association
- 6. Variability
- 7. Heritability and Genetic advance

2.1 Methods of biometrical analysis

Estimation of genetic parameters forms an important aspect of rational plant breeding programme. There are several methods to assess the breeding values of genotypes for polygenic traits.

Fisher (1918) integrated biometry and genetics and partitioned the heriditary variance into additive, dominance and epistatic components. Mather (1949) outlined the procedure to estimate the fixable (D) and non-fixable (H) components with their respective standard deviations, based on the least square technique. Later, different designs were developed to estimate the additive and non-additive variations. Diallel analysis is one such technique by which inheritance pattern of quantitative characters can be studied.

Jinks and Hayman (1953), Jinks (1954, 1956) and Hayman (1954a, 1958 and 1960) developed the theory of diallel cross method which involves crossing a set of inbreds in all possible combinations for genetic analysis in F1. The second degree statistics such as variance (V_r) and co-variance (W_r) were calculated and regression of W_r on V_r was used to indicate graphical representation of the degree of Further the genetic model of Hayman (1954b) dominance. allows the estimation of different genetic components like the variation due to additivity (D), dominance effects and H₂), the co-variance of additive and dominance (H) effects of a single array (F_r) , in the absence of epistasis. Later Jinks (1956) extended the application of this model to advanced generations like F2, F3 and back crosses.

Griffing (1956a and 1956b) emphasized the statistical concepts of general and specific combining ability. He outlined four methods involving,

- i) parents, F₁s and reciprocals,
- ii) parents, Fis and no reciprocals,
- iii) one set of F₁s and reciprocals, and
- iv) one set of Fis only.

2.2 Heterosis

The phenomenon of heterosis in rice was first reported by Jones (1926). Since then rice breeders have shown increasing interest in heterosis and several workers have suggested exploiting heterosis commercially by developing hybrid rice varieties. A perusal of Table 2.1 indicates positive heterosis over mid parent has been observed for all the traits while negative heterosis over mid parent has been observed for number of days to 50 per cent flowering, plant height, number of tillers per plant, panicle length, number of filled grains per panicle and test weight. Positive heterosis over better parent has been observed for all traits except for number of tillers per plant and panicle weight per plant. However negative heterosis over better parent has been observed for test weight only. Heterosis over standard has been recorded for only two traits, viz., panicle length and grain yield per plant.

Ch	arator	Mathad of	Natur	e and	Magnitude	
Cha	aracter	Study	M.P.	B.P.	S.P.	Reference
	1	2	3	4	5	6
1)	Plant height	4x4 diallel 6 hybrids 4 hybrids 11 crosses 6 varieties 3 hybrids 6x6 half diallel 8 crosses 2 crosses 6 hybrids 15x15 diallel	+ + + + + + + + + +	+		Chang <u>et al</u> (1973) Cheema <u>et al</u> (1988) Dzyuba (1975) Guo (1986) Mallick & Hajra (1978) Nijaguna & Mahadevappa (1983) Richharia & Singh (1983) Singh & Singh (1979) Singh & Singh (1978) Singildin & Shilovskll (1977) Srivastava & Seshu (1982)
2)	Total tillers	3 hybrids	+/-			Nijaguna & Mahadevappa (1983)
3)	Produ- ctive tillers	4x4 diallel 6 hybrids 7x7 diallel 5x5 half diallel 6 crosses 6 varieties 8 crosses 8 crosses 2 crosses 28 F ₁ hybrids	+ + + + + + + + + + + + + + + + + + +	+ + + +		Chang <u>et al</u> (1973) Cheema <u>et al</u> (1988) Kalaimani & Sundaram (1987) Kumar & Saini (1983) Madhusudhan Rao (1965) Mallick & Hajra (1978) Shanmugasundaran & Sivasubramanian (1983) Singh & Singh (1979) Singh & Singh (1978) Zhuang & Wu (1982)
4)	Panicle length	4 x 4 diallel 4 hybrids 5x5 half diallel	+ + +	+		Chang <u>et al</u> (1973) Dzyuba (1975) Kumar & Saini (1983)

Table 2.1 Review of literature on heterosis in rice

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	1	2	3	4	5	6	
		6 crosses 6 varieties 6x6 half diallel	+ - +		+	Madhusudhan Rao (1965) Mallik & Hajra (1978) Richharia & Singh (1983)	
		8 crosses 2 crosses	•	+	• 	Singh & Singh (1979) Singh & Singh (1978)	
5)	Panicle weight	4 hybrids	+			Dzyuba (1975)	
	5	-	+			Srivastva & Sheshu (1982)	
6)	No.of spike- lets/ panicle	6 hybrids 4 hybrids 6x6 half diallel 15 x 15 diallel	+ + +	+		Cheema <u>et al</u> (1988) Dzyuba (1975) Richharia & Singh (1983) Srivastava & Sheshu (1982)	
7)	No.of grains/ panicle	7x7 diallel 5x5 half diallel 6 varie- ties 8 crosses	+ + -	+		Kalaimani & Sundaram (1987) Kumar & Saini (1983) Mallick and Hajra (1978) Shanmugasundaram &	
		2 crosses 6 hybrids	+ +			Snivasubramanyan (1983) Singh & Singh (1978) Singildin & Shilovskll (1977)	
8)	Test weight	7x7 diallel 5x5 half diallel 3 hybrids 8 crosses 2 crosses	+ + +/- +	+/-		Kalaimani & Sundaram (1987) Kumar & Saini (1983) Nijaguna & Mahadevappa (1983) Singh & Singh (1979) Singh & Singh (1978)	
9)	Grain yield	L x T 13 parents 17 hybrids 4 x 4 diallel	+ +	+	+ .	Devarathinam (1983) Anandakumar & Rangaswamy (1984) Chang <u>et al</u> (1973)	

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 1	2	3	4	5	6
 	l2xl2 diallel		+		Devarathinam (1984)
	ll crosses	÷			Guo (1986)
	lOxlO half diallel		+	÷	Panwar <u>et al</u> (1983)
	27 crosses	+	÷		Paramasivan & Sreerangaswamy (1990)
	89 hybrids	+	+		Voc & Luat (1987)
 	ll hybrids	÷		+	Rao <u>et</u> al (1985)

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2.3 Combining ability

The concept of combining ability plays a significant role in crop improvement, since it helps the breeder to determine the nature of gene action involved in the expression of quantitative traits of economic importance. Combining ability studies help in the identification of parents with gca effects and in identifying cross combinations showing high sca effects. Table 2.2 indicates that highly significant GCA variance has been observed by many workers for many traits except panicle weight per plant, grain length, grain breadth and spikelet fertility/sterility. Significant GCA variances have been observed for all traits. Similarly significant and highly significant values were also observed for SCA variances. Certain GCA and SCA variance were also found to be nonsignificant as recorded by some workers.

2.4 Gene action

Additive and non-additive gene action have been observed by many workers for all the traits as is evident from the table 2.3. Epistatic gene action has been observed for the traits number of days to 50 per cent flowering and number of tillers per plant. Table 2.2 Review of literature on combining ability in rice.

	Character	Method of Study	GCA	SCA	Reference
	1	2	3	4	5
1)	Plant height	6 hybrids 7x7 diallel 5x5 diallel (7x11) LxT	* * * *		Cheema <u>et al</u> (1988) Dhaliwal & Sharma (1990) Haque <u>et al</u> (1980) Peng & Virmani (1990)
		6x6 diallel	*	*	Kumar & Sreerangaswamy (1986) Maatafigur Babman at al
		7x7 diallel	*	*	$\begin{array}{c} \text{MOSCALLZUL Ranman } \underline{e} \\ (1981) \\ \text{Bac et al } (1990) \end{array}$
		5x5 half diallel	*	*	Sardana & Borthakur (1987)
		6x6 diallel 6x6 half diallel	*	* * *	Singh & Richharia (1978) Singh <u>et al</u> (1980)
		lOxlO half diallel 4x÷ diallel	* *	*	Subramanian & Rathinam (1984) Zagvazdin (1983)
2)	Total tillers	5x5 half diallel	* *		Singh & Srivastava (1982)
3)	Productive tillers	6 hybrids 7x7 diallel 7x7 diallel 5x5 diallel 7x7 diallel 5x5 half diallel 5x5 diallel 6x6 diallel 6x6 half diallel	* * * * * * *	* * * * * *	Cheema <u>et al</u> (1988) Dhaliwal & Sharma (1990) Maurya & Singh (1977) Mostafizur Rahman <u>et al</u> (1981) Rao <u>et al</u> (1980) Sardana & Borthakur (1987) Singh & Nanda (1976) Singh & Richharia (1978) Singh <u>et al</u> (1980)
4)	Panicle length	7x7 diallel 5x5 diallel	* *	*	Dhaliwal & Sharma (1990) Mostafizur Rahman <u>et al</u> (1981)
		5x5 half diallel	*	*	Sardana & Borthakur (1987)
		6x6 half diallel	*		Singh <u>et al</u> (1979)
		6x6 diallel 5x5 half diallel 4x4 diallel	* * * * *	*	Singh (1977) Singh & Srivastava (1982) Zagvazdin (1983)

	1	2	3	4	5
5)	Panicle weight	7x7 diallel	*	*	Rao <u>et al</u> (1980)
6)	No.of spikelets/ panicle	6 hybrids 6x6 diallel 12x12 half	* * *	*	Cheema <u>et al</u> (1988) Ish Kumar (1975)
		diallel	*	*	Mohapatra & Mohanty (1985)
		/X/ diallel	*	^ *	Rao et al (1980) Singh (1977)
		4x4 diallel	* *		Zagvazdin (1983)
7)	No.of	7x7 diallel	*	*	Dhaliwal & Sharma (1990)
	grains/	5x5 diallel	* *	- 1 -	Haque et al (1980)
	panicle	/x/ diallel	*	*	Kalaimani & Sundaram (1988) Vim (1987)
		7x7 diallel	**		Maurya & Singh (1977)
		12x12 half diallel	*	*	Mohapatra & Mohanty (1985)
		5x5 diallel	*	*	Mostafizur Rahman <u>et al</u> (1981)
		7x7 diallel	*	*	Rao <u>et al</u> (1980)
		5x5 half	*	*	Sardana & Borthakur (1987)
		diallel 5x5 diallel	*	*	Singh & Nanda (1976)
8)	Tost	7x7 diallel	*	*	Dhaliwal & Sharma (1990)
07	weight	5x5 diallel	*		Haque et al (1980)
		6x6 diallel	* *		Ish Kumar (1975)
		7x7 diallel	*		Maurya & Singh (1977)
		lOxlO half diallel	*	*	Panwar & Paroda (1983)
		7x7 diallel	*	*	Rao <u>et al</u> (1980)
		5x5 half	*	*	Sardana & Borthakur (1987)
		diallel			Cinch & Norda (1076)
		5x5 diallel	ns. *	ns. *	Singh & Nanda (1976) Singh (1977)
		4x4 diallel	* *		Zagvazdin (1984)
9.)	Grain length	7x7 diallel 10x10 half diallel	*	* *	Dhaliwal & Sharma (1990) Panwar & Paroda (1983)

	1	2	3	4	5
10)	Grain	7x7 diallel	*	*	Dhaliwal & Sharma (1990)
	breadth	lOxlO half diallel	*	*	Panwar & Paroda (1983)
			~		
11)	L/B	lOx10 half	*	*	Panwar & Paroda (1983)
	Lacio	4x4 diallel	* *		Zagvazdin (1983)
12)	Grain	LxT analysis	*	*	Amirthadevarathinam (1983)
	yield	7x7 diallel	*	*	Dhaliwal & Sharma (1990)
		6x6 diallel	**	**	Ish Kumar (1975)
		LXT analysis	**	*	Peng & Virmani (1990) Kalaimani (Cundamam (1088)
		AXA diallel	*	*	Kalalmani & Sundaram (1988) Kuo (jun (1987)
		7x7 diallel	**	* *	Maurya & Singh (1977)
		l2xl2 half diallel	*	*	Mohapatra & Mohanty (1985)
		5x5 diallel	*		Mostafizur Rehman <u>et al</u> (1981)
		lOxlO half diallel	*	*	Panwar <u>et al</u> (1985)
		6x6 half diallel	*		Richharia & Singh (1983)
		5x5 half	*	*	Sardana & Borthakur (1987)
		7x7 diallel	*	*	Sasmal & Baneriee (1986)
		15x15 half diallel		* *	Shrivastava & Seshu (1983)
		5x5 diallel	*	*	Singh & Nanda (1976)
		6x6 half diallel		*	Singh <u>et</u> <u>al</u> (1979)
		6x6 diallel	*	*	Singh (1977)
		6x6 half diallel	*	* *	Singh <u>et al</u> (1980)
		lOxlO half diallel	**	*	Subramaniam & Rathinam (1984)
13)	Spikelet	5x5 diallel	*		Haque et al (1980)
/	sterilitv/	12x12 half	*	*	Mohapatra & Mohanty (1985)
	fertility	diallel 7x7 diallel	*	*	Rao <u>et</u> <u>al</u> (1980)

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			Gene	Action	
	Character	Methcd of Study	Add	Non-Add	Reference
	1	2	3	4	5
1)	Plant height	LxT analysis		+	Anandakumar & Rangaswamy (1986)
		6 hybrids	+	÷	Cheema et al (1988)
		7x7 diallel		+	Dhaliwal & Sharma (1990)
		LxT analysis	· +	+	Peng & Virmani (1990)
		7x7 partial		+	Jun & Kwak (1984)
		diallel			
		7x7 diallel	+		Kalimani & Sundaram (1987)
		7x7 half	+		Kaushik & Sharma (1987)
		diallel			
		6x6 diallel	+	÷	Kumar & Sreerangaswamy (1986)
		5x5 diallel	+	÷	Mostafizur Rahmen <u>et al</u> (1981)
		5x5 half diallel	+	÷	Sardana & Borthakur (1987)
		6x 6 half dial	lel	÷	Singh <u>et al</u> (1980)
2)	Total tillers	7x7 half diallel		+	Kaushik & Sharma (1988)
		5x5 half diall	el +		Singh & Shrivastava (1982)
3)	Productive	6 hybrids		+	Cheema et al (1988)
	tillers	7x7 ^{diallel}		+	Dhaliwal & Sharma (1990)
		5x5 diallel	+		Haque et al (1980)
		7x7 partial diallel		+	Jun & Kwak (1984) <u>et al</u>
		7x7 diallel		+	Kalaimani & Sundaram (1987)
		5x5 diallel	÷	+	Mostafizur Rehman <u>et al</u> (1981)
		5x5 half	+	+	Sardana & Borthakur (1987)
		diallel			
		5x5 diallel	+		Singh & Nanda (1976)
		5x5 diallel		+	Singh & Shrivastava (1982)
		6x6 diallel		+	Singh <u>et al</u> (1980)
۵)	Panicle	IvT analysis		+	Anandakumar & Rangaswamy
	length	TYI GUATADID		, 	(1986)

Table 2.3 Review of literature on gene action in rice.

	1	2	3	4	5
		4x4 diallel		+	Chang et al (1973)
		7x7 full diallel		+	Dhaliwal & Sharma (1990)
		7x7 partial		+	Jun & Kwak (1984)
		diallel			
		7x7 half	+		Kaushik & Sharma (1988)
	-	diallel			
•		5x5 diallel	+	÷	Mostafizur Rahmen <u>et al</u> (1981)
		5x5 half diallel	+	+ • •	Sardana & Borthakur (1987)
		6x6 half diallel		+	Singh et al (1979)
		5x5 half diallel	÷		Singh & Shrivastava (1982)
5)	Panicle	l2xl2 half	+	+	Mohanty & Mohapatra (1973)
	weight	diallel			• • •
	-	5x5 half diallel	+	+	Singh & Shrivastava (1982)
		-	+	+	Rao <u>et al</u> (1980)
6)	No.of spikelets/	32 Varieties	÷		Balakrishna Rao <u>et al</u> (1973)
	panicle	6 hybrids	+	+	Cheema et al (1986)
		7x7 partial		+	Jun & K w ak (1984)
		diallel			
		7x7 half diallel	+		Kaushik & Sharma (1988)
		12x12 half	+		Mohapatra & Mohanty (1985)
		diallel			
		5x5 half diallel		+	Singh & Shrivastava (1982)
7)	No.of	7x7 diallel		+	Dhaliwal & Sharma (1990)
	grains/	5x5 diallel	+		Hague <u>et al</u> (1980)
	panicle	7x7 diallel		+	Kalaimani & Sundaram (1987)
		12x12 half	÷		Mohapatra & Mohanty (1985)
		diallel 5x5 diallel	÷	+	Mostafizur Rahman <u>et al</u>
		5x5 half	+	+	(1981) Sardana & Borthakur (1987)
		diallel		·	
		5x5 diallel		÷	Singh & Nanda (1976)
ρ١	Tost	7×7 diallal		Ŧ	Dhaliwal & Sharma (1990)
0)	woight	5x5 diallel	+	т	Hadue e^{-} al (1980)
	WEIGHL	7x7 half diallel	k	÷	Kaushik & Sharma (1988)

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1	2	3	4	5
	lOxlO half	+	+	Panwar & Paroda (1983)
	diallel			
	6x6 diallel	+	+	Rui & Zhao (1983)
	5x5 diallel	+	+	Sardana & Borthakur (1987)
	5x5 diallel		+	Singh & Nanda (1976)
	6x6 half diallel	+	+	Singh (1982)
	7 vaireties	+		Tripathy & Misra (1985)
9) Crain				Dhaling (1000)
) Grain			+	Dhallwal & Sharma (1990)
rengtu	JUXIU NAII diallel	÷	+	Panwar & Paroda (1983)
	Své diallal	+		P_{11} (1983)
	6x6 half diallel	, _	+	Singh (1982)
	5x5 half diallel	+	1	Singh (1902) Singh & Shrivastava (1982)
	SAS HULL GIULLEI			eingh a bhrivastava (1962)
10) Grain	7x7 diallel		+	Dhaliwal & Sharma (1990)
breadth	lOx10 half	+	+	Panwar & Paroda (1983)
	diallel			\mathbf{P}
	oxo diallel	+	+	Rui & Znao (1983)
	5x5 half diallel	+ +	+	Singh (1982) Singh & Shrivastava (1982)
11) L/B	lOx10 half	+	+	Panwar & Paroda (1983)
Latio	6x6 half diallel	+	÷	Singh (1982)
			1	Singh (1982)
12) Grain	LxT analysis	+	÷	Amirthadevarathivan (1983)
yield	LxT analysis		+	Anandakumar & Rangaswamy (1986)
	4x4 diallel	+		Chang et al (1973)
	7x7 diallel		+	Dhaliwal & Sharma (1990)
	5x5 diallel	+		Hague et al (1980)
	LxT analysis	+	+	Peng & Virmani (1990)
	7x7 diallel	+		Kalaimani & Sundaram (1987)
	7x7 half diallel		+	Kaushik & Sharma (1988)
	9x9 diallel	+	+	Kuo & Liu (1987)
	12x12 half	+		Mohapatra & Mohanty (1985)
•	diallel			
	5x5 diallel	+	+	Mostafizur Rahmen <u>et al</u> (1981)
	8x8 half diallel	+	+	Sarathe <u>et al</u> (1986)

	1	2	3	4	5
		5x5 half diallel 5x5 diallel 6x6 half diallel 6x6 half diallel 5x5 diallel 5x5 half diallel 10x10 half diallel	÷	+++++++++++++++++++++++++++++++++++++++	Sardana & Borthakur (1987) Singh & Nanda (1976) Singh <u>at al</u> (1979) Singh <u>at al</u> (1980) Singh (1991) Singh & Shrivastava (982) Subramanian & Rathinam (1984)
13)	Spikelet sterility/ fertility	5x5 diallel 7x7 half diallel 5x5 half diallel 7x7 partial diallel 12x12 half diallel	÷	+ + +	Haque <u>et al</u> (1980) Kaushik & Sharma (1988) Singh & Shrivastava (1982) Jun & Kwak (1984) Mohapatra & Mchanty (1985)
14)	Harvest index	9x9 diallel LxT analysis 12x12 half diallel	+ +	+ +	Kuo & Liu (1987) Peng & Virmani (1990) Mohapatra & Mohanty (1985)
15)	Dry matter	9x9 diallel LxT analysis	+ +	+ +	Kuo & Liu (1987) Peng & Virmani (1990)

2.5 Character associations

Yield is a complex entity. There may not be genes for yield <u>per se</u> but rather for various components, the multiplicative interaction of which results in the artifact of yield. The study on association of yield components with grain yield is made by the breeders to fix up the characters which contribute for the yield.

Yield is positively correlated with all the traits observed by many workers (Table 2.4). Yield is also negatively correlated with many traits viz., plant height, number of tillers per plant, panicle length, number of filled grains per panicle, and test weight, as observed by some workers.

2.6 Variability

Improvement in any crop depends on the available genetic variability. A wide survey of genetic variability and a thorough understanding of genetic make up of the crop is indispensable for initiating an effective breeding programme. Table 2.5 indicates the amount of phenotypic variability, genotypic variability, phenotypic coefficient of variation, genotypic coefficient of variation and the coefficient of variation observed for different traits by many workers.

	aractor	Type of co with yi	rrelation eld	References		
character		Positive Negative				
	1	2	3	4		
1)	Plant height	÷ ÷	-	Devarathinam (1983) Choudhury et al (1976) Dzyuba et al. (1980) Eunus et al. (1976) Goud et al. (1969) Peng & Viramani (1990)		
			-	Kaul & Kumar (1982) Khaleque <u>et al.</u> (1978) Majumdar <u>et al.</u> (1971) Sukanya Subramanian & Rathinam (1984) Sun (1982)		
2)	Number of tillers	÷ ÷ + + +	-	Devarathinam (1983) Kaul & Kumar (1982) Reddy & Goud (1972) Sarathe et al. (1969) Singh et al. (1980) Sukanya Subramainiam & Rathinam (1984) Sun (1982) Wong Perez & De (1983)		
3)	No. of productive tillers	+ + + + + + + + + + + + + + + + + + + +		Devarathinam (1983) Balakrishna Rao et al. (1973) Choudhury et al. (1976) Dhanraj et al. (1987) Eunus et al. (1976) Hegde et al. (1977) Majumdar et al.(1971) Paramasivan (1986) Rao & Jagadish (1987) Singh (1980) Singh et al.(1980) Singh et al. (1980) Sun (1982)		

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Table 2.4 Review of literature on character association in rice.

	l	2	3.	4
4)	Panicle length	+ + + + +	_	Dhanraj <u>et al.</u> (1987) Khaleque <u>et al.</u> (1978) Lin (1969) Rao & Jagadish (1987) Sarathe <u>et al.</u> (1969) Shamsuddin (1986) Singh <u>et al.</u> (1980) Sukanya Subramaniam & Rathinam (1984) Sun (1982)
5)	Number of spikelets per panicle	+ +		Choudhury <u>et al.</u> (1980) Prasad <u>et al. (1</u> 988)
6)	Number of grains per panicle	+ + + + + + + + + + + +	_	Dhanraj et al. (1987) Dzyuba et al.(1980) Eunus et al. (1976) Hegde (1987) Kaul & Bhan (1974) Majumdar et al. (1971) Prasad et al. (1988) Rai & Murthy (1979) Rao & Jagadish (1987) Singh (1980) Singh et al. (1980) Sun (1982)
7)	Panicle weight	+ + +		Balakrishna Rao <u>et al.</u> (1973) Choudhury <u>et al.</u> (1973) Lin (1969)
8)	Test Weight	+ + + + + + +	-	Choudhury <u>et al.</u> (1980) Choudhury <u>et al.</u> (1973) Dhanraj <u>et al.</u> (1987) Majumdar <u>et al.</u> (1987) Prasad <u>et al.</u> (1988) Reddy & Goud (1972) Sarathe <u>et al.</u> (1969) Shamsuddin (1986) Singh (1980) Sukanya Subramanian & Rathinam (1984)

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Table 2.5.	Review of	literature	on variaility	y in rice.
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Cha	aracter	 PV	GV.	PCV	GCV	CV	Type of Study	Reference
	1	2	3	4	 5	 0	7	8
1)	Plant height	-	Н	-	Н	-	32 varieties	Balakrishna Rao <u>et al</u> (1973)
		-	Н	-	-	-	5 F ₂ lines	Chauhan (1990)
		Н	-	-	-	-	2 F ₂ crosses	Choudhury <u>et</u> <u>al</u> (1976)
		Н	-	_	-	-	34 varieties	Ghosh et al (1981)
		-	Н	-	-	-	40 varieties	Jogi & Hassan Baba (1971)
		-	-	Н	Н	-	30 varieties	Kaul & Bhan (1974)
		H	-	Н	Н	-	21 varieties	Kaul & Kumar (1982)
		Н	-	-	-	-	48 cultivars	Maurya et al (1986)
		-	-	Н	Н	-	10 ecotypes	Nema & Tiwari (1968)
		Η	-	-	-	-	2 crosses	Reddy & Goud (1972)
		-	L	-		-	30 varieties	Roychoudhury (1967)
		-	Н	-	-	-	5x5 half diallel	Sardana & Borthakur (1987)
		-	-	-	L	-	(16 lines) 13 crosses	Sen <u>et al</u> (1969)
		Н	-	Н	H	-	98 cultivars	Singh <u>et al</u> (1986)
2)	No.of tillers	Н	Н	-	-	Н	162 accessions	Amirthadevarathinam (1983)
		-	Н	-	-	-	5 F ₂ crosses	Chauhan (1990)
		Н	-	-	-	-	21 varieties	Kaul & Kumar (1982)
		-	-	Н	Н	-	10 ecotypes	Nema & Tiwari (1968)
			-	Н	Н	-	3 crosses	Sen <u>et al</u> (1969)
		Н	-	Н	Н	-	98 cultivars	Singh et al (1986)
		-	-	Н	Н	-	4 varieties	Sivasubramanian &
							(F ₂)	Madhava Menon (1973)
3)	No.of	H	H	-	-	H	162 accessions	Amirthadevarathinam
	produ- ctive	-	Н	Н	H	-	32 varieties	(1983) Balakrishna Rao <u>et al</u>
	CILLERS	-	Н	-	-	-	5 F ₂ crosses	(1973) Chauhan (1990)
		Н	-	-	-	-	2 inter varietal cross (F ₂)	Chaudhury <u>et al</u> (1976)

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	1	2	3	4	5	6	7		
		-	_	H	н		23 varieties	Chaudhury <u>et</u> <u>al</u> (1973)	
		Н	-	-	-	-	34 varieties	Ghosh et al (1981)	
		-		Н	-	-	40 varieties	Jogi & Hassan Babu (1971)	
		-	-	Н	Н	-	30 varieties	Kaul & Bhanl (1974)	
		-	-	Н	Н	-	10 ecotypes	Nema & Tiwari (1968)	
		-	н	-	-	-	5x5 half diallel	Sardana & Borthakur (1987)	
		Н	-	Н	H	-	179 varieties	Shukla <u>et al</u> (1972)	
		Н	-	H	H	-	98 cultivars	Singh <u>et al</u> (1986)	
		-	-	н	n	-	4 varieties	Sivasubramanian & Madhava Menon (1973)	
4)	Panicle	Н	_	-	_	_	2 crosses	Reddy & Goud (1972)	
- ,	length	_	L	-	-		30 varieties	Roychoudhury (1967)	
	-	-	Н	-	-	-	5x5 half	Sardana & Borthakur	
							diallel	(1987)	
		-	Н	-	-		53 varieties	Shamsuddin (1986)	
5)	Panicle	_	Н	H	Н	_	32 varieties	Balakrishna Rao et al	
	weight							(1973)	
		-	-	Н	Н	-	23 varieties	Choudhury <u>et</u> al (1973)	
		-	-	Н	Н	-	4 varieties	Sivasubramanian & Madhava Menon (1973)	
6)	No.of	-	Н	H	Н	-	32 varieties	Balakrishna Rao <u>et al</u>	
	panicle	Н	-		-	_	2 inter	Choudhury et al	
	L						varietal cross	(1976)	
		H	-	Н	Н	-	179 varieties	Shukla <u>et al</u> (1972)	
7)	No.of grain/	-	H	-	-	-	40 varieties	Jogi & Hassan Baba (1971)	
	panicle	-	-	Н	Н	-	30 varieties	Kaul & Bhan (1974)	
		Н				-	48 cultivars	Maurya <u>et</u> <u>al</u> (1986)	
		-	Н	-	-	-	5x5 half	Sardana & Brothakur	
		_	н		_	ਸ	53 varieties	(1907) Shamsuddin (1986)	
		-	_	H	H	-	4 varieties	Madhava Menon (1973)	
				<i>_</i>					

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		۔ ـ ـ ـ ـ	د 	4 		ю 	/ 	8
8)	Test weight	-	Н	Н	Н	-	32 varieties	Balakrishna Rao <u>et</u> <u>al</u> (1973)
		Η	-	-		-	2 inter varietal crosses (F ₂)	Choudhury <u>et al</u> (1976)
		H -	— Н	-	- -	-	34 varieties 40 varieties	Ghosh <u>et al</u> (1981) Jogi & Hassan Baba (1971)
		H	-	-	-	-	2 crosses	Reddy & Goud (1972)
		-	H H	L 	-	-	30 varieties 5x5 half diallel	Roychoudhury (1967) Sardana & Borthakur
		- Н	Н —	— Н	— Н	H -	53 varieties 179 varieties	Shamsuddin (1986) Shukla <u>et al</u> (1972)
9)	Yield/ plant	Η	Н	-	-	Η	162 accessions	Amirthadevarathinam (1983)
		-	-	Н	Н	-	l2 varieties	Awasthi & Borthakur (1986)
		-	Н	Н	Н	-	32 varieties	Balakrishna Rao <u>et al</u> (1973)
		Н	-	-	-	-	2 inter varietal crosses (Fa)	Choudhury <u>et al</u>
		-	-	Н	Н	-	23 varieties	Choudhury <u>et</u> <u>al</u> (1973)
		Н	Н	-	-	Н	2 crosses	Jangale et al (1985)
		-	Н	-	-	-	40 varieties	Jogi & Goud (1972)
		H	-	-	-	-	2 crosses	Reddy & Goud (1972)
		-	H	-		-	30 varieties	Roychoudhury (1967)
		-	Н	-	-	-	5x5 half diallel	Sardana & Borthakur (1987)
		-	-	Н	Н	-	3 crosses	Sen <u>et al</u> (1969)
		-	Н		-	Н	53 varieties	Shamsuddin (1986)
		H	-	H	H	-	179 varieties	Shukla et al (1972)
		н -	-	H H	H H	-	98 cultivars 4 varieties	Singh <u>et al</u> (1986) Sivasubramanian & Madhava Menon (1973)

H = High

L = Low

Ch	aracter	Herit- ability	Genetic advance	References
	1	2	3	4
1)	Plant	Н	Н	Balakrishna Rao <u>et</u> al (1973)
	height	Н	Н	Chauhan (1990)
		Н	H	Choudhury <u>et al</u> (1976)
		М	H	Ghosh <u>et al</u> (1981)
		М	M	Ghosh & Bhaumik (1985)
		L		Goud <u>et al</u> (1969)
		Н	H	Goud <u>et al</u> (1974)
		Н	Н	Kaul & Kumar (1974)
		Н	Н	Kaul & Kumar (1982)
		H		Kumar & Sree Rangaswamy (1986)
		н		Lin (1909)
		п u	п u	Majumdar et ar (19/1)
		п 5	п	Nome 6 Tivari (1966)
		п ч		Saratho ot al (1960)
		н		Sen et al (1969)
		н		Shukla et al (1972)
		н Н	ਸ	Singh et al. (1980)
		н		Singh et al (1980)
		Н		Singh et al (1986)
		Н	н	Singh & Sharma (1982)
		H		Singh & Patnaik (1969)
		H		Sivasubramanian & Madhava Menon (1973)
		H		Sun (1979)
		H	Н	Swamy Rao & Goud (1969)
		Н	Н	Talwar <u>et al</u> (1974)
2)	No.of	H	H	Amirthadevarathinam (1983)
	tillers/	Н	H	Chauhan (1990)
	plant	Н		Nema & Tiwari (1968)
		·H		Sarathe <u>et al</u> (1969)
		Н		Sivasubramanian & Madhava Menon (1973)
3)	No.of	Н	Ħ	Amirthadevarathinam (1983)
- /	productive	Н	Н	Balakrishna Rao et al (1973)
	tillers/	H	Н	Chauhan (1990)
	plant	н	Н	Chaudhury et al (1976)
	-		Н	Ghosh <u>et al (19</u> 81)
		H		Huang (1983)

Table 2.6. Review of literature on heritability and genetic advance in rice.

	1	2	3	4
		H H L M H H	H H L M H	Kaul & Bhan (1974) Majumdar et al (1971) Neema & Tiwari (1968) Paramasivan (1981) Shukla et al (1972) Singh & Nanda (1976) Singh et al (1980)
4)	Panicle length	H H H H H H H H H H	H	Choudhury et al (1976) Choudhury et al (1973) Ghosh et al (1981) Jogi & Hasan Baba (1971) Lin (1969) Paramasivan (1981) Sarathe et al (1969) Sen et al (1969) Shamsuddin (1986) Sinha & Patnaik (1969)
		H H		Sun (1979) Swamy Rao & Goud (1979)
5)	Panicle weight/ plant	H H H H H	H H H H	Balakrishna Rao <u>et al</u> (1973) Choudhury <u>et al</u> (1973) Lin (1969) Shukla <u>et al</u> (1972) Sivasubramanian & Madhava Menon (1973) Tripathi <u>et al</u> (1973)
6)	Grain yield/ plant	H H L H H H H H H H H H H H	Н Н Н Н Н Н Н Н Н Н Н Н Н	Amirthadevarathinam (1983) Awasthi & Borthakur (1986) Balakrishna Rao <u>et al</u> (1973) Ceng (1977) Choudhury <u>et al</u> (1976) Choudhury <u>et al</u> (1973) Ghosh & Bhaumik (1985) Jangale <u>et al</u> (1985) Kuo & Lin (1987) Paramasivan (1980) Shamsuddin (1986) Shukla <u>et al</u> (1972) Singh <u>et al</u> (1972) Singh <u>et al</u> (1974) Talwar <u>et al</u> (1974) Tripathi <u>et al</u> (1973)
	1	2	3	4
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7)	No.of	 H	н	Balakrishna Rao et al (1973)
. ,	spikelets/	H	Н	Choudhury et al (1980)
	panicle	H	н	Choudhury et al (1976)
	panioic	M		Huang (1984)
		M	м	Shukla et al (1972)
		н		Singh et al (1980)
		Н		Sinha & Patnaik (1969)
8)	No.of	H	H	Choudhury <u>et al</u> (1973)
	grains/	Н	H	Goud <u>et al</u> (1974)
	panicle	Н		Jogi & Hasan Baba (1971)
		Н	Н	Kaul & Bhan (1974)
		Н		Kim (1987)
		Н	Н	Majumdar <u>et al</u> (1971)
		Н	Н	Maurya et al (1986)
		Н	Н	Paramasivan (1980)
			Н	Paramasivan (1981)
		H	Н	Rai & Murthy (1979)
		Н		Sarathe et al (1969)
		Н	Н	Shamsuddin (1986)
		Н	Н	Singh et al (1980)
			Н	Singh & Sharma (1982)
		Н	Н	Sivasubramanian & Madhava Menon (1973)
		Н	Н	Sivasubramanian & Madhava Menon (1973)
	•	Н		Sun (1979)
		Н	Н	Swamy Rao & Goud (1969)
		Н	Н	Talwar (1974)
		H	н	Talwar et al (1974)
		H	Н	Tripathi et al (1973)
		••		
9)	Test	Н	Н	Balakrishna Rao et al (1973)
	weight	Н	H	Choudhury et al (1980)
		Н	Н	Choudhury et al (1976)
		Н		Choudhury et al (1973)
		Н		Ghosh & Bhaumik (1985)
		Н		Guo (1986)
		Н		Huang (1984)
		Н	Н	Maurya et al (1986)
		H	Н	Shamsuddin (1986)
		н	Н	Shukla et al (1972)
		H		Singh et al (1980)
		H		Singh &Sharma (1986)
		н		Sun (1979)
		H	Н	Tripathi <u>et al</u> (1973)
H	= High		 L =	Low M = Moderate

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2.7 Heritability and genetic advance

High heritability estimates have been reported for all the traits by many workers, while some workers have reported low heritability estimates for the traits days to 50 per cent flowering, plant height, number of productive tillers per plant, panicle length, and grain yield per plant as is evident from table 2.6. High genetic advance has been reported for all traits except for number of productive tillers per plant and panicle length which also showed low genetic advance.

MATERIAL AND METHODS

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III. MATERIAL AND METHODS

The present investigation was carried out at the Main Research Station (MRS) of the University of Agricultural Sciences, Hebbal, Bangalore during Kharif season of 1989-90 and summer season of 1990. The experiment included six fine-grained varieties of rice. The soil type of the experimental plot was sandy loam with a pH of 6.5. Irrigation was provided throughout the growth period.

3.1 Selection of Materials

The base material for the present study comprised of six fine grained lines of rice - Ambrose, HP-32, Pak-Basumathi, HP-33, HP-5 and HP-20 The salient features of the parental lines are presented below:

Varieties/Lines

Parentage

Salient features

1)	Ambrose	Variety from Iron	Semi-dwarf, high tillering, aromatic, long fine grain, very good quality.
2)	HP-32 (Parimala)	Pusa 150/ Basmathi-370	Medium tall, high tillering, aromatic, long fine grain, maturing in 130-135 days.
3)	Pak-Basmathi	Introduction from Pakistan	Tall, high tillering, aromatic, fine grain, late maturing, very good quality

4)	HP-33	Pusa 150/ Basmathi-370	Semi-dwarf, high tillering, aromatic, fine grain, early maturing, good elonga- tion on cooking.
5)	HP-5	KMS-1/ Basmathi-370	Semi-dwarf, moderate tillering, non-aromatic, long fine grain, early maturing.
6)	HP-20	Jaya/IET 7031// Jaya	Semi-dwarf, high tillering, mildly aromatic, long fine grain, early maturing, good grain elongation ratio.
7)	Basumathi-370 (Used as Check)		Tall, Sparse tillering, susceptible to lodging, very high good quality, not well suited for South Indian conditions (best under semi- temperate conditions), very high yielders, late maturing

3.2 Methods

3.2.1 Crossing programme

In order to derive 15 F_1 combinations, seeds of both female and male were raised. At the time of flowering each spikelet was emasculated by hand and pollinated with pollen from the other parents in diallel fashion to obtain 15 F_1 combinations. Since hand emasculation and pollination did not yield enough amount of F_1 seeds, the F_1 material was forwarded to the F_2 generation by selfing. This F_2 material constituted the material for diallel study.

3.2.2 Layout of the experiment

The trial comprising 21 treatments (15 $F_{2}s$ and 6 parents) were sown during summer 1990 in a randomised complete block design with three replications.

The recommended package of practices were carried out timely for the crop.

3.2.3 Recording of observations

The pre and post-harvest observations were recorded on 300 F_2 plants and on ten randomly setected plants in each of the parents and check. Data was recorded on the following quantitative characters.

3.2.3.1 Plant height

Plant height was measured in centimeters from the ground level to the tip of the plant at the time of harvest.

3.2.3.2 Number of tillers per plant

The total number of tillers produced per plant was recorded at the time of harvest.

3.2.3.3 Number of productive tillers per plant

The number of productive tillers per plant was recorded after full heading as the number of panicle bearing tillers.

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3.2.3.4 Panicle length

Length of the panicle was measured in centimeters from the base to the tip of the panicle at maturity.

3.2.3.5 Total dry matter per plant

The total dry matter production per plant was measured in grams after the harvested plant was completely dried.

3.2.3.6 Panicle weight per plant

The total weight of all the panicles per plant was recorded in grams.

3.2.3.7 Seed weight per plant

The total weight of all the filled grains per plant was measured in grams and expressed as seed weight per plant.

3.2.3.8 Number of spikelets per panicle

The total number of spikelets per panicle were counted.

3.2.3.9 Number of grains per panicle

The total number of grains per panicle were counted.

3.2.3.10 Grain length

Ten rice grains, of each treatment were arranged lengthwise, for the cumulative measurement of length in millimeters of the ten grains. The average length of the grains was computed and taken as grain length.

3.2.3.11 Grain breadth

Ten rice grains, of each treatment were arranged breadthwise, for the cumulative measurement of breadth in millimeters of the ten grains. The average breadth of the grains was computed and taken as grain breadth.

3.2.3.12 L/B grain ratio

The ratio of length to breadth (L/B) was obtained by dividing the length of each grain by its corresponding breadth.

3.2.3.13 Test weight

In each of the treatments, 100 grains were counted and their weights were recorded in grams as the test weight.

3.2.3.14 Harvest index

It was obtained by dividing the grain yield per plant by the total dry matter produced per plant and expressed as percentage.

3.2.3.15 Tiller fertility

It was obtained by dividing the number of productive tillers by the total number of tillers produced per plant and expressed as percentage.

3.2.3.16 Spikelet fertility

It was obtained by dividing the number of grains per panicle by the total number of spikelets produced per panicle and expressed as percentage.

3.3 Statistical analysis

The statistical analysis of the data on individual character was carried out on the mean values of each treatment over three replications. The statistical methods adopted were as follows.

3.3.1 Analysis of variance

Analysis of variance for individual character was done on the basis of mean values of each treatment over three replications. The model of analysis of variance is given below.

Source	Degrees of freedom	Mean sum of squares	Calculated F
Replications	(r-1) = 2	Mr	M _r /E
Treatments	(t-1) = 20	Mt	M _t /E
Parents	(p-1) = 5	Mp	M _p ∕E
Crosses	p (p-1)/2 =	l4 M _C	M _C /E
Parents vs. Crus∺es	1	M _{pc}	M _{pc} /E
Erro	(t-1) (r-1) =	40 E	
Total	(r.t-1) = 62		
Where, r = numb	er of replicatio	ns	
t = numb	er of treatments		
dmun = q	er of parents		

ANOVA TABLE FOR PARENTS AND CROSSES

3.3.2 Estimation of genetic variability and heritability

The coefficient of variability both at phenotypic and genotypic levels for all characters were calculated as suggested by Burton and Devane (1953).

a) Phenotypic coefficient of variability (PCV)

 $PCV = \frac{\sigma}{x} p$ Where σp = phenotypic standard deviation \overline{x} = population mean b) Genotypic coefficient of variability (GCV)

$$GCV = \frac{\sigma q}{----- X \ 100}$$
Where $\sigma g = genotypic standard deviation$

$$\frac{\pi}{X} = population mean$$

c) Estimation of heritability

Broadsense heritability was calculated using the formula suggested by Hansen et al.. (1956).

Percentage h² =
$$\sigma^2 g \times 100$$

 $\sigma^2 p$

d) Estimation of genetic advance

The genetic advance was calculated by using the formula as suggested by Lush (1949) and Johnson et al. (1956 b).

Genetic advance (GA) = $\frac{h^2}{---} \cdot \sigma^r p$. k

Where h² = heritability in broad sense
k = selection differential = 2.06 at
five percent selection intensity
p = phenotypic standard deviation.
Expected Genetic advance = GA
X
Where GA = genetic advance

X = Mean value for a particular trait.

These estimates were obtained using the programme GENO on VAX/VMS Microsystem II at UAS computer centre. 3.3.3 Heterosis

The overall mean value for each parent and F_2 cross from all the three replications for each character was taken to calculate heterosis. Heterosis of the F_2 crosses over mid-parent (MP), better parent (BP) and standard (SP) were calculated following the method proposed by Hayes <u>et al.</u> (1955) using the programme DIAL2 on VAX/VMS Microsystem II at UAS computer centre

Mid-parental value $(\overline{MP}) = ------2$

$$\overline{F_2} - \overline{MP}$$

Per cent heterosis over MP = ----- x 100

$$\overline{F}_2 - \overline{BP}$$

MP

Per cent heterosis over BP = ----- x 100

 $\overline{F_2} - \overline{SP}$ Per cent heterosis over standard (SP) = ----- x 100 \overline{SP}

Significance of the estimates of heterosis was tested by 't' test at error degrees of freedom as: 't' for heterosis over MP = ------Me 3 -- x r 2

't' for heterosis over BP and SP = $F_2 - \overline{BP}$ or \overline{SP} Me $--x \ 2$ r

Where, Me = error variance, and

r = number of replications,

3.3.4 Estimation of Correlations

The phenotypic and genotypic correlations among the traits studied in F_2 generation were computed by adopting the programme GENO on VAX/VMS Microsystem II at the UAS comouter centre as per the formula suggested by Robinson et al. (1957).

3.3.5 Path coefficient analysis

The direct path co-efficient was computed by using the programme GENO on VAX/VMS Microsystem II at the UAS computer centre by the abbreviated Doolittle technique as suggested by Goulden (1959).

3.3.6 Selection indices

The discriminant function analysis was done using the programme SELINDEX on VAX/VMS Microsystem II at the UAS

computer centre as per the method of Smith (1936) which expresses the phenotypic value of an individual in a linear form such as $Y = b_1x_1 + b_2x_2 + \dots + b_nx_n$ where, b_1 to b_n values are the weightage coefficients associated with the respective characters x_1 to x_n considered for selection.

The expected genetic gain through selection was predicted by the following formula

 $G = (Z/v) \sum_{i=1}^{i} \sum_{j=1}^{i} G_{ij} / (\sum_{i=1}^{i} \sum_{j=1}^{i} D_{j} P_{ij})^{1/2}$ Where Z/v is the standardized selection differential (S), indicating the intensity of selection (i), a_i is the economic weightage, b_i is the regression coefficient, G_{ij} is the genotypic variance - covariance matrix, and P_{ij} is the phenotypic variance - covariance matrix.

The relative efficiency of the selection indices was calculated using the formula:

Relative efficiency = Genetic gain from discriminate Genetic gain from straight selection

3.3.7 DIALLEL ANALYSIS

3.3.7.1 Combining ability analysis

General combining ability (GCA) of parents and specific combining ability (SCA) of the F_2 s were estimated using the programme DIALL on VAX/VMS Microsystem II by employing the procedure detailed by Griffing (1956 b), Method-2, Model-1, since reciprocal crosses were not included in the study, the mathematical model on which the analysis is based was assumed to be

$$x_{ij} = \mathcal{M}_{+g_{i} + g_{j} + s_{ij} + \frac{1}{---} \sum_{k} \sum_{h} \sum_{e_{ijkl}}^{t}$$

i, j = 1, n
k = 1, b
l = 1, c

Where, M = population mean

n = number of parental lines

- b = number of replications
- c = number of plants per family

i and j = the male and the female parents of ijth cross
g_i and g_j = the general combining ability (gca) effect for
the i and jth parents.

- S_{ij} = specific combining ability (sca) effect for the cross between ith and jth parents such that $S_{ij} = S_{ji}$
- eijkl = environmental effect associated with the ijklth
 individual observation.

The following restrictions are imposed on the combining ability elements:

 $\Sigma_i g_i = 0$ and $\Sigma_j S_{ij} - S_{ji} = 0$ (for each i)

This model further assumes that error (e_{ijkl}) is normally and independently distributed with zero mean and e^2 as variance.

Analysis of variance for combining ability

The ANOVA table for combining ability was constructed as below:

Source	d.f.	Sum of squares	Mean sum of squares	F-ratio
GCA	p-1	Sg	Mg	Mg/Me'
SCA	p(p-1)/2	Ss	Ms	M _s /M _e '
Error	(p-1)(p+2)(b-1)	S _e	M _e '	
	2			

The error term in the table was obtained as $M_e' = M_e/b$ where, M_e = error variance of the experiment as determined

by the general ANOVA, and

b = number of replications.

The two combining ability variances were tested for the 'F' ratio against M_e ' to test the significance.

The variances due to general and specific combining ability were calculated as follows:

$$s_{g} = \frac{1}{p+2} \sum_{i}^{2} (x_{i} + x_{ii})^{2} - \frac{4}{p} x^{2}$$

$$\begin{split} s_{s} &= \sum_{i} \sum_{j} x_{ij}^{2} - \frac{1}{p+2} \sum_{i} (x_{i} + x_{ii})^{2} + \frac{2}{(p+1)(p+2)} x^{2} \\ \end{split}$$

$$\begin{split} \text{Where, } s_{g} &= \text{sum of squares due to general combining ability} \\ s_{s} &= \text{sum of squares due to specific combining ability} \\ p &= \text{number of parents,} \\ x_{i.} &= \text{total of array of ith parent in diallel table} \\ x_{ii} &= \text{mean of ith parent,} \\ x_{..} &= \text{grand total of } p(p+1)/2 \text{ values of the diallel} \\ &= \text{table} \end{split}$$

 X_{ii} = value of each cell of the diallel table

Estimation of combining ability effects

The general combining ability (gca) effects and specific combining ability (sca) effects were estimated as follows:

gca effects $(g_i) = \frac{1}{p+2} \begin{bmatrix} (X_i + X_{ii}) - \frac{2}{p-x} \\ p \end{bmatrix}$ sca effects $(s_{ij}) = X_{ij} - \frac{1}{p+2} \\ x_{ii} + X_{ii} + X_{ij} + X_{jj} \end{bmatrix}$

(p+1)(p+2)

Where, X_{jj} the value of the jth parent in the diallel table.

Testing the significance of the combining ability

The variances of the different estimates were calculated by multiplying the error variance from the

combining ability with their respective coefficients as shown below:

Error variance $(X_{ij}) = Me = error variance from the$ RCBD analyşis

(p-1)Variance of $(g_i) = -----$ Me = variance of gca effects p(p+2)Variance of $(S_{ij}) = \frac{p^2 + (p+2)}{(p+1)(p+2)}$ Me = variance of sca effects

Testing the significance of difference between estimates

To test the significance of the difference between two estimates, the least significant difference was calculated by the product of table value of 't' at appropriate degrees of freedom for error and the standard error of the difference of the two estimates. The variances were obtained as follows:-

gca effects.

Variance of $(S_{ij} - S_{ik}) = \frac{2(p + 1)}{(p + 2)}$ Me- for testing differ-(p +2) ences between two estimates of sca effects in the same array.

Variance of $(S_{ij} - S_{kl}) = ------ Me - for testing (p + 2) differences$ differences between two estimates of sca effects in different arrays.

3.3.7.2 Analysis of diallel table for genetic components of variance

After construction of diallel table for each trait, the genetic components were computed by the methods of Jinks and Hayman (1953), Hayman (1954a, 1954b) and Jinks (1954, 1956) using the programme DIALL on VAX/VMS Microsystem II at UAS computer centre.

The diallel analysis by Hayman's (1954b) approach implies the following assumptions:

- i) homozygosity of parents
- ii) diploid segregation
- iii) no difference between reciprocals
- iv) independent action of non-allelic genes or no epistasis
- v) uncorrelated distribution of genes among the parents
 or no linkage
- vi) absence of multiple allelism

It is important to test the validity of these assumptions before proceeding with the genetic analysis. Hence, the t^2 test (Hayman 1954b) was applied in the present study, the value of t^2 was obtained by the formula,

 $(Var, V_r - Var, W_r)^2$ $t^2 = -\frac{p-2}{4}$ $(Var, V_r) (Var, W_r) - Cov^2 (V_r, W_r)$

which follows 'F' distribution with 4 and (p-2) degrees of freedom. Significance of t^2 value indicates the heterogenity of $(W_r - V_r)$ values and thereby indicating the failure of one or a few assumptions.

Calculation of various statistics of the
$$F_2$$
 diallel table

The following statistics were calculated from the diallel table. Each row was considered as an array.

$$V_r$$
 = Variance of the rth array

 W_r = Covariance between parents and their offspring in the r^{th} array

 $V_0L_0 = Variance of the parents$

 V_0L_2 = Variance of the array means

 V_1L_2 = Mean variance of the arrays

 W_0L_{02} = Mean covariance between the parents and the arrays ML₂ = Mean of 'p²' progeny

The above statistics comprised combinations of various genetical and environmental components and were as follows: $V_0L_0 = D+E$ $V_0L_2 = 1/4D + 1/16H_1 - 1/16H_2 - 1/8F + 1/pE_2$ $V_r = 1/4D - 1/4F_r + 1/4H_1 + [E + 1/2(p-1)E]/p$ $W_r = 1/2D - 1/4F_r + E/p$ $V_1L_2 = 1/4D + 1/16H_1 - 1/8F + E_2$ $W_0L_{02} = 1/2D - 1/8F + 1/pE_2$ $(ML_2 - ML_0) = 1/4p^2 + (p-1)(p-2)E + E/p^3$ Estimation of components of variation

With the expectations given above from F_2 diallel the six genetic components were estimated by using the following formulae:

 $D = V_0L_0 - E$ $F = 4 V_0L_0 - 8 W_0L_{02} - \frac{4(P-2)}{p}$ $H_1 = 16 V_1L_2 - 16 W_0L_{02} + 4V_0L_0 - \frac{4(5P-4)}{p} E_2$ $H_2 = 16 V_1L_2 - 16 V_0L_2 - \frac{16(p-1)}{p} E_2$ $h^2 = (4ML_2 - 4ML_0)^2 - 16(p-1) - E_2$ P $E = \frac{Error SS X Replication SS}{df}$ $E = \frac{df}{df}$ Number of replications

- Where, D = the variance due to additive effects of genes F = the mean of F_r values over the arrays H₁ = the variance due to dominance effects of genes H₂ = the proportion of dominance variance due to positive (u) and negative (v) effects of genes h² = the net dominance effects expressed as the algebraic sum over all loci in heterozygous phase in all crosses.
 - E₂ = the error variance obtained from the analysis of variance.

Testing the significance of the genetic components

The variance of $(W_r - V_r)/2$ was used as "S²" and the standard error of the various genetic parameters were calculated using the terms of the main diagonal of the covariance matrix of genetic components given by Hayman (1954b) and Jinks (1956). The formulae are as follows:



Where, p = number of parents.

The significance of the various statistics is tested by 't' test at p-2 degrees of freedom as

Proportion of the genetic components

With the help of six genetic components, the different types of proportions and differences of genetic components were worked out and the indications they give about the genetics of the trait are given below:

$$[1/4(H_1/D)]^{1/2}$$
 = mean degree of dominance over all loci.
(Verhalen et al., 1971)

- $H_2/4H_1 = 0.25$, proportion of genes with equal positive and negative effects
- $H_1-H_2 = 0$, showed that the positive (u) and negative (v) alleles at the loci controlling the character are in equal proportion in the parents.

 $KD = \frac{1/4(4DH_1)^{1/2} + 1/2F}{1/4(4DH_1)^{1/2} - 1/2F}$ the ratio of the total number of $1/4(4DH_1)^{1/2} - 1/2F$ dominant and recessive genes in all the parents.

K = h²/H₂ = estimate of number of groups of genes controlling a character and exhibiting dominance.

Heritability in narrow sense was calculated for each character using the formula given by Verhalen and Murray (1969) as:

Heritability = $\frac{1/4D}{1/4D+1/16H_1-1/8F+E}$

The correlation between Y_r (parental value) and order of dominance (W_r+V_r) was calculated by following the usual procedure adopted for calculation of correlation coefficient. High negative or positive correlation between Y_r and (W_r+V_r) indicates that positive or negative dominant genes are in excess, while decreasing value of either sign indicates that both positive and negative genes tend toward equal proportions in constituting dominance.

3.3.7.3 Graphical analysis

The graphic analysis was done following the method of Hayman (1954b) and Jinks (1956) to obtain the informations on the degree of dominance, order of dominance of parents and the genetic relationship among the parents. According to Hayman (1954b) statistical analysis coupled with the graphic representation provides the vivid genetic properties than the statistical analysis alone.

Regression of W_r on V_r

The regression of W_r on V_r was calculated as.

The expected regression line was drawn with unit slope and the co-ordinates were obtained by using straight line regression equation.

Y = a + bX

Where, $Y = W_r$ and $X = V_r$

The value of intercept 'a' was calculated as:

$$a = \overline{W_r} - b \overline{V_r}$$

The obserred regression line was obtained as:

 $W_r = a + b V_{ri}$

The standard error of the regression coefficient 'b' was calculated by using the formula: 1/2

 $S_{b} = \begin{bmatrix} (Y-\overline{Y})^{2} - b & (X-\overline{X}) & (Y-\overline{Y}) \\ (n-2) & (X-\overline{X})^{2} \end{bmatrix}$

Where, $X = V_r$, $Y = W_r$, and n = number of parents

The array values of V_r and W_r were plotted on the graph taking V_r along the x-axis and W_r along the Y-axis. The point of intersection of \overline{V}_r and \overline{W}_r was also plotted and joined by broken lines to their respective axes. The expected regression line was drawn for W_r , V_r values with unit slope. If the value of 'b' is not equal to unity, it indicates the presence of a large quantity of epistasis. Therefore, b-0 should be significant, while b-1 should S_b S_b S_b not be significant at n-2 degrees of freedom when 't' test

not be significant at n-2 degrees of freedom when 't' test is used. The values of limiting parabola (W_r 's) were calculated corresponding to each of the observed V_r values as: W_r for parabola = ($V_r \times V_0 L_0$)^{1/2}

The limiting parabola was drawn by plotting V_r , $(V_r \times V_0 L_0)^{1/2}$ points with minor intrapolation and extrapolation.

Wr' - Wr graph

Sometimes the non-significance of 'b' value from unity may not indicate the absence of epistasis. To establish the interactions $(W_r' - W_r)$ graph was constructed where $W_{r'}$ was the covariance of array members with array means of their non-recurring parents and W_r was the covariance of array members with their non-recurring parents. The theoretical regression line was drawn with 0.50 slope.

Standardized deviation graph

The standardized deviation graph of parental measurements (Y_r) and the order of dominance (W_r+V_r) was drawn by the method described by Johnson and Aksel (1959). The standardized deviation of Y_r and (W_r+V_r) was obtained using the formula:

x_i - x

Where, X_i = the value of the ith parent

X = the mean of the parents, and

S = standard deviation.

Correlation between standardized deviation ${\tt Y}_r$ and ${\tt W}_r {+} {\tt V}_r$ value was obtained by the formula.

 $r = \frac{(W_r + V_r)}{Var. std. Y_r x Var. std. (W_r + V_r)}$

3.4 Abbreviations used

P	arents	Symbol	assigned
	Ambrose	Pl	
HP-32	(Parimala)	P ₂	
	Pak-Basumathi	P3	
HP-33	(Vyshaki)	P ₄	
HP-5	(Sharavathi)	P5	
HP-20	(Nethravathi)	P ₆	

EXPERIMENTAL RESULTS

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IV EXPERIMENTAL RESULTS

The experimental results of $6x6 F_2$ diallel analysis in fine grained rice are presented under the following heads.

1. Mean performance of parents and F₂ crosses

- 2. Analysis of variance
- 3. Variability and heritability
- 4. Heterosis
- 5. Character associations

6. Path coefficient analysis

- 7. Diallel analysis
 - i) Combining ability analysis
 - ii) Genetic component analysis
 - iii) Graphical analysis, and
- 8. Selection indices
- 4.1 Mean performance of parents and F₂ crosses

The mean values of parents and crosses with respect to the sixteen characters are presented in the Table 4.1

4.1.1 Total dry matter per plant

The parental means ranged from 41.52 g (P_1) to 64.22 g (P_5), while of the crosses ranged from 44.07 g ($P_1 \times P_4$) to 77.89 g ($P_3 \times P_5$). The crosses transgressed the parental means only on the higher side.

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Parents/	the set of second set of set of a				2	urusses :	for yield	and yiel	d componen	ts in ri	ce,							
Crosses		Dry matter (g)	Plant heigh (cm)	Tota t tille:	l Pi rs i	roductive Fillers	Panicle length	Grain	Grain	L/B	Grain	Panicle	No. of					
	100 mil 10 mil 10 mil 10 mil 10 mil		*******				(cm)	(mm)	breadth (mm)	ratio	∀ield (g)	weight (g)	spikelet per	No.of grains per	Test weight (g)	Tiller fertility (%)	Fertility (%)	index (%)
rents										*****			panicle	panicle				
lmbrose	(P) 1	41.52	68,43	25,78		19,45	19.29	10										
2~32	(P) 2	46,70	80.59	26.33	1	19,25	22,47	9,03	2,31	4,35	22,31	27,70	102.39	71.83	1.88	75.52	70.18	53,75
sumathi	(P) 3	59,81	86,70	28,19	2	2 47	22.00	- 1 0 0	1.94	4.65	19,35	25.14	98.67	57.25	1.76	73.35	58,03	41.43
-33	(P) 4	60,65	77,77	25,50	2	2.69	22.77	9,74	2.44	3,99	20.00	28.15	119.97	69.17	1.82	79.79	57.65	33.50
-5	(P)	64,22	74,36	23,22	à	9.17	24.96	9166	8.34	3,95	33.03	42.61	102,72	70.50	2.93	89.01	68.68	54.51
-30	(8)	55.38	77.72	31.47			04.40	9.11	2.37	3.85	38.59	45.73	133.25	98.45	1.94	82.61	73.87	69.06
8865	6					s.78 .	21.13	10.21	8.21	4.63	22.71	30,68	96.19	58.30	1.65	78.79	60.62	h1 - A
8 P 8	1	18,18	77,91	24,50	21	.98 2	2,34	10.15	8,35	4.33	38,70	44,65	100.43	84,22	2,03	86.06	83.87	65.
3		8.22	83,04	\$3.03	34	,78 3	3.11	10.52	8,80	6.78	26,92	34,06	131.07	89,17	1.63	67,15	79.11	65,1
		8-87	88,73	17,76	33	. 83 - 2	1.35	10,10	3,30	6.38	11.21	81.83	100.30	68.30	1.84	67,43	68.16	85,4
1			88.86	83.85 19.25	10	.04 2 01 2	2.69	9.67	8.61	6.01	36,55	37.62	119,97	86.83	1.45	69.68	78,49	46.B
.*	63	.04 11	0.67	25.64	19		5.19	10.10	4.47	8.43	12.36	30.55	101.39	69.30	1.66	72.70	48,66	29.1
1			1.55	20.00			0.20	10.15	4.44	4,22	44.69	49.90	123.63	77.38	1.64	16.44	64,68	44
1			3.91	18.59	13.	1.2 21		9.50	6.64	8.78	48.78	44.80	114.24	69.59	4 - 6-4	88.69	71;6R	144 J
•	58.	63 Pi	6.61	83.62	16.	64 23	. 85	8.85		4.55	25.80	44.48	100.00	88.65	1.64	14.34	子利士植植	he.
1	¥9.	10 81		20.48	84.	61 33	. 10	10.41	4 418	6.63	17.60	23.65	114.117	00.17	1.74	99.79	fē:88 80.00	64
	19.1		.00	16.18	88.1	10 17	68	0.00	4.44.5	3,86	84. FA	64.67	444.44	86.61	6.88	99.39	61.26	44
	46.7	0 87	07 1	F, FA	11.1		10	8.44	6. 16.16	k:07	64.03	+4.10	100-10	1014 - 4 (4	1.41	84,84	86,88	
	£9,8		81 B	8,89	17.1	ið (†4	88	£0.90	6.24	6;10	88,16	18.99	149.74	68.64	1.00	19.64	65,69	
	69,00	78.	63 P	9.99	16.E	4 4	33	0.00	1.18	8.87	88.81	44,69	98.19	68.48	9:84	88,88	91.19	θ
	80,81	99,	(0 H		19.4	7	68	8.99	+ 14	ð,89	88,88	11.01	110.10	89.99	8,03	86,81	61.1	8
										1.25	26.55	4.94	104.10	67.34	1.65	87.41	64.1	

4.1.2 Plant height

The parental means ranged from 68.43 cm (P_1) to 86.70 cm (P_3), while of the crosses ranged from 75.65 cm (P_4xP_6) to 118.08 cm (P_3xP_5). The crosses transgressed the parental means only on the higher side.

4.1.3 Number of tillers per plant

The parental means ranged from 23.22 (P₅) to 31.47 (P₆), while of the crossed ranged from 17.73 (P₃xP₆) to 26.18 (P₃xP₅). The crosses transgressed the parental means only on the lower side.

4.1.4 Number of productive tillers per plant

The parental means ranged from 19.17 (P₅) to 24.78 (P₆), while of the crosses ranged from 11.93 (P₁xP₄) to 22.56 (P₃xP₅). The crosses transgressed the parental means only on the lower side.

4.1.5 Panicle length

The parental means ranged from 19.29 cm (P_1) to 24.25 cm (P_5), while of the crosses ranged from 17.68 cm (P_3xP_5) to 25.49 cm (P_2xP_3). The crosses transgressed the parental means on either limits.

4.1.6 Grain length

The parental means ranged from 9.03 mm (P_2) to 10.21 mm (P_6), while of the crosses ranged from 8.8 mm (P_4xP_6)

to 10.52 mm (P_1xP_3). The crosses transgressed the parental means on either limits.

4.1.7 Grain breadth

The parental means ranged from 1.94 mm (P_2) to 2.44 mm (P_3), while of the crosses ranged from 2.00 mm (P_2xP_5 and P_3xP_6) to 2.51 mm (P_3xP_5 and P_4xP_5). The crosses transgressed the parental means only on the upper limit.

4.1.8 Length to breadth ratio of grain

The parental means ranged from 3.85 (P₅) to 4.65 (P₂), while of the crosses ranged from 3.87 (P₄xP₆) to 4.80 (P₂xP₅). The crosses transgressed the parental means only on the upper limit.

4.1.9 Grain yield per plant

The parental means ranged from 19.35 g (P_2) to 38.59 g (P_5), while of the crosses ranged from 11.21 g ($P_1 x P_4$) to 38.70 g ($P_1 x P_2$). The crosses transgressed the parental means on either limits.

4.1.10 Panicle weight per plant

The parental means ranged from 25.14 g (P_2) to 45.73 g (P_5), while of the crosses ranged from 21.23 g ($P_1x P_4$) to 48.00 g ($P_4x P_5$). The crosses transgressed the parental means on either limits. 4.1.11 Number of spikelets per panicle

The parental means ranged from 96.19 (P_6) to 133.25 (P_5), while of the crosses ranged from 98.19 ($P_4x P_6$) to 156.10 (P_5xP_6). The crosses transgressed the parental means only on the upper limit.

4.1.12 Number of filled grains per panicle

The parental means ranged from 57.25 (P_2) to 98.45 (P_5), while of the crosses ranged from 48.30 ($P_1x P_4$) to 95.14 ($P_5x P_6$). The crosses transgressed the parental means only on the lower limit.

4.1.13 Test weight (100 seed weight)

The parental means ranged from 1.65 g (P_6) to 1.94 g (P_5), while of the crosses ranged from 1.62 g ($P_1x P_3$ and $P_2x P_5$) to 2.04 g ($P_4x P_6$). The crosses transgressed the parental means on either limits.

4.1.14 Tiller fertility

The parental means ranged from 73.35 per cent (P_2) to 89.01 per cent (P_4) , while of the crosses ranged from 67.15 per cent $(P_1x P_3)$ to 88.69 per cent $(P_2x P_4)$. The crosses transgressed the parental means only on the lower limit.

4.1.15 Spikelet fertility

The parental means ranged from 57.65 per cent (P_3) to 73.87 per cent (P_5) , while of the crosses ranged from 48.15 per cent $(P_1x P_4)$ to 83.87 per cent $(P_1x P_2)$. The crosses transgressed the parental means on either limits.

4.1.16 Harvest index

The parental means ranged from 33.50 per cent (P_3) to 60.06 per cent (P_5) , while of the crosses ranged from 25.43 per cent $(P_1 x P_4)$ to 65.39 per cent $(P_1 x P_2)$. The crosses transgressed the parental means on either limits.

4.2 Analysis of variance

Analysis of variance for RBD comprising of 21 treatments (6 parents and 15 F_2 crosses) grown in three replication, is presented for the sixteen characters studied in Table 4.2.

The treatment effects were highly significant for all the characters studied. Further partitioning of the treatment sum of squares revealed that the parents varied highly significantly for all the characters studied. The crosses also showed highly significant differences for all the characters studied. Similarly interaction effect, parents vs. crosses also exhibited high significance for most of the characters studied except spikelet fertility .

Table 4.2 Mean squares due to different sources for some traits in rice.

Characters	means sum of squares que to										
	Treatment (20 d.f.)	Parents (5 d.f.)	Crosses (14 d.f.)	Pa.vs.cr. (l d.f.)	Error (40 d.f.)						
Dry matter	228.73**	234.13**	243.03**	1.63	2.75						
Plant height	565.17**	111.80**	620.80**	2053.18**	2.43						
Total tillers	38.45**	23.72**	21.85**	344.42**	2.34						
Productive tillers	35.67**	16.56**	26.65**	257.61**	1.94						
Panicle length	10.93**	8.87**	11.59**	11.92**	1.02						
Grain length	0.78**	0.78**	0.71**	1.78**	0.03						
Grain breadth	0.07**	0.09**	0.07**	0.002	0.004						
L/B ratio	0.32**	0.37**	0.31**	0.23**	0.02						
Grain yield	170.53**	187.57**	176.57**	0.77	2.40						
Panicle weight	152.71**	223.53**	232.97**	75.02**	2.46						
No.of Spikelets per panicle	748.79**	637.30**	766.27**	1061.52**	4.33						
No.of grains per panicle	627.31**	664.71**	615.94**	599.54**	3.63						
Test weight	0.06**	0.04**	0.08**	0.004	0.001						
Tiller fertility	134.12**	92.26**	154.87**	52.90**	5.52						
Spikelet fertility	227.33**	144.36**	272.11**	15.13*	2.27						
Harvest index	423.11**	312.43**	492.72**	2.00	6.35						
* Significant at			** Sia	nificant at							

t

percentage which was significant only at 5% level of significance and also total dry matter per plant, grain breadth, grain yield per plant, 100 seed weight and harvest index, which were non-significant.

4.3 Components of variability and heritability

The phenotypic and genotypic variances, phenotypic and genotypic coefficent of variability and the values of genetic advance and heritability (broad sense) are presented for the 15 F_2 crosses in Table 4.3.

4.3.1 Total dry matter per plant

The estimated values of phenotypic and genotypic coefficient of variation were 16.54 and 16.24, respectively for the crosses. The phenotypic and genotypic variances were 82.96 and 80.03, respectively. Heritability and genetic advance estimates were 96.48 per cent and 18.10, respectively. The genetic advance as percentage of the mean was 32.87.

4.3.2 Plant height

The character showed phenotypic and genotypic coefficient of variation values of 16.10 and 15.91, respectively. The phenotypic and genotypic variance were 208.60 and 206.11, respectively. The heritability and genetic advance values were 98.81 per cent and 29.40,
Table 4.3 Varia in ri	nces, coeff ce.	icients of v	Ariances, heri	tability and g	enetic advance	for differ	ent trait
Characters	Phenotypic varíance	Genotypic variance	Phenotypic coefficient of variation	Genotypic Genotypic coefficient of variation	Heritabi- lity (%) (broad sense)	Genetic advance	GA as percent of mean
Dry matter	82.96	80.03	16.54	16.24	19.48	18.10	32.87
Plant height	208.60	206.11	16.01	15.91	98.81	29.40	32.58
Total tillers	8.90	6.47	13.83	11.79	72.70	4.47	20.72
Productive tillers	10.37	8.14	19.14	16.96	78.48	5.21	30.98
Panicle length	4.38	3.60	9.19	8.33	82.22	3.55	15.58
Grain length	0.25	0.23	5.01	4.84	93.12	0.95	9.67
Grain breadth	0.03	0.02	7.02	6.57	87.49	0.29	12.72
L/B ratio	0.11	0.10	7.59	7.22	90.89	0.62	14.19
Grain yield	60.52	58.03	30.20	29.57	95.89	15.37	59.67
Panicle weight	45.98	43.50	18.97	18.45	94.49	13.21	36.95
No.of Spikelets per panicle	258.46	253.89	13.63	13.51	98.23	32.53	27.58
No.of grains per panicle	207.68	204.13	18.54	18.38	98.29	29.18	37.53
Test weight	0.03	0.02	8.82	8.70	97.40	0.32	17.68
Tiller fertility	55.51	49.68	9.58	9.06	89.51	13.74	17.66
Spikelet fertility	92.23	89.94	14.57	14.39	97.52	19.29	29.26
Harvest ind ex	168.36	162.18	27.62	27.11	96.33	25.75	54.81
8 8 8 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		c 8 1 1 1 1 1 1 1	t 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	7 4 4 1 1 1 1 1 1 1 1 1 1		1 1 1 1 1 1 1 1 1 1	60

respectively. The genetic advance as a percentage of mean was 32.58.

4.3.3 Number of tillers per plant

The phenotypic and genotypic coefficient of variation values were 13.83 and 11.79, respectively. The phenotypic and genotypic variance values were 8.90 and 6.47, respectively. The heritability and genetic advance values were 72.70 per cent and 4.47, respectively. The genetic advance as percentage of mean was 20.72.

4.3.4 Number of productive tillers per plant

The phenotypic and genotypic coefficient of variation were 19.14 and 16.96, respectively. The phenotypic and genotypic variance values were 10.37 and 8.14, respectively. The heritability and genetic advance estimates were 78.48 per cent and 5.21, respectively. The genetic advance as percentage of mean was 30.98.

4.3.5 Panicle length

The phenotypic and genotypic coefficient of variation estimates were 9.19 and 8.33, respectively. The phenotypic and genotypic variances were 4.38 and 3.60, respectively. The heritability and genetic advance estimates were 82.22 per cent and 3.55, respectively. The genetic advance as percentage of mean was 15.58.

4.3.6 Grain length

The phenotypic and genotypic coefficient of variation estimates were 5.10 and 4.84, respectively. The phenotypic and genotypic variance values were 0.25 and 0.23, respectively. The heritability and genetic advance estimates were 93.12 per cent and 0.95, respectively. The genetic advance as percentage of mean was 9.57.

4.3.7 Grain breadth

The phenotypic and genotypic coefficient of variation values were 7.02 and 6.57, respectively. The phenotypic and genotypic variance values were 0.03 and 0.02, respectively. The heritability and genetic advance values were 87.49 per cent and 0.29, respectively. The genetic advance as percentage of mean was 12.72.

4.3.8 Length to breadth ratio of grain

The estimated values of phenotypic and genotypic coefficient of variation were 7.59 and 7.24, respectively. The values of phenotypic and genotypic variances were 0.11 and 0.10, respectively. The heritability and genetic advance values were 90.89 per cent and 0.62, respectively. The genetic advance as percentage of mean was 14.19.

4.3.9 Grain yield per plant

The values of phenotypic and genotypic coefficient of variation were 30.20 and 29.57, respectively. The phenotypic and genotypic variances were 60.52 and 58.03, respectively. The heritability and genetic advance values were 95.89 per cent and 15.37, respectively. The genetic advance as percentage of mean was 59.67.

4.3.10 Panicle weight per plant

The estimates of phenotypic and genotypic coefficient of variation were 18.97 and 18.45, respectively. The phenotypic and genotypic variance values were 45.98 and 43.50, respectively. The heritability and genetic advance values were 94.59 per cent and 13.21, respectively. The genetic advance as percentage of mean was 36.95.

4.3.11 Number of spikelets per panicle

The phenotypic and genotypic coefficient of variation were 13.63 and 13.51, respectively. The phenotypic and genotypic variance values were 258.46 and 253.89, respectively. The heritability and genetic advance estimates were 98.23 per cent and 32.53, respectively. The genetic advance as percentage of mean was 27.58.

4.3.12 Number of filled grains per panicle

The values of phenotypic and genotypic coefficient of variation were 18.54 and 18.38, respectively. The values of phenotypic and genotypic variances were 207.68 and 204.13, respectively. The values of heritability and genetic advance were 98.29 per cent and 29.18, respectively. The genetic advance as percentage of mean was 37.53.

4.3.13 Test weight

The values of phenotypic and genotypic coefficient of variation were 3.82 and 8.70, respectively. The phenotypic and genotypic variances were 0.03 and 0.02, respectively. The heritability and genetic advance estimates were 97.40 per cent and 0.32, respectively. The genetic advance as percentage of mean was 17.68.

4.3.14 Tiller fertility

The phenotypic and genotypic coefficient of variation values were 9.58 and 9.06, respectively. The values of phenotypic and genotypic variances were 55.51 and 49.68, respectively. The heritability and genetic advance estimate values were 89.51 per cent and 13.74, respectively. The genetic advance as percentage of mean was 17.66.

4.3.15 Spikelet fertility

The phenotypic and genotypic coefficient of variation values were 14.57 and 14.39, respectively. The phenotypic and genotypic variance values were 92.23 and 89.94, respectively. The heritability and genetic advance estimates were 97.52 per cent and 19.29, respectively. The genetic advance as percentage of mean was 29.26.

4.3.16 Harvest index

The estimated values of phenotypic and genotypic coefficient of variation were 27.62 and 27.11, respectively. The phenotypic and genotypic variances were 168.36 and 162.18, respectively. The heritability and genetic advance estimates were 96.33 per cent and 25.75, respectively. The genetic advance as percentage of mean was 54.81.

4.4 Heterosis

The extent of heterosis expressed as percentage increase or decrease over mid parent (MP), better parent (BP) and standard parent (SP) are presented in Table 4.4. The results obtained are presented here under.

4.4.1 Total dry matter per plant

Five of the fifteen crosses showed highly significant positive heterosis over mid parent. Six out of fifteen crosses showed negative and significant heterosis, Table 4.4 Estimates of percentage of heterosis over mid-pare

Lare	^c , better par
	Parent and standard for yield and yield attributes in rice.

Crosses		otal dry ma	atter		Plant he	i ch t												
0100000	H M.P	leterosis % B.P	Over		Heterosis %	0ver		Total till	ers	Prod	uctive til	lers	Panic	le length	3	G	rain leng	th
				M.P.	B.P.	Standard	He M.P.	terosis % B.P.	Over Standard	Het M.P.	erosis % B.P.	Over Standard	Heter M.P.	osis % (B.P.	Dver Standard	Het M.P.	erosis % B.P.	Over Standard
P x P 1 2	34.15**	26.71**	- 2.36	4.57**	-3.33*	-18.70**	- 5.97											
P x P 1 3	-4.83*	-19.38**	-20.44**	7.06**	-4.22**	-13.35**	-18.40**	-6.96	21.4/**	8.95	8.40	19.91**	6.98*	-0.59	-7.46*	6.34**	0.86	2.94
P x P 1 4	-13.74**	-27.34**	-27.29**	36.42**	28.22**	4.06**	-30.73**	-31.10**	-11.95**	-43.40**	-47.44**	-13.87*	5,14	-2.90	-8.41*	6.28**	4.5/**	2 43
P x P 1 5	11.95**	-7.83**	-2.34	34.36**	29.00**	0.09	-10.81*	-15.23**	8.33	-22.12**	-22.68**	-14.45*	4.22	-6.45	-6.01	0.89	-3.88*	-1.93
P x P 1 6	7.90**	-5.60*	-13.74**	56.94**	47.56**	19.68**	-32.76**	-38,85**	-4.56	-32.55**	-39.81**	-15.19*	22.13**	16.73**	2.32	-2.68*	-3.36*	0.00
P x P 2 3	20.06**	6.91**	5.94*	32.31**	27.65**	15.49**	-5.06	-8.49	28.31**	-7.77	-14.39**	9.44	12.70**	11.96**	5.59	11.83**	7.73**	6.39**
P x P 2 4	-15.18**	-24.93**	-24.88**	3.00*	1.20	-14.89**	-19.40**	-20.67**	3.57	-11.60*	-18.30**	5.46	1.98	-1.39	-8.20*	14.54**	13.29**	5.98**
P x P 2 5	-2.08	-15.43**	-10.39**	8.04**	,3.86 *	-12.65**	-24.97**	-29.41**	-7.83	-30.13**	-30.29**	-23.66**	4.45	0.62	1.08	5.62**	5,12**	-2.84
PxP	-2.96	-10.57**	-18.28**	-3.22*	-4.94**	-20.06**	-18.28**	-24.95**	17.10**	-11.25*	-21.15**	11.15	1.07	-1.88	~8.66*	2.46	-3.46*	-0.10
PxP	-12.51**	-13.12**	-13.05**	10.10**	4.43**	-5.52**	-23.83**	-27.47**	1.39	-35.29**	-35.61**	-16.89**	1.26	-2.71	-8.24*	9.74**	6.84**	5.58**
P x P	25.60**	21.29**	28.51**	46.63**	36.20**	23.22**	1.83	-7.15	29.80**	8.34	0.37	28.33**	-24.79**	-27.09**	-26.76**	5.66**	2.26	1.01
3 5 P x P	-18.92**	-21.92**	-22.95**	5.91**	0.43	-9.14**	-40.56**	-43.66**	-12.10*	-37.30**	-40.21**	~15.76*	9.74**	5.86	-0.17	-6.25**	-8.39**	-5.17**
3 6 P x P	0.34	-2.45	3.37	6.77**	4.43**	-15.26**	-7.13	-11.28*	12.15*	-14.33**	-20.99**	1.99	8.36**	1.06	1.53	11.89**	11.20**	4.06*
4 5 P x P	-15.47**	-19.14**	-19.09**	-2.70	-2.73	-21.05**	-29.62**	-36.30**	-0.59	-3.45**	~33.38**	-0.09	8 69**	1.76	2 24	-1.00	-6.30*	* -3.04
4 6 P x P	1.74	-5.26*	0.38	1.39	-0.80	-19.55**	-18.77**	-29.42**	10.11	-20.4/**	-29.48	-0.03				-1.00		
5 6		1.25	1.35	1.12	1.29	1.29	1.07	1.22	1.22	0.98	1.09	1.09	0.73	0.89	0.89	0.13	0.16	0.16
5.£. (+)	1.18	1.35																

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*********	7.25- ** 51.5	10- **†C'9	- 22.2-	-2.11	++61.34-	**/1.02-	+*09.66-	**87.72-	**50.88-	**87.65-	90.5	11.0		SZ"T-	/C*T-	1	I
10** 30.02**	8.11- 66.1	1.92**	I **16*6-	1.62	-2° 02	**71.81-	50.1	00.0	-31.19**	-12.90**	+2°°2+	-)*8544	57.7-	54.5	E8.1	90.5	
10100 - 38 1244	1.23** -31.3	2- **14.2.	- 81.0-	11.5	-35.48**	14.0-	49.4	-15' 25	-32.79**	-32.20**	5.35	+44.5-	76°Z-	-5"28	-5" 05	22.0	I P axa
*****************	11 ++27.22	**6S.AI	2.38	15.36**	**20°6-	56.11**	33.22**	*ES'II-	**74.71	**51.01	*90*4	-5*12	*S5.33*	98.0-	+91"5-	*25°S	5 3 5 X 5
19 61 19 61	56, 03 ** 11	s.16**	** £7.6	** 26.11	-16.52**	**87.22-	78.2-	SL*0	-13.02**	2.13	**65*01	1.22	a.42**	24.7-	66**-	TQ*E	5 T
10101 01	13.61** -10	**86.41	**05*1-	e*52**	+*90.81-	-27,66**	-9*92-	**£3.61-	**65 *01-	-20.96**	12.94**	0E*E	15"8**	++91.41-	**S1"SI-	++27-4-	s a a x b
-Co'IC	15 ++09"25	12,86**	22.60**	24.16**	**96.8-	**26.91-	28.54**	-5.82	*65*EI-	-55' 68**	*90°L	-5' 12	48°T-	+28*9-	96.1-	55.4	9 X 5
TOTE TE		7.26**	**/1'*-	3.25*	-24.74**	**07*0E-	**/1.91-	**17.55-	**11.91-	++19"6E-	*65*9	**17.EL		-1.29	.00*9-	26°E-	t E X
	51- 16.1-	54.26**	S0.0-	2*50**	2.69	*0S-11-	**LS*6	10.6-	-33.28**	-15.11**	-6.82*	65.0-	11.1	** 57.77	2.86	• 57 "7	5 2 3
561	- ++L1"L	66.0-	-1.48**	92°T-	**75.21-	-10.05*	**87.41	-10*35*	48.4	**02.11-	**88.6	80.1	**52.8	**91.41	- **10.8	I- ++06°EI	- 2
1 65 **59.6	- **05"5	**95° <i>L</i> Z	2.61*	**88*SI	**08.12	12.4	**89.8	** 57.54	-1-15	*22.9	-3*23	17.E	*00*S	*57.7	*11.8	*****	E.
	·91'6	**07.8-	**14.4-	12.1-	**90.11-	**£7,71-	46.4-	6.63	**82.41-	65°T	** 76.8-	-16.23**	**69*6	- 51.5	- 99"	2- 22°0	9.9
-2.54 42.	22.42**	**63.22	**SI.TI	36*07**	11.72**	-3.72	15.24**	35"32**	** 26*9-	**88.41	*09*2-	**{S.\$4	- **28.8	3- 98.5	sz.	2 ** 28.6	
t <u>1</u> 5.t	1.35	£7.1	£7.1	05.1	1.33	£E.1	1.14	05.1	0E.I	51.1	0.12	0.12	60.	0 90*0	0 90	"0 SO'	·o (-

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** Significant at 1% level.

* Significant at 5% level

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66.64	\$\$1.67	**17'48 .	**78.66	**28°61	** 18,05	vs.1-	**86'ET	**19.81	** 66'01	**68*2	**99'TT	a ×	
55.75	78.5	\$27,98	**10.91	*01.4	**86.41	**81.62-	**90*9T-	**62.61-	**84.11-	**68*61-	-12,49**	d × z	Y
06'17-	**76.52-	**10°£5-	-22,32	**66.16-	**29,05-	22,86**	-24.24**	** 60.01-	55.0	++25.4-	*74.6-	a x E	1
64,5	**05.32-	-21.16**	**62.21	10.2-	05"0	** 64.15-	++90'91-	** 61 * 61-	60°T	*69.4-	*20*8-	d x	
ALL CE-	**12*57-	-38.42**	**05*22-	-30'67**	**09.25-	**11,11-	75.1-	97.0	49.1	09.1-	**00*9	s	
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34.32*	=98*/	95'77		- 20*2	12.78**	97*1	95*0-	**97'6	10*01-	85'ST-	0/*11-	7	×
86.6-	-50'28**	**99.91-	**87*71	-5.69	**66'8	**95.71-	-15'28**	**75.7-	**87'II-	**75-91-	++96'31-	s ď	×
96.81	**69'52	56.32	**/0'91	\$\$*72'02	**28.22	**6£'S-	*60'S	8.78**	**97'5-	ZS*1-	£8°T	d	×
-22,69**	** 26.75-	-53'10**	**/S'S-	-13.67**	**71.8-	**06'21-	**86.01-	**86.41	**97'5-	**20°0T-	**85'/-	d 9	×
*07.42-	*16'77-	**72.25-	79°T-	**07'91-	**60.9-	0T.I-	*95*7	**86.8	2.73	-3.00	11.0	d 7	2
*E7'9T	**52.42	**67.35	2*36	**70.8	**£7.8-	*22-7-	2E.4	*70*5	**95'9-	**72*9-	29.1-	d S	
*05.6£	69.1	*09.9	3.62	**66,11-	**27.8-	**98.8-	**22.01-	**61 2-	**72.8	75 6	*80 2	9	
	28.9	**08 00	***** 71	*96 /	**32 01	**32 3-	**17 2-	52 1-	**0 / **			S	
0110	5010	00107	C0.161	0715	0/107	C/'C-	hh*/-	C/*T-	DH*TT	2*93.	TO * #T	9	
	15.4-	**17.51	-2.12	**08.31-	**19'8-	**56*6-	+72.12*	-2°71	**66.01	**IE'7	12.75**	9 3	t
					<i>,</i>								
2'1'	2.17	78°T	72°1	1.24	7.07	18.1	1.82	19.1	0.03	£0.03	920.0	(+)	5

of which five were highly significant. Hybrid vigour ranged from -18.92 (P₃x P₆) to 34.15 (P₁x P₂) per cent over mid parent.

In the present study the parent with maximum total dry matter per plant was considered as better parent. Three of the fifteen crosses showed significant positive heterosis over better parent. Eleven out of fifteen crosses manifested negative and significant heterosis over better parent. The heterosis over better parent ranged from -27.34 (P₁x P₄) to 26.71 (P₁x P₂) per cent.

Two out of fifteen crosses showed significant positive heterosis over standard parent. Nine of the fifteen crosses showed significant negative heterosis over standard parent. The heterosis over standard parent ranged from -27.29 (P₁x P₄) to 28.51 (P₃x P₅) per cent.

4.4.2 Plant height

Twelve of the fifteen crosses showed significant positive heterosis over mid parent, while only one cross showed significant negative heterosis over mid parent. The hybrid vigour ranged from -3.22 (P₂x P₆) to 56.94 (P₁x P₆) per cent over mid parent.

Eight out of fifteen crosses showed significant positive heterosis over better parent. Three of the fifteen crosses showed a negative and significant heterosis over better parent. The heterosis over better parent ranged from -4.94 (P₂x P₆) to 47.56 (P₁x P₆) per cent.

Four of the fifteen crosses showed significant positive heterosis over standard parent and ten of the fifteen crosses showed a significant, negative heterosis over standard parent. The heterosis over standard parent ranged from -21.06 (P₄x P₆) to 23.22 (P₃x P₅) per cent.

4.4.3 Number of tillers per plant

Of the fifteen crosses, eleven crosses showed a significant negative heterosis over mid parent, while none of the crosses showed a significant positive heterosis over mid parent. The heterosis over mid parent ranged from -40.56 (P₃x P₆) to 1.83 (P₃x P₅) per cent.

Twelve of the fifteen crosses showed a significant negative heterosis over better parent, while none of the crosses showed significant positive heterosis over better parent. The heterosis over better parent ranged from -43.66 ($P_{3}x P_{6}$) to -6.96 ($P_{1}x P_{2}$) per cent.

Five of the fifteen crosses showed a significant positive heterosis over the standard. Two of the fifteen crosses showed a significant negative heterosis over standard parent. The heterosis over standard ranged from -12.10 (P₃x P₆) to 29.80 (P₃x P₅) per cent.

4.4.4 Number of productive tillers per plant

Twelve out of the fifteen crosses showed a significant negative heterosis over the mid parent, while none of the crosses showed a significant positive heterosis over mid parent. The range of heterosis over mid parent was from -43.40 (P₁x P₄) to 8.95 (P₁x P₂) per cent.

A significant and negative heterosis over the better parent was shown by thirteen of the fifteen crosses, while none of the crosses showed a significant positive heterosis over better parent. The heterosis over better parent ranged from -47.44 (P₁x P₄) to 8.40 (P₁x P₂) per cent.

Two of the fifteen crosses showed a significant positive heterosis over standard, while seven of the crosses showed a significant negative heterosis over the standard. The heterosis over the standard ranged from -32.14 (P₁x P₄) to 28.33 (P₃x P₅) per cent.

4.4.5 Panicle length

Only one of the fifteen crosses showed significant negative heterosis over mid parent, while six of the crosses showed significant positive heterosis over mid parent. The range of heterosis over mid parent varied from -24.79(P₃x P₅) to 22.13 (P₁x P₆) per cent. Only one of the fifteen crosses showed significant negative heterosis over better parent, while two of the crosses showed a significant positive heterosis over better parent. The heterosis over better parent ranged from -27.09 (P₃xP₅) to 16.73 (P₁xP₆) per cent.

Eight of the fifteen crosses showed significant negative heterosis over the standard, while none of the crosses showed a significant positive heterosis over the standard. The heterosis over the standard ranged from -26.76 (P₃xP₅) to 5.59 (P₂xP₃) per cent.

4.4.6 Grain length

Nine of the fifteen crosses showed significant positive heterosis over the mid parent. Three of the fifteen crosses showed a significant and negative heterosis over the mid parent. The heterosis over mid parent ranged from -9.47 (P₄x P₆) to 14.54 (P₂x P₄) per cent.

Six out of the fifteen crosses showed a significant positive heterosis over the better parent, while another six crosses showed significant negative heterosis over the better parent. The range of heterosis over better parent varied from -13.81 ($P_4x P_6$) to 13.29 ($P_2x P_4$).

Five of the fifteen crosses showed a significant positive heterosis over the standard, while two other crosses showed significant negative heterosis over the

standard. The heterosis over standard ranged from -10.75 (P₄x P₆) to 6.69 (P₁x P₃) per cent.

4.4.7 Grain breadth

Five of the fifteen crosses showed a significant positive heterosis over mid parent, while three other crosses showed significant negative heterosis over mid parent. The range of heterosis over mid parent varied from -13.90 (P₃x P₆) to 10.26 (P₁x P₂) per cent.

Five of the fifteen crosses showed a significant negative heterosis over better parent, while only one of the other crosses showed a significant positive heterosis over better parent. The heterosis over better parent ranged from -18.01 (P₃x P₆) to 5.77 (P₄x P₅) per cent.

Four of the fifteen crosses showed a significant negative heterosis over the standard, while two of the other crosses showed a significant positive heterosis over the standard. The heterosis over the standard ranged from $-14.16(P_{2}x P_{5} \text{ and } P_{3}x P_{6})$ to 7.73 ($P_{3}x P_{5} \text{ and } P_{4}x P_{5}$) per cent.

4.4.8 Length to breadth ratio of grain

Eight of the fifteen crosses showed a significant positive heterosis over mid parent while two of the other crosses showed a significant and negative heterosis over mid parent. The range of heterosis over mid parent varied from $-9.69 (P_4 x P_6)$ to 14.75 $(P_1 x P_3)$ per cent.

Two of the fifteen crosses showed a significant positive heterosis over better parent, while five of the other crosses showed significant negative heterosis over better parent. The heterosis over better parent ranged from -16.23 (P₄x P₆) to 13.71 (P₃x P₄) per cent.

Seven of the fifteen crosses showed significant positive heterosis over the standard, while four of the other crosses showed a significant negative heterosis over the standard. The heterosis over standard ranged from -8.94(P₄x P₆) to 12.94 (P₂x P₅) per cent.

4.4.9 Grain yield per plant

Seven of the fifteen crosses showed a significant positive heterosis over mid parent, while six other crosses showed significant negative heterosis over mid parent. The heterosis over mid parent ranged from -59.48 ($P_1x P_4$) to 85.81 ($P_1x P_2$) per cent.

Four of the fifteen crosses showed a significant positive heterosis over better parent, while nine other crosses showed significant negative heterosis over better parent. The range of heterosis over better parent varied from -66.05 ($P_1x P_4$) to 73.45 ($P_1x P_2$) per cent.

Three of the fifteen crosses showed a significant positive heterosis over the standard, while six other crosses showed significant negative heterosis over standard. The heterosis over standard ranged from -57.78(P₁x P₄) to 45.76 (P₁x P₂) per cent.

4.4.10 Panicle weight per plant

Eight of the fifteen crosses showed significant positive heterosis over mid parent, while three other crosses showed significant negative heterosis over mid parent. The range of heterosis over mid parent varied from -39.60 (P₁x P₄) to $69.01(P_1x P_2)$ per cent.

Five out of fifteen crosses showed significant positive heterosis over better parent, while seven other crosses showed significant negative heterosis over better parent. The heterosis over better parent ranged from -50.17 (P₁x P₄) to 61.22 (P₁x P₂) per cent.

Three of the fifteen crosses showed significant positive heterosis over standard, while ten other crosses showed a significant and negative heterosis over standard. The range of heterosis over standard varied from -46.13 $(P_1 x P_4)$ to 21.80 $(P_4 x P_5)$ per cent.

4.4.11 Number of spikelets per panicle

Nine of the fifteen crosses showed significant positive heterosis over mid parent, while none of the crosses showed significant negative heterosis over mid parent. The range of heterosis over mid parent ranged from $-2.11(P_1xP_4)$ to 36.07 (P5xP6) per cent.

Four out of fifteen corsses showed significant positive heterosis over better parent, while five other crosses showed significant negative heterosis over better parent. The heterosis over better parent ranged from -11.48 (P₃xP₆) to 22.60 (P₂xP₆) per cent.

Ten of the fifteen crosses showed significant positive heterosis over standard, while four others showed a significant negative heterosis over standard. The heterosis over the standard ranged from $-8.40 (P_4 x P_6)$ to 45.63(P_5 x P_6) per cent.

4.4.12 Number of filled grains per panicle

Ten out of the fifteen crosses showed a significant and positive heterosis over mid parent, while only two other crosses showed significant negative heterosis over mid parent. The heterosis over mid parent ranged from -32.13 (P₁ x P₄) to 52.60 (P₂ x P₆) per cent.

Five of the fifteen crosses showed significant positive heterosis over better parent, while six other crosses showed significant negative heterosis over better parent.The range of heterosis over better parent varied from -32.76 (P₁x P₄) to 51.22 (P₂x P₆) per cent.

Only two of the fifteen crosses showed significant negative heterosis over standard, while ten of the crosses showed significant positive heterosis over standard. The heterosis over standard ranged from -28.23 (P₁x P₄) to 42.56 (P₅x P₆) per cent.

4.4.13 Test weight

Five of the fifteen crosses showed significant positive heterosis over mid parent, while seven of the crosses showed significant negative heterosis over mid parent. The range of heterosis over mid parent varied from -12.49 (P₁xP₃) to 14.01(P₄xP₆) per cent.

Eight of the fifteen crosses showed significant negative heterosis over better parent, while only three other crosses showed significant positive heterosis over better parent. The heterosis over better parent ranged from -16.54 (P₂xP₅) to 7.89 (P₁xP₂) per cent.

Four out of the fifteen crosses showed significant positive heterosis over standard, while seven other crosses showed a significant and negative heterosis over standard.

The heterosis over standard ranged from -11.48 ($P_1x P_3$ and $P_2x P_5$) to 11.48 ($P_4x P_6$) per cent.

4.4.14 Tiller fertility

Five of the fifteen crosses showed significant positive heterosis over mid parent, while six other crosses showed significant negative heterosis over mid parent. The range of heterosis over mid parent varied from -18.03(P₁x P₄) to 15.61 (P₁x P₂) per cent.

Nine of the fifteen crosses showed significant negative heterosis over better parent, while only three other crosses showed significant positive heterosis over better parent. The heterosis over better parent ranged from -24.24 (P₁x P₄) to 13.95 (P₁x P₂) per cent

Twelve of the fifteen crosses showed significant negative heterosis over standard, while none of the crosses showed significant positive heterosis over standard. The heterosis over standard ranged from -23.18 ($P_1x P_3$) to 1.46 ($P_2x P_4$) per cent.

4.4.15 Spikelet fertility

Eight of the fifteen crosses showed significant positive heterosis over mid parent, while six other crosses showed significant negative heterosis over mid parent. The

range of heterosis over mid parent ranged from -30.65 (P₁ x P₄) to 30.84 (P₁ x P₂) per cent.

Seven of the fifteen crosses showed significant positive heterosis over better parent, while six other crosses showed significant negative heterosis over better parent. The heterosis over better parent ranged from -31.39(P1x P4) to 20.24 (P2x P6) per cent.

Seven of the fifteen crosses showed significant positive heterosis over standard, while three other crosses showed significant negative heterosis over standard. The heterosis over the standard ranged from -23.32 (P₁x P₄) to 33.57 (P₁x P₂) per cent.

4.4.16 Harvest index

Eight of the fifteen crosses showed a significant and positive heterosis over mid parent, while six other crosses showed significant negative heterosis over mid parent. The range of heterosis over mid parent varied from -53.01 $(P_1 x P_4)$ to 37.41 $(P_1 x P_2)$ per cent.

Four of the fifteen crosses showed significant positive heterosis over better parent, while seven other crosses showed significant negative heterosis over better parent. The heterosis over better parent ranged from -53.34 ($P_1 x P_4$) to 25.69 ($P_2 x P_6$) per cent.

Eight out of the fifteen crosses showed significant positive heterosis over the standard, while five other crosses showed significant negative heterosis over standard. The heterosis over standard ranged from -41.90 (P₁x P₄) to 49.39 (P₁x P₂) per cent.

4.5 Character association

The phenotypic and genotypic correlations were worked out among sixteen characters studied, to determine the nature of association prevalent between the characters studied. The results are presented in Table 4.5 and 4.6 for the F_2 crosses. The significant correlations are discussed below.

Among the F₂ crosses (Table 4.5), number of tillers per plant showed highly significant positive phenotypic correlation with number of productive tillers per plant and total dry matter per plant. Grain yield per plant showed highly significant positive phenotypic correlation with panicle weight per plant, number of grains per panicle, spikelet fertility and harvest index. Panicle weight per plant also showed highly significant positive phenotypic correlation with number of productive tillers per plant, number of grains per panicle, and harvest index. Other character combinations which showed highly significant positive phenotypic correlation were number of productive tillers per plant with tiller fertility, number of spikelets

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							2								
Characters	, ,	·····		, 5	X 6	X 7	X	X 9	X 10	X 11	x 12	X 13	X 14	X 15	X 15
					0.1012	0,6331*	-0 5112	0,3912	0.6360*	0.5617*	0.4011	0.3261	0.1921	0.0384 -	0.0927
x 1	0.4307	0.7065	0.01/1	-0.1299	0.2246	0.2612	-0.0970	-0.5440*	-0.2791	-0.0896	~0.4836	-0.1475	-0.1635	-0.6168*	-0.8029**
2		9,1824	0.475**	-0,1801	0.3508	0.5122	-0,2483	0.4837	0.5867*	0.3908	0,4991	0.1192	0.2523	0.3363	0.1770
, J				-0.2317	9,1761	0.4123	-0,2689	0.5673*	0.6439**	0.2628	0,4290	0.2268	0.7080**	0.3793	0.3396
Ĵ.					0.0130	-0.2580	0.2400	0.1197	0.1325	0.1327	0.0430	-0.1297	-0.1862	-0.0824	0.1550
Ĵs -						0.2232	0.4798	-0.0511	-0.0363	0.1351	0,0631	-0.4055	-0.1709	-0.0636	-0.1169
_ ⊊ X							-0.7822**	0.3497	0.4785	0.3918	0.1450	0.6303*	0.0556	-0.1545	0.0052
7 X								-0.3439	-0.4486	-0.2476	-0.0682	-0.8516**	-0.1632	0.1094	-0.0754
e x									0.8329**	0.4405	0.7564**	0.4697	0,4365	0.6625**	0.8683**
♥ X										0.5628*	0.7178**	0.5023	0,4338	0,4866	0.5674**
10 2		•									0.7050*	0.0750	0.0372	0.0004	0.1723
11 X												0.0133	0,1516	0,7066	• 0.6355•
17 X													0.2617	0.0050	0.2689
23 X														0.2936	0,4338
34 X															0,7463*

Phenetypic correlation coefficients between different traits emong f crosses in rice.

. Stantficer

Test weight x . Grein ylold - - The president - - - illey x - Panicia weight ent halght 10 Selet fortility x . Mo.of spikelets per paniele 11 7 x · Harvest index z . Ro,of grains per panicle X . L/B satio 16 12 . 4

panicle with number of filled grains per panicle, per number of filled grains per panicle with spikelet fertility, and spikelet fertility with harvest index. The character combinations which showed a highly significant negative phenotypic correlation were plant height with harvest index, grain breadth with length to breadth ratio of grain, and length to breadth ratio of grain with test weight. Α significant and positive phenotypic correlation was observed between the character combinations total dry matter per plant with number of productive tillers per plant, grain breadth, panicle weight per plant and number of spikelets per panicle, number of tillers per plant with panicle weight per plant, number of productive tillers per plant with grain yield per plant, grain breadth with test weight, panicle weight per plant with number of spikelets per panicle, and number of grains per panicle with harvest index. The character combinations which showed significant negative phenotypic correlations were plant height with grain yield and spikelet fertility. Other character per plant combinations showed insignificant correlations.

Among the F₂ crosses (Table 4.6), number of tillers per plant had highly significant positive genotypic correlation with total dry matter per plant and number of productive tillers per plant. Total dry matter per plant showed highly significant positive genotypic correlation with number of productive tillers per plant, grain breadth,

	velght r fertility let fertilit	Test Tille Spike	X 13 X 14		er panicle	yleld e weight spikelets p	= Grain • Panicl	۲. × ۲. × ۳. ×		icle lengt n length n breadth	- Pani 5 - Graf			Dry matter Plant height Totel tiller
													: 5% level 1% level	ignificant at ignificant at
														15
0.														x 14
76 0.0	0.21													13 X
17 0.7	0171 0.16	0.0												ж 12
50 0.0	762 -0.02	6** 0.0	0.709											x
00 0.5	269* 0.47.	9** 0.5	0.747	0.5794										x 10
17 0.65	910 0.47	6** 0.4	0,783	0.4482	0.9327**									9 X
1 0,10	810** -0.205	6 -0.8	-0.075	-0.2505	-0.4736	-0.3592								а ×
4 -0.14	540** 0.089	1 0.6	0.156	0.4020	0.5057	0.3633	-0.7740**							X 7
7 -0.062	259 -0.199	5 -0.4	0.061	0.1333	-0.0505	-0.0657	0.4469	0.2190						6 ×
7 -0.090	459 -0.246	1 -0.1.	0.049	0.1494	0.0912	0.0868	0.2808	-0.3030	8600.0					5 X
5** 0.415	921 0.746	5 0.25	0.477	0.3067	0.6913**	0.6070*	-0.3289	0.4909	0.1714	-0.3691				• ×
0.3673	748 0.3324	2* 0.1;	0.569	0.4676	0.6536**	0.5303*	-0.3060	0.6249*	0.3991	-0.2712	0.8889**			ω ×
-0.6283	548 -0.1772	4 -0.11	-0.490	-0.0703	-0.2978	-0.5669*	-0.0944	0.2756	0.2401	-0.1733	0.0520	0.1950		22
0.0318	989 0.2064	5 0.33	0.407	0.5798	0.6463**	0.3914	-0.5348*	0.6898**	0.1075	-0.2087	0.6649**	0.7782**	0.4419	× 1
Х 15	X 14	×	X 12	X 11	X 10	6 X	B	х 7	6 Х	5 5	X 4	ω X	2	Characters

and panicle weight per plant. Grain yield per plant showed highly significant positive genotypic correlation with panicle weight per plant, number of filled grains per panicle, spikelet fertility, and harvest index. Highly significant positive genotypic correlations were also observed between panicle weight per plant with number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, and harvest index. The character combinations number of productive tillers per plant with tiller fertility, grain breadth with test weight, number of spikelets per panicle with number of filled grains per panicle, number of filled grains per panicle with spikelet fertility and harvest index, and spikelet fertility with harvest index also showed highly significant positive genotypic correlations. The character combinations plant height with harvest index, grain breadth with length to breadth ratio of grain, and length to breadth ratio of grain with test weight showed highly significant negative genotypic correlations. The character combinations which showed only a significant positive genotypic correlation were total dry matter per plant with number of spikelets per panicle, number of tillers per plant with grain breadth, grain yield per plant, and number of grains per panicle, number of productive tillers per plant with grain yield per plant and panicle weight per plant with number of spikelets per panicle, test weight, and spikelet fertility. The

character combinations total dry matter per plant with length to breadth ratic of grain and plant height with grain yield per plant, and spikelet fertility showed significant negative genotypic correlation. The other character combination showed insignificant genotypic correlations.

4.6 Path coefficient analysis

The path coefficients at phenotypic and genotypic levels of grain yield cer plant with total dry matter per plant, number of productive tillers per plant, panicle weight per plant, number of filled grains per panicle, test weight and harvest index is presented in Table 4.7 and 4.8 respectively.

4.6.1 Phenotypic path coefficient analysis

The direct contribution to grain yield per plant by harvest index (0.7029) was highest followed by total dry matter per plant (0.2860), panicle weight per plant (0.2442), test weight (0.0725) and number of filled grains per panicle (0.0344). However, the direct contribution of number of productive tillers per plant (-0.0363) to grain yield was negative. The residual effect was 0.0105 (Table 4.7).

The effect of total dry matter per plant on grain yield per plant through panicle weight per plant (0.1553), number of filled grains per panicle (0.0138) and test weight

Character	s X l	X 2	X 3	X 4	x 5	X 6
x 1	0.2860	-0.0224	0.1553	0.0138	0.0237	-0.0651
X	0.1765	-0.0363	0.1572	0.0147	0.0165	0.2387
x 3	0.1819	-0.0234	0.2442	0.0247	0.0364	0.4691
X	0.1147	-0.0156	0.1753	0.0344	0.0010	0.4467
4 X 5	0.0933	-0.0082	0.1226	0.0005	0.0725	0.1890
Х б	-0.0265	-0.0123	0.1629	0.0218	0.0195	0.7029
Residual	= 0.0105	GA	= 15.4308	(GA (%) =	681.1856

Table 4.7 Direct (diagnol) and Indirect effect of some selected traits on grain yield at phenotypic level.

X	=	Dry matter	X =	No.of grains per panicle
X	=	Productive tillers	4 X =	Test weight
2 X	=	Panicle weight	5 X =	Harvest index
3		5	6	

(0.0237) was positive. However, the indirect effect of total dry matter per plant on grain yield, through, number of productive tillers per plant (-0.0224) and harvest index (-0.0651) was negative.

Number of productive tillers per plant influenced grain yield per plant indirectly and positively through total dry matter per plant (0.1765), panicle weight per plant (0.1572), number of filled grains per panicle (0.0147), test weight (0.0165) and harvest index (0.2387). However, it did not show any indirect negative effects.

Panicle weight per plant showed indirect and positive influence on grain yield through total dry matter per plant (0.1819), number of filled grains per panicle (0.0247), test weight (0.0364) and harvest index (0.4691), while, it showed indirect negative influence on grain yield through number of productive tillers per plant (-0.0234).

Number of filled grains per panicle influenced grain yield indirectly and positively via total dry matter per plant (0.1147), panicle weight per plant (0.1753), test weight (0.0010) and harvest index (0.4467), while, it showed indirect negative influence on grain yield through number of productive tillers per plant (-0.0156).

The contribution of test weight to grain yield per plant through total dry matter per plant (0.0933), panicle

weight per plant (0.1226), number of filled grains per panicle (0.0005) and harvest index (0.1890) was positive, while, its influence on grain yield through number of productive tillers per plant (-0.0082) was negative.

Harvest index contributed indirectly and positively to grain yield through total dry matter per plant (0.0265), panicle weight per plant (0.1629), number of filled grains per panicle (0.0218) and test weight (0.0195), while it contributed indirectly and negatively to grain yield through number of productive tillers per plant (-0.0123).

4.6.2 Genotypic path coefficient analysis

The direct contribution to grain yield per plant by harvest index (0.7316) was highest, followed by total dry matter per plant (0.3197), panicle weight per plant (0.2140), test weight (0.0823) and number of filled grains per panicle (0.0382). However, the direct contribution to grain yield by number of productive tillers per plant (-0.0617) was negative. The residual effect was 0.0069 (Table 4.8).

Total dry matter per plant influenced grain yield per plant positively through panicle weight per plant (0.1383), number of filled grains per panicle (0.0156) and test weight (0.0279), while, it influenced grain yield negatively

Character	s X l	x 2	x 3	x 4	x 5	X 6
x 1	0.3197	-0.0410	0.1383	0.0156	0.0279	-0.0691
X 2	0.2125	-0.0617	0.1480	0.0182	0.0240	0.2659
x 3	0.2066	-0.0427	0.2140	0.0286	0.0434	0.4828
X 4	0.1303	-0.0295	0.1601	0.0382	0.0014	0.4831
Х 5	0.1083	-0.0180	0.1128	0.0007	0.0823	0.2049
х 6	-0.0302	-0.0224	0.1413	0.0252	0.0231	0.7316
Residual	= 0.0069	GA	= 15.4308	(GA (%) =	681.1856

Table 4.8 Direct (diagnol) and Indirect effect of some selected traits on grain yield at genotypic level.

X I	=	Dry matter	X =	No.of grains per panicle
x	=	Productive tillers	X =	Test weight
X X	=	Panicle weight	5 X =	Harvest index
5			0	

through number of productive tillers per plant (-0.0410) and harvest index (-0.0691).

The effect of number of productive tillers per plant on grain yield was positive through total dry matter per plant (0.2125), panicle weight per plant (0.1480), number of filled grains per panicle (0.0192), test weight (0.0240) and harvest index (0.2659). However, it showed no negative effect on grain yield through any character.

Panicle weight per plant influenced grain yield per plant positively through total dry matter per plant (0.2066), number of filled grains per panicle (0.0286), test weight (0.0434) and harvest index (0.4828), while its influence on grain yield through number of productive tillers per plant (-0.0427) was negative.

The contribution of number of filled grains per panicle to grain yield per plant was positive through total dry matter per plant (0.1303), panicle weight per plant (0.1601), test weight (0.0014) and harvest index (0.4831), while, its contribution to grain yield through number of productive tillers per plant (-0.0295) was negative.

The effect of test weight on grain yield per plant was positive through total dry mater per plant (0.0183), panicle weight per plant (0.1128), number of filled greins per panicle (0.0007) and harvest index (0.2049), while, its

effect on grain yield was negative through number of productive tillers per plant (-0.0180).

Harvest index influenced grain yield per plant positively through panicle weight (0.1413), number of filled grains per panicle (0.0252) and test weight (0.0231), while, it influenced grain yield through total dry matter per plant (-0.0302) and number of productive tillers per plant (-0.0224) negatively.

4.7 Diallel analysis

4.7.1 Combining ability analysis

4.7.1.1 Analysis of variance for combining ability

The analysis of variance for combining ability for different traits are presented in table 4.9. The mean sum of squares due to general combining ability, specific combining ability and the ratio of GCA to SCA for each of the characters studied are given in the table.

The mean sum of squares due to GCA and SCA were highly significant for all the traits. The GCA/SCA ratio was maximum in case of number of spikelets per panicle (4.68), while it was minimum for number of productive tillers per plant (0.31). The GCA/SCA ratio of more than one was observed for total dry matter per plant, grain breadth, grain yield per plant, panicle weight per plant,

		Means sum of	squares	
characters	G.C.A. (5 d.f)	S.C.A. (15 d.f.)	Error (40 d.f.)	G.C.A./S.C
Dry matter	155.31**	49.89**	0.92	3.11
Plant height	107.21**	215.45**	0.81	0.50
Total tillers	5.03**	15.41**	0.78	0.33
Productive tillers	4.42**	14.38**	0.65	0.31
Panicle length	2.29**	4.09**	0.34	0.56
Grain length	0.20**	0.28**	0.009	0.71
Grain breadth	0.05**	0.02**	0.001	2.50
Grain yield	74.65**	50.91**	0.80	0.47
Panicle weight	84.49**	39.71**	0.82	2.13
No.of Spikelets per panicle	608.42**	129.99**	1.44	4.68
No.of grains per panicle	389.74**	148.89**	1.21	2.62
Test weight	0.03**	0.02**	0.0004	1.50
Tiller fertility	38.39**	46.81**	1.84	0.82
Spikelet fertility	45.09**	86.00**	0.76	0.52
Harvest index	97.82**	155.44**	2.12	0.63

Table 4.9 Analysis of variance for combining ability in rice.

** Significant at 1% level.

number of spikelets per panicle, number of filled grains per panicle and test weight. Plant height, number of tillers per plant, number of productive tillers per plant, panicle length, grain length, tiller fertility, spikelet fertility and harvest index showed GCA/SCA ratio less than one.

4.7.1.2 Combining ability effects

The estimates of general combiing ability (gca) effects for the parents in respect of the different traits are presented in Table 4.10, while estimates of specific combining ability (sca) effects are given in Table 4.11. The character wise gca and sca effects are presented in the following pages.

Total dry matter per plant

All the six parents showed highly significant gca effects of which four were negative and two were positive. The magnitude of gca effects ranged from -4.85 (P₁) to 7.32 (P₅).

The sca effects were significant in 12 crosses of which 11 were highly significant. Five crosses showed positive significant sca effects and the remaining seven crosses showed negative significant sca effects. The magnitude of sca effects ranged from -9.35 (P_3xP_6) to 12.57 (P_3xP_5).

and the state of the state	; 0.23 0.20 0 -qj)	r 0.096 0.085 (5 -1.95 -2.47	5	4 7 33** _0.00	3 -1.19** -2.77** -	2 3.04** 7.05**	P -2.36** -1.84**		matter height t	farents
	. 195	0,08	0.56*	0.43		1.07**	.91**	-0.55		Total I illers	
	0.16	0.07	0.76**	-0.25		-0.23	0.53*	-1.26**		Productive tillers	
	0.09	0.04	0.20	0.61**		-0.51*	-0.06	-0.72**		Panicle length	
	0.0023	0.001	-0.12**	-0.19**	0.04	5 02	0.18**	0.20**	44	Grain length	
	0.0004	0.00015	-0.05**	0.08**	0.04**	0.03		0.03*		Grain	GC
	0.20	0,08	-0.88**	5.61**	0.91**	-2.90*	-0.55	-2.19**	held	Grain	effects
	0.20	0.09	-0.60*	6.13**	0.83**	-1.96**	-0.64**	-2.76**	weight	Panicle	
	0.36	0.15	-4.03**	16.03**	-4.88**	3.95**	-3.75**	-7.32**	spikelet per panicle	No.of	
	0.30	0.13	-5.24**	13.59**	-4.17**	-0.88*	0.33	-3.63**	grains per panicle	No.of	
	0,00009	0,00004	-0.008	0.07**	0.04**	-0.06**	-0.07**	0.03**	weight	Test	The second s
	0,46	0.19	1.68**	0.27	2.40**	-0.78	0.25	-3.83**	fertility	Tiller	
	0.19	0.03	-2,40**	2.62**	-0.80**	-2.82**	2.48**	0.90**	Fertility		
	0.5	0.22	-0.03	3.65*	2.02*	-6.52**	1.07*	-0.19	Index		

(135-	8E*T	1.22	21.1	26*0	15.0	10.0	200*0	1,20	E2.1	2.17	18.1	9000*0	97.2	ντ ·τ	3.17
(475-1	19.1	24.1	1.36	ET ' I	09.0	20.0	0,002	07'1	£7°I	£5°Z	5,12	2000.0	22.5	25.1	0 <i>1</i> ,£
(fis) .	22.0	79.0	19.0	12.0	72.0	200-0	100.0	69.0	79°0	EI . I	96°0	0000.0	77°T	65*0	99"T
9 4 X	IS:0		95'0-	•T•T-		coo	TT '0	9C*b			08'II		79'I-	65'1-	, , ,
9	**64'7-	**£4.5-		-2.13**	/8.0		800.0		7Z*0-	**SZ 00		**81.0	80.0-	**81'6	.19'8
s a x	55.1	** 77.2-	80.1	05.0	06'1	/9.0		**08'9	09.0	**ZZ*0I	a.EL'E	**69*0	27*1-	**86.2-	.62'9
e e	**SE*6-	**£1.4-	**84*9-	**85.4-		*******	-0*56**	*//.1	92.1	**80.6-	7E.1	*70°0-	**96'£	**68.5	
s e a x	12.57**	**09**7	**59'2	**/1*7	86*5-	51.0	0"15**	**62.2-	.7Z°I	*SI'Z-	**0£.ð-	**90.0	**05*8	-3.66**	**71°11-
3 ¢ d × b	-4.12**	۲٤.0-	**77.5-	**62.5-	12.0	**77°0	90*0-	-9'53**	-4.27**	75°0		**10°0-	**SZ*8-	-5"11 **	**97.8-
5 e	£1.1-	**02"5-	65.0-	£2.0	*70°I-	*/1.0	*20°0	07'1	**90°£	**66.52	17.28**	600°0-	2°58*	**81*2	**76°E
s z 6 × 6	**19'S-	88.0-	** 69 * 7-	**68*7-	08.0	£0°0-	-0.23**	**S6' <i>L</i> -	**/7'9-	**66°7-	72.1-	**61*0-	**78.8-	91.1	**25.6-
5 ¢ 5 × 5	**68°5-	97*0-	+69°T-	0.22	-0.32	**69.0	0.03	95.0	56°T-	**66*5	**7S*8	**/1.0-	**S3.7	**91.4	**19°8
5 3 b x b	**05.8	18°83**	25.1	91.0	s*25**	**ZS*0	**10°0	1.12	**70*7	**12.rT	5.13**	**S0.0-	**35.e-	-2.28*	**98°7
5 × 5	4.12**	30.32**	-3'81**	-5'69**	5.71**	S0.0-	10.0	**67*2-	60.1-	-5.61*	-17.62**	20°0	97°T	**L7*ST-	**01.11-
5×5	*ST.15*	**8 * *	12.0-	*92.1-	62.0	*LI.0-	£0.0	-2.70**	10.1-	**01-7-	80°T	**90*0-	**SI.8-	3°52.	**01.2-
E X B	**98.4-	**79°SI	-3'99*	**69*7-	80.0	11.0	70°0-	**7E.EI-	**68.11-	-2.76**	**69°6I-	**S0°0-	**85.6-	**LS'LT-	-53.50**
E X E	**76"7-	-10'86**	65.1-	-5°28**	85.0	**15.0	**71.0-	**81.8	3*12**	**86.0	**88.71	**91'0-	-9'95**	**17'6	**77°ST
d x d	11.42**	**60.7-	07"1	**6 <i>L</i> *E	80.0	71.0	**/[`0	29.21	**00°7I	**98.6-	**57.21	4436 0		*26 75	**27"11
								aratik		per panicle	per per per	aj jubiaw	er friiter	ATTIT	Tabel
8550 10	Dry	tasig .	Total	Productive Fillers	Pantcle dtpnsf	Grain length	Grain	Grain blobs	Panicle Panicle	To.oW	la.oH	T test T	q2 Tall1	1919AI	TRATIER
000010								toelle AD2	5						

.1 Significant at 18 level.
Plant height

Four of the six parents showed highly significant gca effects of which three were negative and one was positive. The magnitude of gca effects ranged from -2.77 (P₄) to 7.05 (P₃).

Twelve crosses showed significant sca effects, all of which were highly significant. Five crosses showed significant positive sca effects while seven crossed showed significant negative sca effects. The magnitude of sca effects ranged from -10.86 (P1xP3) to 30.32 (P1xP6).

Number of tillers per plant

Four parents showed significant gca effects of which two were highly significant. Only one of the parents showed a highly significant negative gca effect. The magnitude of gca effects ranged from -1.07 (P₄) to 0.91 (P₃).

Eight crosses showed significant sca effects, seven of which were highly significant. Seven crosses showed significant negative sca effects while only one cross showed significant positive sca effect. The magnitude of sca effects ranged from -6.78 (P₃xP₆) to 2.65 (P₃xP₅).

Number of productive tillers per plant

Three parents showed significant gca effects of which two were highly significant. Only one of the parents showed a highly significant negative gca effect. The magnitude of gca effects ranged from -1.26 (P₁) to 0.76 (P₆).

Ten crosses showed significant gca effects, nine of which were highly significant. Two crosses showed significant positive sca effects while eight crosses showed significant negative sca effects. The magnitude of sca effects ranged from -4.89 (P₂xP₅) to 4.17 (P₃xP₅).

Panicle length

Four parents showed significant gca effects of which two were highly significant. Two parents showed significant negative gca effects while two others showed significant positive gca effects. The magnitude of gca effects ranged from -0.72 (P₁) to 0.61 (P₆).

The sca effects were significant in seven crosses of which six were highly significant. Five crosses showed significant positive sca effects while two crosses showed significant negative sca effects. The magnitude of sca effects ranged from -5.38(P₃xP₅) to 2.71 (P₁xP₆).

Grain length

Four parents showed highly significant gca effects of which two parents should positive gca effects and two showed negative gca effects. The magnitude of gca effects ranged from -0.19 (P₅) to 0.20 (P₁).

The sca effects were significant for nine crosses of which seven were highly significant. Six crosses showed significant positive sca effects while three crosses showed significant negative sca effects. The magnitude of sca effects ranged from -0.87 (P₄xP₆) to 0.69 (P₂xP₄).

Grain breadth

All the six parents showed significant gca effects of which four were highly significant. Two parents showed significant negative gca effects while four showed significant positive gca effects. The magnitude of gca effects ranged from -0.13 (P₂) to 0.08 (P₅).

Nine crosses showed significant sca effects of which eight were highly significant. Six crosses showed significant positive sca effects while three crosses showed significant negative effects. The magnitude of sca effects ranged from -0.26 (P₃xP₆) to 0.17 (P₁xP₂)

Grain yield per plant

Five of the parents showed highly significant gca effects of which three were negative and two were positive. The magnitude of gca effects ranged from -2.90 (P₃) to 5.61 (P₅).

The sca effects were significant in twelve crosses of which eleven were highly significant. Six crosses showed significant positive sca effects while other six showed significant negative sca effects. The magnitude of sca effects ranged from -13.34 ($P_1 \times P_4$) to 15.62 ($P_1 \times P_2$).

Panicle weight per plant

All the six parents showed significant gca effects of which five were highly significant. Two parents showed significant positive gca effects while four showed significant negative gca effects. The magnitude of gca effects ranged from -20.76 (P_1) to 6.13 (P_5).

Eight crosses showed highly significant scaleffects of which five showed positive gcaleffects and three showed negative scaleffects. The magnitude of scaleffects ranged from -11.89 ($P_1 \times P_4$) to 14.00 ($P_1 \times P_2$).

Number of spikelets per panicle

All the six parents showed highly significant gca effects of which four parents showed negative gca effects and two showed positive gca effects. The magnitude of gca effects ranged from -7.32 (P₁) to 16.03 (P₅).

Fourteen crosses showed significant sca effects of which twelve were highly significant. Eight crosses showed significant negative sca effects while six showed significant positive sca effects. The magnitude of sca effects ranged from -9.08 ($P_3 \times P_6$) to 28.75 ($P_5 \times P_6$).

Number of filled grains per panicle

Five of the six parents showed significant gca effects of which four were highly significant. Four parents showed significant negative gca effects while only one showed significant positive gca effect. The magnitude of gca effects ranged from -5.24 (P₆) to 13.59 (P₅).

Twelve crosses showed highly significant scaleffects of which eight crosses showed positive scaleffects and four crosses showed negative scaleffects. The magnitude of scaleffects ranged from -19.69 (P₁ x P₄) to 17.88 (P₁ x P₃).

Test weight

Five parents showed highly significant gca effects of which three were positive and two negative. The magnitude of gca effects ranged from $-0.07(P_2)$ to 0.07 (P₅).

Thirteen of the fifteen crosses showed significant sca effects of which eleven were highly significant. Eight crosses showed significant negative sca effects while five crosses showed significant positive sca effects. The magnitude of sca effects ranged from $-0.19(P_2xP_5)$ to 0.63 $(P_4 \times P_5)$.

Tiller fertility

Three parents showed highly significant gca effects of which two were positive and only one negative. The magnitude of gca effects ranged from -3.83 (P₁) to 2.40(P₄).

. . .

Eleven of the fifteen crosses showed significant sca effects of which ten were highly significant. While six crosses showed significant negative sca effects. The magnitude of sca effects ranged from -9.53 (P_1xP_4) to 11.25 (P_1xP_2).

Spikelet fertility

All the six parents showed highly significant qca effects of which three were positive and three negative. The magnitude of qca effects ranged from $-2.82(P_3)$ to $2.62(P_5)$.

Fourteen of the fifteen crosses showed significant sca effects of which twelve were highly significant. Seven crosses showed significant positive sca effects while seven others showed significant negative sca effects. The magnitude of sca effects ranged from $-17.57(P_1xP_4)$ to $14.87(P_1xP_2)$.

Harvest index

Four parents showed significant gca effects of which three were highly significant. Three parents showed significant positive gca effects while only one parent showed significant negative sca effect. The magnitude of gca effects ranged from -6.52(P₃) to 3.65(P₅).

All the fifteen crosses showed highly significant sca effects of which nine crosses showed positive sca effects and six showed negative sca effects. The magnitude of sca effects ranged from $-23.50(P_1xP_4)$ to $17.42(P_1xP_2)$.

4.7.2 Genetic components of variance

The genetic components of variation like D (variation due to additive effect), E (environmental component of variation), F (mean of the co variance of additive and dominance effects over arrays), H1 (variation due to dominance effect of the genes), H2(proportion of dominance variance due to positive and negative gene effects), h²(net dominance effects expressed as the algebraic sum over all loci in heterozygous phase in all crosses) with their respective standard errors in parenthesis and their ratios (H_l/D)^{1/2} (mean differences viz., and degree of dominance), H₂/4H₁ (proportion of genes with positive and negative effects in the parents), KD/KR (proportion of dominant and recessive gene in the parents), $K=h^2/H_2$ (number of group of genes controlling the character and exhibiting dominance), H1-H2(showing whether positive (u) and negative (v) alleles were in equal proportion in the parents), $r((W_r+V_r) Y_r)$ (the correlation coefficient between parental order of dominance and parental means), heritability in narrow sense and t^2 and b (regression coefficient) (to test the validity of diallel assumptions) are presented in the table 4.12 for the fifteen characters studied. Traitwise results are presented below.

Tabile 4.12 Generic components of verietion and their proportion for some traits in rice.

10,0003 14.0 4.14 380,83 0.86* 1.52 5.05 272 112 Add to Date 1.12 - SE BEST H 11.42 The state 도 되 날 년 4.67 3.42 0.002 20.572 0.19 1.95 6.2 19.10 0.20 2.85 (15.35) 5.64 andreader Served an 366., 551 576 (DE-MES SIE. 13* 円 日 日 日 0.15 3.85 146.69 0.58 0.02 1.75 0.20 11,12 (24,45) 1.84 (8.65) 5.25 ESI. 56^m (01,000) 11.11 AST LEA 82.73 (111.35) anna Merrinal 16.12 0.0006 (0.005) 0.004 (0.002) 0.002 -0.65 0.05 0.06 3.73 ##LZ"D Tess 5.24 0.20 1.42 1.33 (30.05) 0.00 (0.06) 878 (878) 74.67** 8.82 -0.56 100,357 1.21 (25.74) 479.84 2042.255** 0.06 21.9M PERSON 1000 (53, 525) 115.87 (115.04) 8E.E 0.20 1.40 (2772, 66) No.uef Praties Peer peerliche No...of spikelet per pericle 10.15) (21.15) 228.52 [142.13] 1.44 (35.21) 248.64 2.37 (ST 181) *DE" DEIE 845.02) -0.62 10. Mei 01°E 0.22 8.78 S45.32 0.79 0.13 Perciplic 71.65 (54.42) 13 (S1 (81) 12.25 (74.24) *13-303 [51'5BZ 555, 52* (11)四日 0.19 119.83 0.82 (10.75) 18.11 3,03 0.21 1.82 0.03 0.74 Grain 81"72 (24"72) 57°58() (157°58() 1257,1258 (357-36) 13. BI -0.0004 [11, 11] 878) (15-23) 0.80 (13.12) 3.71 400.0 1.55 86.82 0.22 0.73 7.56 Contra Contra 0.03** (600°0) 8,8 (8,8) 0.257** (G..05) (30.05) 0.001 -0.001 3.03 0.22 1.41 0.007 0.03 -0.01 10.68 Goration Leangert (g. 16) 1.00 (0.73) **05"3 *B]*F (2.45) 85°0 (25°0) 0.009 (0.05) 4.42 0.17 2.63 0.11 -0.32 1.57 0.13 5.97 Particle Jengch 2.52 6.61 (04.65) 19. ES (Sh-02) -52-15 (02"12) 2.38 (4.58) 0.34 6.9 0.23 1.69 0.04 6.26 7.55* 0.62 4.29 Productive tillers (15-E) 97°C) (97°53) 198,65* HATE"EVI (50.3) (6.05) (55°52) 0,65 (02.1) 8079 0.22 11.1 0.32 25.43 0.78 2.58 0.25 Jaccel tilliers (227%) 16"E) 214,525** 172,45** (95°°L) (35-37) (92.52) 0.73 (1.52) 5.35 0.21 1.97 0.43 31.63 *88*0 3.76 0.55 Filent 315,465 (117,485) 80°31 (16°192) 1000°, 700° THE (EIE.ET) (EU "US) [367.95] 0.81 ((52.53) 9.51 2.23 1.25 0.15 -0.40 322.67 1.12 1.67 (127.12) (73,127) (121,127) 1987, GGP [12] 13Z (275 712) -0.15 0.35.0 ((35..6) -0,,0002 0°.19 EE-I General Gamerica/ Componenca/ 157,04 1 2 r[(W +V],Y] 0.55 r r r Heritability 8.61 65.0 2/11 B m = H₁ HI FI ы ((日/) 王)) 2 1 1 1 1 1 м (.......) ~ ~

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** Significant at 1% level.

* Significant at 5% level

Total dry matter per plant

The t² value was not significant indicating fulfilment of diallel assumptions. Genetic components D, H₁ and H₂ were highly significant. The F value was positive but not significant. The role of environment as indicated by E component was not significant. The h² value was negative and not significant. The mean degree of dominance $(H_1/D)^{1/2}$ exceeded one (3.39), H₂/4H₁ was less than 0.25 (0.19), KD/KR was more than one (1.33) and H₁-H₂ value was not equal to zero (197.04). The K value was -0.0002 and correlation coefficient between(W_T + V_T) and Y_T was positive and non-significant (0.55). Narrow sense heritability was low(8.61 per cent).

Plant height

The t^2 value was not significant indicating confirmity to the diallel assumptions. Additive component (D) was not significant but dominance components H₁, H₂ and h² were highly significant. The environmental component E and the F value were non-significant. Mean degree cf dominance was more than one (9.51). KD/KR was also more than one (1.25). Value of H₂/4H₁ was less than 0.25(0.23) and H₁-H₂ was not equal to zero (322.67). K value was 0.15. Narrow sense heritability was low (1.12 per cent) and the correlation coefficient between (W_r+V_r) and Y_r was negative and non-significant(-0.40).

Number of tillers per plant

The diallel assumptions were satisfied as the t² test was non-significant. Dominance components H₁, H₂ and h² were highly significant but additive component D was not significant. Environmental effect E and F value were non-significant. $(H_1/D)^{1/2}$ was more than one (5.35), H₂/4H₁ was lower than 0.25 (0.21) and H₁ - H₂ was not equal to zero (31.63). KD/KR value was more than one (1.97) and the K value was 0.43. Narrow sense heritability was low (3.76 per cent) and the correlation coefficient between(W_r+V_r) and Y_r was positive and significant(0.88).

Number of productive tillers per plant

The t² value was not significant indicating the validity of diallel assumptions. The dominance components H₁, H₂ and h² were highly significant. The F value and environmental effect E were also non-significant. $(H_1/D)^{1/2}$ was more than one (6.38), H₂/4H₁ was less than 0.25(0.22) and H₁-H₂ was not equal to zero(25.43). KD/KR value was more than one (1.77) and the K value was 0.32. Narrow sense heritability was low (2.58 per cent) and the correlation between (W_r+V_r) and Y_r was positive and non-significant(0.78).

Panicle length

The t² value was significant indicating the failure of one or a few diallel assumptions. The dominance components H₁ and H₂ were significant while h² was nonsignificant. Additive component D was non-significant. The F value and environmental effect E were also nonsignificant. $(H_1/D)^{1/2}$ was more than one (4.93), H₂/4H₁ was less than 0.25(0.23) and H₁-H₂ was not equal to zero(6.26). KD/KR value was more than one (1.69) and the K value was 0.04. Narrow sense heritability was low (4.29 per cent) and the correlation betwen (W_r-V_r) and Y_r was positive and nonsignificant (0.62).

Grain length

Non-significant t^2 value indicated the fulfilment of diallel assumption for this trait. The dominance component H_1 was highly significant while H_2 was significant and h^2 was non-significant. Additive component D and F value were non-significant. Environmental effect E was also nonsignificant. $(H_1/D)^{1/2}$ was more than one (4.42), $H_2/4H_1$ was less than 0.25(0.17) and H_1-H_2 was not equal to zero (1.57). KD/KR value was more than one (2.63) and the K value was Narrow sense heritability was low (5.97 percent) 0.11. and the correlation between (W_r+V_r) and Y_r was negative and nonsignificant (-0.32).

Grain breadth

The diallel assumptions were valid for this trait as t^2 value was non-significant. Additive component D and dominance components H₁ and H₂ were highly significant. F value and h^2 were non-significant. The environmental component E was also non-significant. (H₁/D)^{1/2} value was more than one (3.03), H₂/4H₁, was less than 0.25 (0.22) and H₁ - H₂ was not equal to zero (0.03). KD/KR value was more than one (1.41) and the K value was negative (-0.001). Narrow sense heritability was low (10.68 per cent) and the correlation between (W_r+ V_r) and Y_r was negative and non-significant (-0.01).

Grain yield per plant

The t² value was non-significant indicating confirmity to diallel assumptions. The dominance components H₁ and H₂ were significant while h² was non-significant. Additive component D, environmental effect E and F value were non-significant. $(H_1/D)^{1/2}$ value was more than one (3.71), H₂/4H₁ was less than 0.25 (0.22) and H₁ - H₂ was not equal to zero (86.82). KD/KR value was more than one (1.55) and the K value was negative (-0.004). Narrow sense heritability was low (7.56 per cent) and the correlation between (W_r + V_r) and Y_r was positive and non-significant (0.73).

Panicle weight per plant

The t² value for this trait was not significant fulfiling the diallel assumptions. The dominance components H₁ and H₂ were significant while h² was non-significant. Additive component D was highly significant. The environmental effect E and F value were non-significant. $(H_1/D)^{1/2}$ value was more than one (3.03), H₂/4H₁, was less than 0.25 (0.21) and H₁ - H₂ was not equal to zero (119.88). KD/KR value was more than one (1.82) and the K value was 0.03. Narrow sense heritability was low (11.81 per cent) and the correlation between (W_r + V_r) and Y_r was positive and non-significant (0.74).

Number of spikelets per panicle

The t² value was non-significant indicating the validity of diallel assumptions. The dominance components H₁ and H₂ and additive component D were significant. F value and h² value were non-significant. Environmental effect E was also non-significant. $(H_1/D)^{1/2}$ value was more than one (3.10), H₂/4H₁ was less than 0.25 (0.22) and H₁-H₂ was not equal to zero (248.64). KD/KR value was less than one (0.79) and the K value was 0.13. Narrow sense heritability was low (8.78 per cent) and the correlation between $(W_r + V_r)$ and Y_r was negative and non-significant (-0.62).

Number of filled grains per panicle

The t² value was highly significant indicating the non-fulfilment of one or a few diallel assumptions. The dominance components H₁ and H₂ and additive component D were highly significant. Environmental effect E, F value and h² value were non-significant. $(H_1/D)^{1/2}$ value was more than one (3.38), H₂/4H₁ was less than 0.25 (0.20) and H₁ - H₂ was not equal to zero (479.84). KD/KR value was more than one (1.40) and the K value was 0.06. Narrow sense heritability was low (8.82 per cent) and the correlation between (W_r + V_r) and Y_r was negative and non-significant (-0.56).

Test weight

The t² value was non-significant indicating the validity of diallel assumptions. The dominance components H_1 and H_2 were highly significant while h^2 was non-significant. The additive component D, environmental effect E and F value were non-significant. $(H_1/D)^{1/2}$ value was more than one (5.24), $H_2/4H_1$ value was less than 0.25 (0.20) and H_1-H_2 value was not equal to zero (0.06). The KD/KR value was more than one (1.41) and K value was 0.002. Narrow sense heritability was low (3.73 per cent) and the correlation between ($W_r + V_r$) and Y_r was negative and non-significant (-0.65).

Tiller fertility

The diallel assumptions were valid for this trait as the t² value was non-significant. The dominance components H₁ and H₂ were highly significant while h² was nonsignificant. The additive component D, environmental effect E and F value were non-significant. $(H_1/D)^{1/2}$ value was more than one (5.25), H₂/4H₁ value was less than 0.25 (0.20) and H₁ - H₂ value was not equal to zero (146.69). The KD/KR value was more than one (1.75) and K value was 0.02. Narrow sense heritability was low (3.35 per cent) and the correlation between $(W_r + T_r)$ and T_r was positive and nonsignificant (0.58).

Spikelet fertility

The t² value for this trait was non-significant indicating the confirmity to the diallel assumptions. The dominance components H₁ and H₂ were significant while h² was non-significant. The additive component D, environmental effect E and F value were non-significant. $(H_1/D)^{1/2}$ value was more than one (5.64), H₂/4H₁ value was less than 0.25 (0.20) and H₁ - H₂ value was not equal to zero (279.02). The KD/KR value was more than one (1.95) and K value was 0.002. Narrow sense heritability was low (3.42 per cent) and the correlation between (W_r + V_r) and Y_r was positive and non-significant (0.19). Harvest index

The t² value was non-significant for this trait indicating the validity of diallel assumptions. The dominance components H1 and H2 were highly significant while h^2 non-significant. The additive was component D, environmental effect E and F value were non-significant. $(H_1/D)^{1/2}$ value was more than one (5.05), $H_2/4H_1$ value was less than 0.25 (0.22) and $H_1 - H_2$ value was not equal to zero (263.83). The KD/KR value was more than one (1.62) and K value was -0.003. Narrow sense heritability was low (4.14 per cent) and the correlation between (Wr + Vr) and Yr was positive and significant (0.86).

4.7.3 Graphical analysis

The genetic analysis was also carried out through graphical analysis for ten traits viz. total dry matter per plant, plant height, number of tillers per plant, grain breadth, grain yield per panicle, number of filled grains per panicle, test weight and tiller fertility.

In all the figures graph 'A' represents the variance of each array (V_r) and covariance between parents and their progenies in each array (W_r) as proposed and illustrated by Jinks and Hayman (1953) and Hayman (1954b). The regression of W_r and Vr along with the limiting parabola have been graphically represented. The theoretical regression line

with unit slope (b=1.00) is represented by dotted line whereas the estimated regression line is represented by a solid line and the short dotted lines indicate the mean W_r and V_r values.

Graph 'B' represents covariance of array members with array means of their non-recurrent parent (W_r') and the covariance between parents and their offsprings (W_r) . The theoretical regression line was drawn by a dotted line with a slope of 0.50.

The third graph 'C' is the standardized deviation graph with parental order of dominance (W_r+V_r) plotted against parental mean (Y_r) . The array points have been numbered representing the parents.

The results have been given characterwise here under:-Total dry matter per plant

Graphic analysis for this trait is presented in Fig.1. The regression coefficient for this trait (b=0.34 \pm 0.28) was not significantly different from zero. The observed regression line intercepted the W_r-axis above the origin. Parental array points were scatlered below the limiting parabola. Array point P₆ was the closest to origin while array point P₃ was the farthest from origin. The other array points between these two, in the increasing order of distance, were P₁, P₅ and P₄.



All the array points which were located below the unit regression line of $W_r - V_r$ graph were found above the regression line of $W_r - W_r$ ' graph barring P₄ which remained below the regression line.

Parental array points P_3 , P_4 and P_5 were in the first (++) region of standardized deviation graph while P_6 was in the second (+-) and R_1 and P_2 were in the third (--). None of the array points were found in the fourth (-+) quadrant.

Plant height

Graphical analysis for this trait is presented in Fig.2. The regression coefficient of W_r on V_r (b=0.09 \pm 0.27) was significantly different from one but not from zero. The observed regression line intercepted the W_r -axis below the point of origin. Well distributed parental array points within the limiting parabola indicated greater genetic diversity among the parents. Array points P₄ was the closest to origin while P₂, P₃, P₁, P₅ and P₆ were away from it.

All the parental arrays which were found below the theoretical regression line of $W_r - V_r$ graph were found above the regression line of $W_r - W_r'$ graph except P₂ and P₅ arrays.

Standardized deviation graph revealed that shorter paarents P_1 and P_5 were in the fourth (-+) cuadrant, P_6 and





 P_4 in the second (+-) region while taller parents P_2 and P_3 . were in the first (++) region.

Number of tillers per plant

The regression coefficient for this trait (b=0.36 \pm 0.32) was not significant from zero or unity. The interception of the observed regression line was below the origin (fig.3). Parental array points were distributed within the limiting parabola. Parental array points P₅, P₄ and P₁ were closer to origin whereas P₂, P₃ and P₆ were away from the origin.

All the parental arrays which were below the unit regression line of $W_r - V_r$ graph were found above the regression line of $W_r - W_r$ ' graph except P₂ and P₅ arrays.

Standardized deviation graph showed that parents with higher number of tillers per plant P_6 was in the first (++) region and P_3 was in the second (+-) region, while, P_1 , P_4 and P_5 were in the third (--) quadrant and P_2 was in the fourth (-+) region.

Grain breadth

The regression coefficient for this trait (b=0.77+0.30) was not significantly different from zero or one. The point of interception of the observed regression line was below the origin (Fig.4). Parental array points were well distributed within the limiting parabola. Parental array



points P_1 and P_4 were closer to the origin while P_6 , P_3 , P_2 and P_5 were away from the origin.

All the parental arrays which were below the unit regression line of $W_r - V_r$ graph were found above the regression line of $W_r - W_r$ ' graph except P₄ array point.

Standardized deviation graph showed that parents with broader grains P_3 and P_5 were in the first (++) region, P_4 and P_1 in the second (+-) guardrant and the slender grained parent P_2 was in the fourth (-+) guadrant. Array point P_6 was in the third (--) region.

Grain yield per plant

Graphical analysis for this trait is presented in The regression coefficient for Fig.5. this trait (0.10 + 0.51) was not significant from zero or unity. The observed regression line intercepted the Wr-axis above the of origin. Parental array points were point well distributed within the limiting parabola. Parental array point P3 was the closest to origin while P2, P6, P5, P1 and P_4 were away from the origin.

The parental array points which were below the unit regression line of $W_r - V_r$ graph were found above the regression line of $W_r - W_r$ ' graph except P4, P5 and P6 arrays.



Standardized deviation graph showed that parents with higher grain yield per plant P_4 and P_5 were in the first (++) quadrant and parental arrays P_1 , P_2 and P_3 with lower yield in the third (--) region. Array point P_6 was in the fourth (-+) quadrant.

Panicle weight per plant

The regression coefficient of W_r on V_r for this trait $(b=0.33 \pm 0.59)$ was not significant from zero or unity. The observed regression line intercepted the W_r -axis above the point of origin (Fig.6). Parental array points were well distributed within the limiting parabola. Parental array point P₃ was the closest to the origin and P₄ was the farthest from the origin. The other array points away from the origin were P₆, P₅, P₂ and P₁.

The parental array points which were below the unit regression line of $W_r - V_r$ graph were found above the regression line of $W_r - W_r$ ' graph.

Standardized deviation graph showed that parents with higher panicle weight per plant P_4 and P_5 were in the first (++) region and parental arrays with lower panicle weight per plant P_1 , P_2 , P_3 and P_6 were in the third (--) quadrant.







Number of spikelets per panicle

Graphical analysis for this trait is presented in Fig.7. The regression coefficient of W_r on V_r for this trait (b=0.39 \pm 0.22) was significantly different from unity but not from zero. The observed regression line intercepted the W_r axis above the point of origin. Parental array points were distributed within the limiting parabola. The parental array points in the increasing order of their distance from the origin was P₅, P₃, P₂, P₁, P₄ and P₆.

The parental array points which were below the unit regression line of $W_r - V_r$ graph were found above the regression line of $W_r - W_r$ ' graph.

Standardized deviation graph showed that parents with lower number of spikelets per plant P_1, P_2, P_4 and P_6 were in the fourth (+-) region while parents with higher number of spikelets per plant P_3 and P_5 were in the second (+-) region.

Number of filled grains per panicle

The regression coefficient of W_r on V_r for this trait (b=0.21 ± 0.05) was highly significant from unity and significantly different from zero. The observed regression line intercepted the W_r -axis above the point of origin (Fig.8). The parental array points were distributed within the limiting parabola. The parental array point P5 was the







LEGEND

A. W_r - V_r Graph

B. Wr'- Wr Graph

C. Standardized deviation graph

Limiting parabola

 Theoretical regression line Observed regression line

Parents (🛛)

HP-33 4. 1. Ambrose

HP-5 . ഗ .9 3. Pak-Basmathi HP-32 2. FIG. 8. NUMBER OF GRAINS/PANICLE

125

HP-20

closest to origin while P_1 was the farthest from origin. The other array points away from origin were P_3 , P_2 , P_4 and P_6 in the increasing order of distance from the origin.

All the parental array points of $W_r - V_r$ graph which were below the unit regression line were located above the regression line of $W_r - W_r'$ graph.

The standardized deviation graph showed that parental array point P_1 was in the first (++) quadrant, P_5 was in the second (+-) region, P_2 , P_3 and P_4 were in the third (--) region and P_6 was in the fourth (-+) quadrant.

Test weight

The graphical analysis for this trait is presented in Fig.9. The regression co-efficient of W_r on V_r for this trait (b=0.38 ± 0.52) was not significantly different from zero or unity. The observed regression line intercepted the W_r -axis below the point of origin. The parental array points were well distributed within the limiting parabola. The parental array points in the increasing order of distance from the origin was F₃, P₁, P₅, P₂, P₄ and P₆.

The parental array points which were below the unit regression line of $W_r - V_r$ graph were located above the regression line of $W_r - W_r'$ graph except the array point P₃.





Standardized deviation graph showed that parental array point P_4 was in the first (++) quadrant, P_1 , P_2 , P_3 and P_5 were in the second (+-) region and P_6 was in the fourth (-+) region.

Tiller fertility

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The regression coefficient of W_r and V_r for this trait (b=0.03 \pm 0.41) was not significantly different from zero or unity. The observed regression line intercepted the W_r -axis above the point of origin (Fig-10). The parental array points were well distributed within the limiting parabola. The parental array point P₆ was the closest to the origin and P₄ the farthest from the origin. The other parental arrays away from the origin were P₅, P₂, P₃ and P₁.

The parental array points which were below the unit regression line of $W_r - V_r$ graph were located above the regression line of $W_r - W_r$ ' graph, except the array points P_2 , P_4 and P_5 .

Standardized deviation graph showed that parental array points P_4 and P_5 were in the first (++) quadrant, P_1 and P_6 were in the third (--) region and P_2 and P_3 were in the fourth (-+) quadrant.

4.8 Selection indices

Selection indices for grain yield were formulated by considering the parameters number of productive tillers per

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plant (X_2) , panicle weight per plant (X_3) , number of filled grains per panicle (X_4) , test weight (X_5) and harvest index (X_6) . Grain yield per plant (X_1) was considered as the dependent variable in the analysis.

In the results presented on selection indices, the relative efficiency obtained by straight selection for yield was 100 per cent (genetic gain = 15.37). The values of beta coefficients obtained for the characters in each combination, genetic gain and relative efficiency estimated for each combination are presented in table 4.13.

None of the single character index showed an efficiency greater than 100 per cent. The best single character index was panicle weight per plant (X_3) with an efficiency of 92.64 per cent (genetic gain = 14.24) followed by harvest index (X_6) with an efficiency of 87.05 per cent (Genetic gain = 13.38).

Among the two character combinations highest efficiency of 108.73 per cent (Genetic gain = 16.71) was obtained for X_1 , X_3 combination. The remaining two character combinations showed an efficiency of less than 100 per cent. Among these X_1 , X_6 combination showed an efficiency of 99.18 (genetic gain = 15.24) followed by X_3 , X_6 combination and X_3 , X_4 combination which showed an efficiency of 98.64 and 94.46 per cent, respectively and genetic gain of 15.16 and 14.51 respectively.

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4.13 Genetic gain and relative efficiency of different selection indices in rice.

Characters in index Discriminant function -------Genetic gain -----Relative х efficiency 1 X 15.3663 100,00 Y = 0.3215 X6.0326 39.26 Y = 1.0191 X 14.2354 92.64 Y = 0.4107 X12,1911 79.34 X Y = 23.0843 X5 7.6035 x 49.48 Y = 0.5005 X6 6 13.3768 X + Y 87.05 Y = -0.2703 X + 1.2500 X2 3 2 16.7081 108.73 x + x Y = 0.0726 X + 0.3923 x 2 2 4 12.2548 79.75 X + X Y = 0.2119 X + 19.1476 X2 5 8.4816 55.20 X + X Y = 0.3909 X + 0.5259 X2 2 15.2407 99.18 X + X Y = 0.8099 X + 0.1371 X3 3 4 14.5148 94.46 X + X Y = 0.9973 X + 1.8413 X3 3 14.2451 92.70 X + X Y = 0.6852 X + 0.2615 X3 3 15.1572 98.64 X + X Y = 0.4073 X + 22.5973 X4 5 4 14.2833 92.95 X + X Y = 0.2085 X + 0.3533 X4 6 4 14.2049 6 92.44 X + X Y = 13.1106 X + 0.4570 X 5 14.0085 5 6 91.16 X + X + X Y = -0.2528 X + 1.0538 X + 0.1189 X 2 3 16.7682 2 3 109.12 X + X + X Y = -0.2707 X + 1.2269 X + 1.9800 X 16.7203 3 2 3 108.81 X + X + X Y = 0.2788 X + 0.2140 X + 0.4440 X 15.2593 3 6 2 3 99.30 X + X + X Y = -0.0901 X + 0.4299 X + 24.2449 X 4 5 4 15.0507 97.95 2 X + X + X Y = 0.3705 X + 0.0278 X + 0.5049 X 4 6 15.2493 99.24 2 4 6 X + X + X Y = 0.3573 X + 5.4079 X + 0.5058 X 15.3241 5 6 99.73 2 5 X + X + X Y = 0.5377 X + 0.2274 X + 11.3585 X 4 5 14.7534 95.01 3 4 X + X + X Y = 0.6095 X + 0.0672 X + 0.2404 X 4 6 15.2150 99.02 3 4 6 X + X + X Y = 0.6335 X + 3.7619 X + 0.2670 X 15.1946 6 98.88 3 5 X + X + X Y = 0.2585 X + 17.0713 X + 0.2614 X 15.1589 5 6 98.65

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X =	Grain yield	X = No. of grains per panicle
1		4
X =	No.of productive tillers	X = Test weight
2	and the second second second second	5
X :	Panicle weight	X = Harvest index
3		6

The maximum efficiency of 109.12 per cent (Genetic gain = 16.77) was observed among three character combination for the X₁, X₃, X₄ combination, followed by the combination X₁, X₃, X₅ which showed an efficiency of 108.81 per cent (Genetic gain=16.72). The remaining three character combinations showed efficiency of less than 100 per cent. Among these X₁, X₅, X₆ combination, X₁, X₃, X₆ combination X₁, X₄, X₆ combination and X₃, X₄, X₆ combination showed efficiencies of 99.73 99.30, 99.24 and 99.02 per cent, respectively with genetic gain of 15.32, 15.26, 15.25 and 15.22 respectively.

Among four character combinations highest efficiency of 109.81 per cent (Genetic gain = 16.87) was obtained for X_1 , X_3 , X_4 , X_5 combination followed by X_1 , X_4 , X_5 , X_6 combination and X_3 , X_4 , X_5 , X_6 combination which showed efficiences of 100.38 and 100.08 per cent respectively, with genetic gain of 15.42 and 15.38 respectively. The combinations X_1 , X_3 , X_5 , X_6 and X_1 , X_3 , X_4 , X_6 showed efficiencies of 99.74 and 99.40 per cent respectively with genetic gain of 15.33 and 15.27 respectively.

The selection index with all the five characters included showed an efficiency of 100.39 per cent with a genetic gain of 15.43.

DISCUSSION

V. DISCUSSION

Plant breeding is a continuing enterprise. The unrelenting demand for increased food production due to continuous increase in population, alteration the in spectrum of pests, diseases and environment by the interference of human beings and changes in economic and consumer demands ensure the continuance and hopefully increased efficiency of this enterprise. Crop improvement programme has a set of defined objectives. The success of a clant breeder depends on his ability to define and assemble the requisite genetic variability, recombine this genetic variability and extract from the gene pool those gene combinations which yield superior cultivars according to his The major problem facing the breeder of self objectives. fertilizing plant species is the choice of superior crosses and choice of superior lines with desirable combination of characters within the crosses.

The concept of combining ability in self pollinated crops like rice and wheat is of recent origin. Identification of superior combiners helps the breeders in selecting appropriate parents to be used in the breeding programme to develop superior varieties. Hence, it is contemplated in the present study to identify superior combining parents and to understand the genetic architecture of yield and yield components. The present study was undertaken following the diallel technique developed by Jinks and Hayman (1953), Jinks (1954, 1956), Hayman (1954, 1958, 1960) and Griffing (1956) utilizing 6 fine grained parental lines viz., Ambrose, HP-32, Pak-Basmathi, HP-33, HP-5 and HP-20.

The results obtained from the investigation are discussed under the following heads.

- 1. Mean performance of parents and F_2 crosses
- 2. Variability studies
- 3. Heritability and genetic advance
- 4. Character association
- 5. Path coefficient analysis
- 6. Diallel studies
- 7. Selection indices

5.1 Mean performance of parents and F₂ crosses

The per se performance of parents (Table 4.1) revealed HP-5 (P₅) was the highest yielder. It also had that the highest panicle weight per plant, number of spikelets per panicle, number of filled grains per panicle, test weight, spikelet fertility, harvest index, panicle length and total dry matter per plant. HP-20 (P₆) had the least weight and the longest grain test length and highest number of tillers per plant and highest number

of productive tillers per plant. It also had the least number of spikelets per panicle. HP-32 (P₂) had the least grain yield per plant, panicle weight per plant, number of filled grains per panicle, tiller fertility, grain length and grain breadth, but it had the highest grain length to breadth ratio. Pak-Basumathi (P₃) had the highest plant height and grain breadth, but the least spikelet fertility and harvest index. Ambrose (P₁) had the least plant height, total dry matter per plant and panicle length.

per se performance of the crosses (Table 4.1) The indicated that the cross $P_1 \times P_2$ had the highest grain yield per plant. It also showed the highest spikelet fertility and harvest index. Cross P1x P4 had the least grain yield per plant. It also showed the least panicle weight per plant, number of filled grains per panicle, spikelet fertility, harvest index, total dry matter per plant and number of productive tillers per plant. Cross P1x P3 had the highest grain length, but the least test weight and tiller fertility. Cross P3x P5 had the highest plant height, total dry matter per plant, number of tillers per plant, number of productive tillers per plant and grain breadth, but the least panicle length. Cross $P_4x P_6$ had the least plant height, grain length, grain length to breadth ratio, and number of spikelets per panicle, but the highest test weight.

The analysis of variance revealed highly significant differences among the 21 treatments for all the traits studied (Table 4.2). The partitioning of the treatment sum of squares into parents, crosses and parents vs. crosses showed highly significant differences due to parents indicating greater genetic diversity among them for all the traits studied.

The sum of squares due to the crosses was also highly significant for all the traits studied. The mean sum of squares due to parents vs. crosses was highly significant for plant height, number of tillers per plant, number of productive tillers per plant, panicle length, grain length, grain length to breadth ratio, panicle weight per plant, number of spikelets per panicle, number of filled grains per panicle and tiller fertility and significant at 5 per cent only for spikelet fertility indicating overdominance and the importance of non-additive gene action for these traits. For the rest of the traits the mean sum of squares due to parents vs. crosses was non-significant.

5.2 Variability studies

High phenotypic coefficient of variation was observed for grain yield per plant, panicle weight per plant, number of filled grains per panicle and harvest index. These findings are in confirmation with the results reported by Balakrishna Rao <u>at al</u> (1973) and Sivasubramanian and Madhava Menon (1973). Moderate phenotypic coefficient of variation was observed for total dry matter per plant, plant height, number of tillers per plant, number of productive tillers per plant, number of spikelets per pancicle and spikelet fertility. These results are in confirmation with the findings reported by Balakrishna Rao <u>et al</u>. (1973), Chauhan (1990) and Singh et al. (1986)

Low phenotypic coefficient of variation was observed for panicle length, grain length, grain breadth, length to breadth ratio of grain, test weight and tiller fertility. These results are in concordance with those reported by Roychoudhury (1967) except for that of grain characteristies.

High values of genotypic coefficient of variation were observed for grain yield per plant, panicle weight per plant, number of filled grains per panicle and harvest index. These results were in confirmity with those reported by Sivasubramanian and Madhava Menon (1973). Moderate genotypic coefficient of variation were observed for total dry matter per plant, plant height, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle and spikelet fertility. Choudhury et al. (1973), Shukla et al. (1972), Tripathy et al. (1973) and Ghose et al. (1981) reported similar results. Low genotypic coefficient of variation values were observed for the traits panicle length, grain length, grain breadth, length to breadth ratio of grain, test weight and tiller fertility. Similar findings were reported by Gopal Reddy and Goud (1970), Sukanya (1984) and Sreenatha (1987).

PCV and GCV estimates for all the traits studied were relatively of same magnitude indicating less sensitivity of the characters to environmental changes.

5.3 Heritability and genetic advance

The degree to which the phenotypic variations that can be explained as variation in genotype is estimated as the ratio of genotypic variability to the total phenotypic variability and is called heritability in broad sense, which is otherwise known as 'Degree of genetic determination'. Computation of heritability value will help to know the extent to which a phenotype is susceptible to environmental influence indicating the accuracy with which selection on phenotype would be effective.

Though heritability estimates represents the relative genetic strength of characters and indicate the efficiency of selection system, still their scope is restricted as they are prone to change with change in environment (Swarup and Chougale, 1962; Athwal and Singh, 1966). So heritability values when used in conjugation with genetic advance, can be of importance in selection programme.

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In the present study, grain yield per plant, panicle weight per plant, number of filled grains per panicle, and harvest index recorded very high heritability coupled with high genetic advance. This indicated that the environmental effect was low on the characters. In these characters the hariability may be due to more of additive interaction of genes. Hence selection for these traits can be exercised to increase the yield per se.

Moderately high heritability in broad sense coupled with moderate genetic advance was recorded for total dry matter per plant, plant height, number of tillers per plant, number of productive tiller per plant number of spikelets per plant and spikelet fertility. The variability in these characters may be due to both additive and non-additive interaction of genes.

High heritability in broad sense coupled with low genetic advance was recorded for panicle length, grain length, grain breadth, length to breadth ratio of grain, test weight and tiller fertility. This indicates a greater control by non additive genes on these characters.

5.4 Heterosis

With regard to heterosis for seed yield, cross $P_1 \times P_2$ recorded the highest percentage over mid parent, better parent and standard (Table 4.4). This cross also recorded significant positive heterosis over mid-parent, better parent and standard for panicle weight per plant, number of filled grains per panicle, test weight, spikelet fertility and harvest index.

This cross also had significant positive heterosis over mid parent and better parent for total dry matter per plant and tiller fertility. This cross P1x P2 showed significant positive heterosis over mid parent for panicle length, grain length and grain breadth and significant positive heterosis over standard for number of tillers per plant and number of productive tillers per plant. However the cross P1x P2 showed significant negative heterosis over better parent for plant height and length to breadth ratio of grain. It also showed significant negative heterosis over standard for plant height, panicle length and number of spikelets per panicle. The cross P1x P3 followed P1x P2 in high percentage of positive heterosis over mid parent and better parent. This cross P1x P3 also showed significant positive heterosis over mid parent and better parent for grain length, grain length to breadth ratio, panicle weight per plant, number of filled grains per panicle and spikelet fertility. However, the cross P₁x P₃ showed significant negative heterosis over mid parent, better parent and standard for total dry matter per plant, number of productive tillers per plant, grain breadth, test weight and tiller fertility. It also showed negative and significant

heterosis over mid parent and better parent for number of tillers per plant.

5.5 Diallel studies

5.5.1 Validity of diallel assumptions

Since Hayman's approach of genetic analysis is based the assumptions of homozygosity of parents, diploid on segregation, no difference between reciprocals, independent action of non-allelic genes, uncorrelated distribution of genes in parents and the absence of multiple allelism, it is necessary to test for the conformity of the data to these assumptions before the results are interpreted. Uniformity of $W_r - V_r$ values over the parental arrays and nonsignificance of t² test are used to test the validity of diallel assumptions. Among the assumptions uncorrelated gene distribution, absence of multiple allelism and absence of epistasis are difficult to satisfy practically (Manjunath and Goud, 1978/79). In the present study also, diallel assumptions were not met for two of the traits since the t^2 test revealed highly significant difference for the number of filled grains per panicle and significant difference for panicle length. However, some investigators (Allard, 1956; Crumpacker and Allard, 1962 and Aksel and Johnson, 1963) found that partial invalidity of assumptions did not create a significant source of bias in the genetic analysis of their respective data.

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Rice ($\underline{\text{Oryza}}$ sativa $\underline{\text{L}}$.) behaves as a true diploid forming 24 bivalents although it is an amphidiploid with a somatic chromosome number of 24.

Rice is a strictly self pollinated crop having nil or negligible out-crossing. Hence the parents used for the present study can be assumed to be of homozygous nature and also lacking in the maternal effects. However possibility of heterozycosity for polygenic traits cannot be ruled out, also maternal effects, as reciprocal crosses were not as included in the present study. It is also difficult to establish uncorrelated gene distribution, absence of epistasis and multiple allelism as they are bound to be present in characters governed by polygenes. In fact these three assumptions from "null hypothesis" and their failure enables to detect epistasis, overdominance, linkage and allelism. Jinks and Hayman (1953) multiple proposed homozygosity of parents as an essential assumption basic to diallel analysis. Dickinson and Jinks (1956) examined the possibility of removing this assumption and concluded the that although heterozygosity of parents may bring about departure from homozygous analysis, most of the genetic quantities can be estimated, though somewhat less precisely.

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Labana (1982) observed that Hayman's and Sangha approach provided detailed description of the relative genetic properties of the inbred lines while the Griffing's approach stresses statistical concepts of GCA and SCA though there is some loss of genetic information. A comparative study of Hayman's and Griffing's approaches of diallel analysis led Arunachalam (1976) and Baker (1978) to conclude that Griffing's approach for diallel analysis has more general utility for plant breeders. Since Griffing's approach is based on the sole assumption of parental homozygosity, it provides necessary genetic information of additive or epistatic gene action which could be effectively utilised for the selection of parents and their further usage in the breeding programmes.

In the present study both Hayman's and Griffing's approaches were employed and results are interpreted hereunder.

5.5.2 Combining ability analysis

Analysis of variance for combining ability (Table 4.9) revealed that both GCA and SCA variances were highly significant for all the characters studied which indicates that there was considerable genetic variability in the population of the present study.

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The ratio of GCA/SCA indicates the preponderence of additive gene action over non-additive for total dry matter per plant, grain breadth, grain yield per plant, panicle weight per plant, number of spikelets per panicle, number of filled grains per panicle and test weight. The result for total dry matter per plant corroborates with the findings of Kuo and Liu (1987) and Peng and Virmani (1990) while for grain breadth the result is in confirmity with the findings of Singh and Shrivastava (1982), Panwar and Paroda (1983)and Singh (1982). Preponderance of additive gene action for grain yield per plant have also been reported by Chang et al. (1973), Haque et al. (1980), Kalaimani and Sundaram (1987) and Mohapatra and Mohanty (1985) and for panicle weight per plant has been reported by Rao et al. (1980).Balakrishna Rao et al. (1973) Kaushik and Sharma (1988) and Mohapatra and Mohanty (1985) have reported the preponderance of additive gene action for number of spikelets per panicle while Haque et al. (1980) and Mohapatra and Mohanty (1985) reported the same results for number of filled grains per panicle. Haque et al. (1980) and Tripathy and Misra (1985) also reported similar results for test weight.

The ratio of GCA/SCA variances indicates the preponderance of non-additive gene action over additive gene action for plant height, number of tillers per plant, number of productive tillers per plant, panicle length, grain length, tiller fertility, spikelet fertility and harvest

index. Preponderance of non-additive gene action for plant height have been reported by Anandakumar and Rangaswamy (1986), Dhaliwal and Sharma (1990), Jun and Kwak (1984), and Singh et al. (1980). Similar result have been reported for number of tillers per plant by Singh and Shrivastava (1982). Cheema et al. (1986), Dhaliwal and Sharma (1990), Jun and Kwak (1984), Kalaimani and Sundaram (1987), Singh and Shrivastava (1982) and Singh et al. (1980) reported similar results for number of productive tillers per plant. Nonadditive gene action for panicle length has been reported by Anandakumar and Rangaswamy (1986), Dhaliwal and Sharma (1990), Jun and Kwak (1984) and Singh et al. (1979). Similar results have been reported for grain length by Dhaliwal and Sharma (1990), and for spikelet fertility by Jun and Kwak (1984). Non-additive gene action for harvest index has been reported by Peng and Virmani (1990).

The estimates of gca effects revealed wide differences among the parents. HP-5 (P₅) ranked first as good general combiner for yield per plant and also for total dry matter per plant, panicle length, grain breadth, panicle weight per plant, number of spikelets per panicle, number of filled grains per panicle, test weight, spikelet fertility and harvest index, but was a poor combiner for grain length (Table 4.10). HP-33 (P₄) ranked second as good general combiner for yield and also for dwarf stature, grain breadth, panicle weight per plant, test weight, tiller

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fertility and harvest index, but was a poor combiner for total dry matter per plant, number of tillers per plant, panicle length, number of spikelets per panicle, number of filled grains per panicle and spikelet fertility.

The high gca effect not only for yield per plant but also for a number of other yield components obtained for these two parents suggested that combining ability for grain yield was positively related to combining ability for various yield contributing characters, which corroborates with the findings of Manuel and Palaniswany (1989).

Crosses $P_1 x P_2$, $P_1 x P_3$, $P_4 x P_5$, $P_5 x P_6$, $P_4 x P_6$ and $P_3 x P_6$ were the best specific combinations for yield per plant. These crosses also showed good specific combination for other traits like dwarf stature, number of filled grains per panicle and harvest index.

On comparison of the sca effects with the mean <u>per se</u> performance of the crosses for yield, cross $P_1 \times P_2$ which was the best specific combiner gave the highest grain yield. Cross $P_1 \times P_2$ was also good specific combiner for total dry matter per plant, dwarf stature, number of productive tillers per plant, grain breadth, panicle weight, number of filled grains per panicle, test weight, tiller fertility and harvest index. The cross $P_4 \times P_5$ which ranked second with respect to the <u>per se</u> performance for grain yield, ranked third with respect to the sca effects for the trait. The cross $P_{4x} P_5$ also showed good specific combining ability for dwarf stature, grain length, panicle weight per plant, number of spikelets per panicle, number of filled grains per panicle, spikelet fertility and harvest index. Thus it is clear that the best <u>per se</u> performers for grain yield also has good specific combining ability across the yield and yield attributes.

Information on number of crosses showing significant heterosis over mid parent, better parent and standard value and specific combining ability is given in Table 5.1. It is clear from the table that majority of the crosses showing significant heterosis over mid parent, better parent and standard were in the desirable direction for panicle length (except over standard) grain length, number of spikelets per panicle, number of filled grains per panicle, test weight, spikelet fertility and harvest index (except over better parent). These results were also reported by Madhusudan Rao (1965), Maurya & Singh (1978), Nijaguna (1982), Anandkumar and Sree Rangaswamy (1989a), Kalaimani and Sundaram (1987b) and Dushyant Kumar (1989).

It can also be noted from the table that majority of the crosses showing significant heterosis over mid parent, better parent and standard were not in the desirable direction for total dry matter per plant, plant height (except over standard), number of tillers per plant, number

Tra	its	Het MP	erosis BP	over Standard	sca effects
1.	Total dry matter per plant	11(6)	14(11)	11(9)	12(7)
2.	Plant height	13(1)	11(3)	14(10)	12(7)
3.	Number of tillers per plant	11(11)	12(12)	6(2)	8(7)
4.	Number of productive tillers per plant	12(12)	13(13)	9(7)	10(8)
5.	Panicle length	7(1)	3(1)	8(8)	7(2)
6.	Grain length	12(3)	12(6)	7(2)	9(3)
7.	Grain breadth	8(3)	6(5)	6(4)	9(3)
8.	Grain yield per plant	13(6)	13(9)	9(6)	12(6)
9.	Panicle weight oer plant	11(3)	12(7)	13(10)	8(3)
10.	Number of spikelets per panicle	9(0)	9(5)	14(4)	14(8)
11.	Number of filled grains per panicle	12(2)	11(6)	12(2)	12(4)
12.	Test weight	12(7)	11(8)	11(7)	13(8)
13.	Tiller fertility	11(6)	12(9)	12(12)	11(6)
14.	Spikelet fertility	14(6)	13(6)	10(3)	14(7)
15.	Harvest index	14(6)	11(7)	13(5)	15(6)
Fig	ures in parenthesis	refer	to th	ne freque	ency of
sig	nificantly negative hybr	ids.			

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of productive tillers per plant, grain yield per plant (except over MP) and tiller fertility. For harvest index significantly negative better parent heterosis was observed in high frequency which was in confirmity with the results reported by Nijaguna (1982).

There was a close relationship between the frequency of crosses showing significant sca effects and those showing heterosis over better parents for all traits (Table 5.1). Singh and Richharia (1978) and Kabiraj (1986) also reported high heterotic crosses as good specific combiners. Their observations explain the similarity in the frequencies of significant heterosis over better parent with the frequencies of significant sca effects observed in the present study.

5.5.3 Heterosis and combining ability across the traits

It was observed that heterosis and combining ability effects were in desirable direction for some characters and in undesirable direction for others. Such observation is common as character components are correlated positively or negatively among themselves (Arunachalam and Bandyopadhyay, 1979). Hence an attempt was made to ascertain the overall status of a parent or cross with respect to gca, sca and heterosis for seed yield and other yield component studied. Method outlined by Arunachalam and Bandyopadhyay (1979) for gca and sca and Arunachalam <u>et al</u>. (1984) for heterosis, was followed. The procedure is briefly described below.

5.5.3.1 Heterosis

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For every trait, a cross was assigned +1 score if its mean value significantly exceeded that of superior parent in the desirable direction. The scores were added across the traits and final score obtained which gives the overall heterosis across the characters. This was in slight modification to Arunachalam <u>et al</u>. (1984) who gave +1 score for every trait in a cross if it exceeded the better parent per se and did not consider its signifacance.

5.5.3.2 Combining ability effects

procedure followed was as The described by Arunachalam and Bandyopadhyay (1979). The mean of gca effects significant at 5 percent level was used as a norm for that trait and significant gca effects equal to or greater than the norm were given a score of +1 and the gca effects of the parent whose score was less than the norm were given a score of -1 . Non-significant gca effects received zero score. Final score was obtained by totalling the scores across all the traits. The mean of the final score was taken as final norm and parents whose value exceeded the final norm were given high (H) overall status and parents whose final score was less than final norm were given low(L) status. The same procedure was followed for classifying the hybrids as high or low for their overall sca status.

5.5.3.3 Overall heterosis and Combining ability

The crosses with high overall better-parent heterosis with their final score are presented in Table 5.2. The parents with high or low overall doe and crosses with high or low overall sca status are presented in Table 5.3. It is clear from the Tables 5.2 and 5.3 that all the crosses with an overall score of 5 or more as also cross $P_{4x} P_{5}$ with 3 scores and crosses $P_{4x} P_{6}$ and $P_{5x} P_{6}$ with 2 scores each for heterosis had also high overall sca status. This is supported by Arunachalam <u>et al</u>. (1964) and Kabiraj (1986) who reported that about half of the heterotic crosses in groundnut and cowpea respectively had high sca to explain heterosis.

Score	Parents	Crosses
9	P ₅	P ₁ x P ₂
8		P ₂ x P ₆
7		P ₁ xP ₃ , P ₂ x P ₃
5		P ₂ x P ₄
3		P ₃ x P ₆ , P ₄ x P ₅
2		P3x P5, P4x P6, P5x P6
1	•	P ₁ x P ₆ , P ₂ x P ₅ , P ₃ x P ₅

Table 5.2 Overall better parent heterosis for crosses

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Overall Status	Overall Score	Parents	Crosses
High	1 Ó	-	P ₁ x P ₂
	à	P 5	-
	8	-	P ₂ x P ₆ , P ₄ x P ₅ , P ₅ x P ₆
	Ą	-	P ₂ x P ₃
	3	-	P ₁ x P ₃ , P ₂ x P ₄
	1	-	Plx P6
Low	0	P ₂	-
	~1	P4	P ₃ x P ₅ , P ₃ x P ₆
	-2	P ₃	-
	-4	Pl, P6	-
	-6	-	P ₁ x P ₅ , P ₁ x P ₆
	-9	-	P ₃ x P ₄
	-10	-	P ₂ x P ₅
	-12	-	Plx P4

Table 5.3 Overall gca status of parents and sca status of crosses across traits

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Based on the overall gca effects, the crosses were classified as HH (both the parents in a cross with high overall gca status), HL(one parent with high and other parent with low overall gca status) LL (both the parents in a cross with low overall gca status). The frequency of

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crosses with high overall heterosis over better parents falling in each class was as follows:

gca combination	НН	HL	LL
Frequency of crosses	-	4	9

It is thus clear that parents with high x low or low x low qca effects only give rise to high frequency of heterotic crosses where the LL combination is more useful. This type of results for heterosis was also reported by Arunachalam <u>et al.</u> (1984) and Mohapatra and Mohanty (1985), thus indicating the importance of genetic diversity in gca effects for realising heterosis.

Similarly, the frequency of crosses with high overall scalated was also classified into HH, HL and LL classes based on the overall gca effects of the parents involved in a partiular cross. The results were as follows:

gca	combination	НН	HL	ΓĽ
Freau with	uency of crosses high scaleffects	-	2	6

This also followed a similar pattern as that of heterosis. Crosses with high x low or low x low overall goa status of the parents only give rise to crosses with high overall specific combining ability status where LL combination is more useful. This type of result has also been reported by Mohapatra and Mohanty (1985).

5.5.4 Genetic component analysis

Genetic component analysis showed that the dominance component was relatively larger than the additive component for all the traits studied (Table 4.12). The results substantiated were in accordance with the results obtained by Griffings method. The value of H1 for all the characters were higher than the values of D and were significant, which indicated the predominance of nonadditive genetic variance in the present experimental material. Similar results have also been reported by Khaleque et al (1978) and Singh et al. (1980). The value of H₂ component of genetic variation was positive and significant for all the characters. The H₂ value were also more than D values for all the characters indicating the predominance of non-additive gene action.

F value was negative and non-significant for number of spikelets per panicle indicating recessive alleles were more frequent than dominant alleles which was also corroborated by the lower values of KD/KR. All the other characters showed non-significant positive F value indicating dominant alleles were more frequent than recessive alleles which was also corroborated by higher values of KD/KR. Singh et al. (1980), Subramanian and Rathinam (1984) and Kalaimani and Sundaram (1987) have also made similar observations for certain traits.

The t² estimates to test the uniformity of the N_r , V_r values were not significant for drv matter per plant, plant height, number of tillers per plant, number of productive tillers per plant, grain length grain breadth, grain vield per plant, panicle weight per plant, number of spikelets per panicle, test weight, tiller fertility, spikelet fertility and harvest index indicating the fulfilment of diallel assumption for these traits. For the traits canicle length and number of filled grains per panicle the t² value was significant indicating the failure of one or a few diallel assumptions. Significant regression coefficients deviating from one also revealed the existence of large quantity of linkage and epistasis for plant height, panicle length, grain length, number of spikelets per panicle, number of filled graints per panicle, spikelet fertility and harvest index.

The values of $(H_1/D)^{1/2}$ ratio were found to be more than one for all the characters, indicating the operation of over-dominance (Singh <u>et al.</u>, 1980). The H₂ component is smaller than the H₁, thereby indicating the unequal proportion of positive and negative alleles in the loci governing the characters and the asymmetrical distribution of genes in the parents was evidenced by the value of $H_2/4H_1$, which was less than 0.25 in all the traits, which is similar to the findings of Kalaimani and Sundaram (1987). The number of blocks of genes influencing the character was just one for all the characters as revealed by the h^2/H_2 value. Subramanian and Rathinam (1984) have also reported similarly for a few traits.

The negative correlation between the mean values of the parents Yr and the order of domiance (Wr+Vr) for plant height, grain length, grain breadth, number of spikelets per panicle, number of filled grains per panicle and test weight suggests that the dominant genes are associated with high mean expression. Similar results were obtained by Subramanian and Rathinam (1984) and Kalaimani and Sundaram (1987) for a few traits. All the other traits showed positive correlation suggesting that the recessive genes are associated with high mean expression for these traits.

5.5.5 Graphic analysis

Graphical analysis for the ten traits revealed considerable genetic variability and diversity among the parents used in the present study as the parental array points were well scattered within the limiting parabola. The observed regresson line interecpted the W_r -axis below the point of origin indicating over dominance for the traits plant height, number of tillers per plant, grain breadth and test weight. The observed regression line intercepted the W_r -axis above the point of origin indicating partial dominance for the traits total dry matter per plant, grain yield per plant, panicle weight per plant, number of spikelets per panicle, number of filled grains per panicle and tiller fertility. A perusal of W_r - V_r and W_r' - W_r graph indicated complementary type of epistasis for the traits total dry matter per plant, number of filled grains per panicle weight per plant, number of spikelets per plant, grain breadth, panicle weight per plant, number of spikelets per panicle and number of spikelets per plant, number of spikelets per panicle and number of tilled grains per plant, number of tillers per plant, grain breadth, panicle weight per plant, number of spikelets per panicle and number of tilled grains per plant, test weight and tiller fertility some parents showed duplicate type of epistasis in addition to the complementary type of epistasis.

5.6 Character associations

Yield is polygenically controlled guantitative character which is the total effect of several component factors. The influence of these factors can be known through the correlation studies. Genetic correlation between different characters of plant arises because of linkage and pleiotropism of developmentally induced functional relationships (Harland, 1939).

To determine the extent and nature of relationship between yield and yield components, a knowledge of interaction of characters among themselves and with

environment is very essential. In the present study, both genotypic and phenotypic correlations were estimated for yield and yield component characters.

In the present study, in general, it was observed that the genotypic correlation coefficients were higher than phenotypic correlation coefficients. This indicates that, though there was a strong inherent association between various characters studied, the phenotypic expression of the correlation was influenced by environment.

Plant height was significantly negatively correlated with grain yield per plant. This result was also supported by several other workers namely Amirthadevarathi- nam (1983), Eunus <u>et al</u>. (1976), Goud <u>et al</u>. (1969), Majumdar <u>et al</u>. (1971) and Sukanya Subramanian and Rathinam (1984). Plant height was also significantly negatively correlated with spikelet fertility and harvest index which may be the cause of its negative correlation with grain yield per plant.

Number of productive tillers per plant was found to be asociated positively and significantly with yield. Hence high productive tillering types should be selected for, to increase the yield. Several investigators have reported similar results in rice, namely, Amirthadevarathinam (1983), Dhanraj <u>et al</u>. (1987), Hegde (1987), Paramasivan (1986) and Rao and Jagadish (1987). The significant positive correlation of number of productive tillers per plant with grain yield per plant may be due to the significant positive correlation of number of productive tillers with number of tillers per plant, panicle weight per plant and tiller fertility.

Panicle weight per plant was highly significantly and positively correlated with grain yield per plant. Such findings have also been reported by Balakrishna Rao <u>et al</u>. (1973), Choudhury <u>et al</u>. (1973) and Lin (1969). Panicle weight per plant was significantly and positively associated with total dry matter per plant, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle,test weight, spikelet fertility and harvest index which may be the cause for it to be positively associated with grain yield.

Number of filled grains per panicle was positively and highly significantly correlated with grain yield. Such reports were also given by Dhanraj <u>et al</u>. (1987), Hegde (1987), Prasad <u>et al</u>. (1988) and Rao and Jagadish (1987). Panicle weight per plant, number of spikelets per plant, spielet fertility and harvest index were also significantly and positively associated with number of filled grains per panicle which might have resulted in the positive and significant association of number of filled grains per panicle with grain yield per plant.

Spikelet fertility was positively and highly significantly associated with grain yield per plant. This may be attributed to the highly significant positively correlation of spikelet fertility with number of filled grains per panicle and harvest index.

Harvest index was highly significantly and positively correlated with grain yield per plant. This may be attributed to the highly significant positive association of harvest index with panicle weight per plant, number of filled grains per panicle and spikelet fertility.

5.7 Path coefficient analysis

Correlation does not consider the dependence of one variable over another independent variable. Path coefficient analysis is a statistical tool which helps in detecting the direct and indirect effects of one variable over another dependent variable. The nature and degree of association among any two characters may be the results of several interacting factors which constitute both direct effect of independent variable on dependent variable through other variables.

The path coefficient analysis was conducted for grain yield (dependent variable) with total dry matter per

plant, number of productive tillers per plant, panicle weight per plant, number of filled grains per panicle, test weight and harvest index as independent variables.

At both phenotypic and genotypic level, harvest index attributed maximum direct effect on grain yield followed by total dry matter per plant, panicle weight per plant, test weight and number of filled grain per panicle. Number of productive tillers per plant had direct negative effects on grain yield.

Inspite of the negative direct effect of number of productive tillers per plant on grain yield, the positive indirect effect of number of productive tillers per plant on grain yield, through total dry matter per plant, panicle weight per plant, number of filled grains per panicle, test weight and harvest index, resulted in significant positive corelation between grain yield and number of productive tillers per plant.

The increase in grain yield per plant with an increase in total dry matter per plant was due to the high positive direct effect of total dry matter per plant on yield, along with positive indirect effects of it through panicle weight per plant, number of filled grains per panicle and test weight. A similar phenomenon was observed for the increase in grain yield per plant with an increase in the harvest index.

5.8 Selection indices

The interaction between heritable and non-heritable variation makes yield a very complex character for straight selection. In such a case, improvement in yield can be achieved through indirect selection based on other highly heritable yeild components of plants.

It was first realised by Kozel (1943) that rapid improvement in yield could be achieved by simultaneous selection of component characters combined in the form of an index or a score. He further emphasized that appropriate weightages should be given to each character according to its heritability and genotypic and phenotypic correlations existing between characters.

In the present study, selection indices were generated for grain yield considering five characters viz, number of productive tillers per plant (X_2) , panicle weight per plant (X_3) , number of filled grains per panicle (X_4) , test weight (X_5) and harvest index (X_6) . Grain yield (X_1) was not included as a component by itself and was considered as the dependent variable in all linear discriminate function analysis. All the characters chosen possessed high heritability values.

When the single character indices were considered, the best single character index was panicle weight per plant followed by harvest index and number of filled grains per panicle. However, the same character panicle weight per plant, in combination with number of productive tillers per plant was found to be the best in case of two character Among three character indices the best index indices. included number of filled grains per panicle, in addition to panicle weight per plant and number of productive tillers per plant, followed by the index containing test weight, in addition to panicle weight per plant and number of productive tillers per plant. For four characters selection indices, the combination of number of productive tillers per plant, panicle weight per plant, number of filled grains per panicle and test weight was found to be superior followed by the index including number of productive tillers per plant, number of filled grains per panicle, test weight and harvest index and the index comprising panicle weight per plant, number of filled grains per panicle, test weight and harvest index. Whenever the panicle weight per plant was included in the selection, the relative efficiency of the index increased.

Among all the indices formulated, the one containing the component character number of productive tillers per plant, panicle weight per plant, number of filled grains per panicle and test weight gave the highest relative efficiency of 109.81 per cent. It is suggested from this study that in rice selection for grain yield based on selection index consisting of number of productive tillers per plant, panicle weight per plant, number of filled grains per panicle and test weight would be more advantagenous. The present study was in confirmation with the results of Choudhury <u>et al</u>. (1973), Dhanraj <u>et al</u>. (1987) and Mahajan <u>et al</u>. (1986).

SUMMARY
VI. SUMMARY

The present study on genetic architecture of yield and yield components in F_2 generation of 6 x 6 diallel set of fine grained rice (<u>Oryza sativa</u> L.) was undertaken (i) to assess the amount of genetic variability for grain yield and its components, (ii) to identify potential crosses which could be profitably used for evolving hybrids, (iii) to assess the combining ability and the components of gene action, (iv) to estimate the direct and indirect effects of characters through correlation and path coefficient analysis and (v) to formulate selection indices for grain yield.

The six parents involved were Ambrose, HP-32 Pak-Basumathi, HP-33, HP-5 and HP-20. The six parents and 15 F_2 's were grown during summer 1990 in RCBD with three replication at the wet lands of Main Research Station, University of Agricultural Sciences, Hebbal, Bangalore. Observations were recorded for 16 traits, viz., total dry matter per plant, plant height, number of tillers per plant, number of productive tillers per plant, panicle length, grain length, grain breadth, length to breadth ratio of the grain, grain yield per plant, panicle weight per plant, number of spikelets per panicle, number of filled grains per panicle, test weight, tiller fertility, spikelet fertility and harvest index. The mean values of parents and crosses and analysis of variance have indicated considerable variability for all the characters in the present study. The component parent vs. crosses also revealed highly significant differences for most of the traits except total dry matter, grain breadth, grain yield per plant, test weight and harvest index, indicating the importance of over - dominance for the traits. The mean performance of hybrids revealed that the crosses $P_1 \times P_2$, $P_4 \times P_5$ and $P_5 \times P_6$ were having high values for yield and yield components.

Heterosis for yield and yield components were observed in different degrees over mid parent, better parent and standard values. Cross $P_1 \times P_2$ showed highest significant positive heterosis over mid parent, better parent and standard, for yield and yield components. For plant height, cross $P_2 \times P_6$ was the most desirable as it showed significant negative heterosis over mid parent, better parent and standard.

Analysis of variance for combining ability showed that both GCA and SCA variances were highly significant indicating the importance of both additive and non – additive gene action. Preponderance of additive gene action was recorded for total dry matter per plant, grain breadth, grain yield per plant, panicle weight per plant, number of spikelets per panicle, number of filled grains per panicle and test weight, while for other traits non - additive gene action was predominant. This was also substantiated by analysis of components of genetic variance and graphic analysis.

Analysis of genetic components of variance showed that additive component was higher than dominance for the traits total dry matter per plant, grain breadth, panicle weight per plant, number of spikelets per panicle and number of filled grains per panicle, while for the other traits dominance component was higher than additive component. All the traits showed a low narrow sense heritability. Degree of dominance showed over dominance for all the traits. Asymmetrical gene distribution was observed for all the traits. Number of groups of dominant genes, controlling a character was just one. Graphic analysis indicated genetic divergence among parents. Graphical analysis also showed over dominance for the traits plant height, number of tillers per plant, grain breadth, and test weight, while it showed partial dominance for the traits total dry matter per plant, grain yield per plant, panicle weight per plant, number of spikelets per panicle, number of filled grains per and tiller fertility. Complementary type panicle of epistasis was observed for all the traits in majority of the parents, while duplicate type of epistasis was also observed in some parents (P2 and P5) for the traits plant height, number of tillers per plant, grain yield per plant and

tiller fertility. Standardized deviation graph revealed asymmetrical distribution of dominant and recessive genes in most of the parents for all the characters.

Grain yield had positive significant correlation with panicle weight per plant, number of grains per panicle, spikelet fertility, number of productive tillers per plant and harvest index, at both phenotypic and genotypic level.

The path coefficient analysis revealed maximum direct effect of harvest index on grain yield at both phenotypic and genotypic level.

It was found that selection based on a combination of number of productive tillers per plant, panicle weight per plant, number of filled grains per panicle and test weight would be superior to straight selection for grain yield.

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VII. REFERENCES

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* Original not seen.

