African Journal of Biotechnology Vol. 10(17), pp. 3322-3334, 25 April, 2011
Available online at http://www.academicjournals.org/AJB
DOI: 10.5897/AJB10.2575
ISSN 1684–5315 © 2011 Academic Journals

Full Length Research Paper

Genetic parameters of variability, correlation and path-coefficient studies for grain yield and other yield Attributes among rice blast disease resistant genotypes of rice (*Oryza sativa* L.)

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Accepted 24 March, 2011

Twenty one rice genotypes were selected and screened under artificially controlled conditions to identify the rice blast disease reaction. Sixteen genotypes which were already reported to have resistance genes reacted negatively to the blast disease. Four genotypes were found to be susceptible. Highly significant, lower mean disease reaction score and mean PDI (potential disease incidence) % was recorded for Moroberekan, followed by Columbia 2 and ARBN 142 (Asian rice biological network). All the 21 genotypes along with 64 hybrids were evaluated for nine traits in a randomized block design over five replications. Genetic variability, character association and path-coefficient analysis were studied. Grain yield was kept as a dependant character and the results were analyzed. Analysis of variance revealed considerable variability among the genotypes for all the characters. The phenotypic correlation coefficient (PCV) values were slightly greater than genotypic correlation coefficient (GCV), revealing negligible influence of environment in character expression. High heritability coupled with high genetic advance and high GCV were observed for number of tillers/plant followed by number of productive tillers per plant, plant height and grain yield / plant. Characters like plant height, number of tillers / plant, number of productive tillers / plant, panicle length, filled grains per panicle and test weight had significant positive association with grain yield. Results of path-coefficient analysis revealed that, test weight exhibited maximum positive direct effect on grain yield / plant followed by filled grains / panicle, plant height, panicle length, number of tillers / plant and days to 50% flowering and they contributed primarily to yield and could be relied upon for selection of genotypes to improve genetic yield potential of rice.

Key words: *Oryza sativa,* direct effect, heritability, genetic advance, association, *Magnaporthe grisea,* phenotypic correlation coefficient, genotypic correlation coefficient.

INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food for about 2.5 billion world's population which may escalate to 4.6 billion by the year 2050 (Maclean, 2002). Rice is one of the significant cereal commodities (Lopez and Joseph, 2008). Rice fulfills the nutritional requirements of half of the world's population. It occupies a pivotal place in Indian agriculture as it is a staple food for more than 70% of population and a source of lively hood for about 120 to

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150 million rural house holds. It accounts for about 43% of food grain production in the country. At the current rate of population growth, which is 1.8%, rice requirement by 2020 would be around 140 million tonnes (Directorate of rice research, 2005). More than 2,000 modern varieties have been commercially released in twelve countries of South and Southeast Asia over the past 40 years (Cantrell and Hettel, 2004).

The potentially devastating economic impact resulting from blast infection has prompted worldwide efforts to produce blast-resistant rice varieties / hybrids (Bormans et al., 2003). Rice blast, caused by the filamentous ascomycete fungi *Magnaporthe grisea* (Hebert) Barr, is one of the most devastating diseases of rice and often reduces rice yields greatly in rice-growing countries under disease-conducive conditions (Ou, 1985). Obtaining long-lasting durable resistance to blast from a single gene is not likely, as the fungus has the ability to quickly mutate and attack formerly resistant cultivars (Araujo et al., 2000). One way to improve the durability of blast resistance is to "pyramid" resistance genes by crossing rice varieties with complementary genes to provide multigenic resistance against a wide spectrum of blast races (Hittalmani et al., 2000; Bormans et al., 2003). Introgession of resistance genes from four *indica* cultivars (LAC23, 5173, Pai-Kan-Tao and Tetep) into the susceptible high yielding cultivar CO39 that led to near-isogenic lines (NILs) harboring one or two resistance gene(s) each. These NILs allowed for the discovery of new resistance genes, namely *Pi1, Pi2* (=*Piz*^{5}), *Pi3* and *Pi4b* (Yu et al., 1991; Mackill and Bonman, 1992; Inukai et al., 1994).

Some upland cultivars such as the traditional African cultivars Moroberekan and OS6 have been cultivated for many years in large areas in West Africa without high losses from blast (Notteghem, 1985; Bonman and Mackill, 1988). Five resistance genes have been identified in African cultivar, Moroberekan (Wang et al., 1994; Inukai et al., 1996; Naqvi and Chattoo, 1996; Chen et al., 1999). These cultivars have been widely used as resistance donors in breeding programs (Wang et al., 1994).

Scientists are stumbling because they are looking for a reductionist answer to a complex problem. Both fungicides and breeding efforts failed remarkably to control blast, because they are too static to deal with the dynamic relationships between plants and disease that are deeply tied to the surrounding ecology (Briggs, 2000). Scientists who once hoped to identify one gene or a small set of genes responsible for disease resistance realized that, in most cases, a plant responds to a disease through a complex interactive network of genes and signals (Lamb, 2000). Even within varieties of the same species, the response to a particular disease can be almost entirely different at the genetic level (Briggs, 2000).

The choice of the parents for the current study was based on the earlier reports for the lines and testers. The lines were selected based on three important criteria. They are as follows: The extensive usage of these rice varieties for cooking purpose in Southern parts of India (Tamilnadu, Andhra Pradesh, Karnataka) for its fine grain quality, (for example, White ponni, BPT 5204 and IR 50), grain yield per hectare, consistency of leaf blast disease reaction (TN 1).

The testers namely ARBN 97, ARBN 138, ARBN 139, ARBN 142, ARBN 144 and ARBN 153 harboring major blast resistance genes *Pi-5(t)*, *Pi-9(t), Pi-12(t), Pi-1(t)* + *Pi-2(t)*, *Pi-1(t)* + *Pi-4(t)* and *Pi-5(t),* respectively, were obtained from Central Rice Research Institute (CRRI), Cuttack. The genotypes or the accessions CB98002, CB98004, CB98006 and CB98013 obtained from Paddy Breeding Station, Coimbatore, Tamilnadu, India in the same year (2005) were selected based on the records of the earlier evaluation trials artificially, with moderate to higher yield combined with moderate to resistant leaf blast disease reaction. Other blast resistant genotypes used as testers include Tadukkan (Padmavathi and Mishra, 2005), Te-tep (Dillon et al., 2006), Moroberekan, a West African Landrace (Wu et al., 2004), IR 64 which harbors more than four blast resistance genes (Sallaud et al., 2003; Lawrence et al., 2000). ARBN 153 (Pai-Kan-Tao) a *Japonica* type NIL consisted of major resistance gene for leaf blast as reported by Ahn et al. (1996). IR 50 was used as a susceptible check (Calvero, 1992; Jyothi et al., 2001).

Commercial exploitation of heterosis or hybrid vigor to increase production and productivity of rice has been successfully demonstrated in China. The yields obtained from rice hybrids are 20% higher than conventional varieties. Adoption of hybrid rice on a commercial scale has helped China to produce 33 million tones more rice per year over the past decade (Virmani, 1996). Although more than 30 rice hybrids have so far been released in India, not many could fulfill the just demands of South Indian consumers to get a non-sticky, non-aromatic market and consumer friendly rice hybrid (Thiyagarajan et al., 2009). A big challenge is the assembling process to combine all of the favorable alleles into a single cultivar and ensure their proper functioning. In this regard, it may be more advantageous to breed for hybrids than conventional pure line cultivars, because it may take less effort to have two complementary sets of genes in two parental lines than stacking all of the genes in a single genetic background (Zhang, 2005). In this way, one can try incorporating disease resistance trait along with yield and its contributing traits.

The progress in breeding for yield and its contributing characters of any crop is polygenically controlled, environmentally influenced and determined by the magnitude and nature of their genetic variability (Wright, 1935; Fisher, 1981). It is very difficult to judge whether observed variability is highly heritable or not. Moreover, knowledge of heritability is essential for selection based improvement, as it indicates the extent of transmissibility of a character into future generations (Sabesan et al., 2009). Genetic variability for agronomic traits is the key component of breeding programs for broadening the gene pool of rice and other crops. The genetic coefficient of variation together with heritability estimate would give the best picture of the amount of advance to be expected from selection. The amount of genetic advance under selection depends mainly on the amount of genetic variability. The phenotype of an individual is affected both by genotype (G) and environment (E). Most agronomically significant characters are inherited quantitatively and are known to be affected by environmental factors. Selection based on the phenotype would be difficult for such difficult traits. In breeding programs, it is often difficult to manipulate such traits, since several inter-componential characters indirectly control them (Hittalmani et al., 2003).

Correlation in grouping with path analysis would give a better insight into cause and effect relationship between different pairs of characters (Jayasudha and Sharma, 2010). Knowledge of correlation between yield and its contributing characters are basic and foremost endeavor to find out guidelines for plant selection. Partitioning of total correlation into direct and indirect effect by path coefficient analysis helps in making the selection more effective (Priya and Joel, 2009).

The existing relationships between traits are, generally determined by the genotypic, phenotypic and environmental correlations. The phenotypic correlation measures the degree of association of two variables and is determined by genetic and environmental factors. The environmental correlation is mainly responsible for the association of traits of low heritability, such as grain yield. The genotypic correlation on the other hand, which represents the genetic portion of the phenotypic correlation, is the only one of inheritable nature and therefore, used to orient breeding programs (Falconer, 1989). However, the correlation coefficient between two characters does not necessarily imply a cause and effect relationship. The inter-relationship could be grasped best if a coefficient could be assigned to each path in the diagram designed to measure the direct influence on it.

Before placing strong emphasis on breeding for yield improvement trait, the knowledge on the association between yield and yield attributes will enable the breeder in the improvement of yield. The correlation coefficient may also help to identify characters that have little or no importance in the selection programme. The existence of correlation may be attributed to the presence of linkage or pleiotropic effect of genes or physiological and development relationship or environmental effect or in combination of all (Oad et al., 2002).

The basic objective of most of the crop improvement programs is to realize a marked improvement in crop yield. But yield is a complex character which is controlled by association of various characters. Thus, information on association of yield attributes and their direct and indirect effects on grain yield are of paramount significance. Hence, path analysis is of much importance in any plant breeding program. Genetic variability, character association and path are pre-requisites for improvement of any crop including rice for selection of superior geno-types and improvement of any trait (Krishnaveni et al., 2006).

The major advantage of path analysis is that, it permits the partitioning of the correlation coefficient into its components, one component being the path coefficient that measures the direct effect of a predictor variable upon its response variable; the second component being the indirect effect(s) of a predictor variable on the response variable through another predictor variable (Dewey and Lu, 1959). In agriculture, path analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield (Milligan et al., 1990; Surek and Beser, 2003).

Keeping the stated concepts in mind, an attempt was made to understand the variability for the grain yield and its related attributes, study the correlation and path analysis of yield attributing traits among 20 genotypes (16 testers (male), 4 lines (female)) parents and their 64 hybrids of rice.

MATERIALS AND METHODS

Artificial screening for leaf blast disease reaction

Twenty one rice genotypes (Table 1) obtained from Central Rice Research Institute, Cuttack, India and Paddy Breeding station, Coimbatore, Tamil Nadu, India in the year 2008, which were already reported either to possess higher yield along with susceptibility for rice blast disease or harboring major blast resistance genes were subjected to artificial screening for rice blast disease. The screen house is specially constructed with good irrigation facilities fitted with mist blowers, which can spray water in a fine mist inside the chamber. Subsequently, the seedlings were misted 4 to 5 times at intervals. The screen house was maintained at 32 to 37°C (day temperature) and 94 to 96% relative humidity (RH) for the potential disease occurrence. The rate of sporulation increases with increase in relative humidity provided with lower night temperature with minimum of 25°C. Inoculations with *M. grisea* Hebert (Barr) were performed 3 weeks after sowing by spraying with conidial suspensions. For the spray method, 30 ml of a 50,000 conidia.ml^{-1} suspension with 0.5% gelatin were sprayed on each tray (Sallaud et al., 2003). The experimental setup for artificial rice blast disease screening, isolation and sporulation of rice blast fungus (*M. grisea*) for artificial disease screening is shown in Figure 1.

The observation on the disease incidence was recorded when the susceptible check (IR 50) was severely infected by blast. Observations were recorded from 20 plants in each entry following standard evaluation system (SES, 2002) on 0 to 9 scale at 25th day after sowing. The resistant check used was IR 64. Observations were recorded in plants, when they were at third leaf stage. The grade and criterion based on standard evaluation system is as follows: Score 0, no lesions observed; score 1, small brown specks of pin point size or larger brown specks without sporulating centre; score 3, small roundish to slightly elongated necrotic grey sporulating spots about 1 to 2 mm in diameter with a distinct brown margin; score 5, narrow or slight elliptical lesions, 1 to 2 mm in breadth, more than 3 mm long with brown margin; score 7, broad spindle shaped lesion with yellow, brown or purple margin; score 9,

Table 1. Details of rice genotypes involved in this study.

S/no.	Genotypes	Parentage	Habit	Duration (days)	Place of collection	Geographic origin
1	ARBN 153	C-101-Pai Kan Too (*japonica*)	Tall	110-115	China	Central Asia
2	ARBN 97	RIL 45 (Moroberekan / CO 39)	Semi dwarf	135	India	South Asia / Africa
3	ARBN 139	RIL 10 (Moroberekan / CO 39)	Dwarf	140	India	South Asia / Africa
4	ARBN 144	RIL 249 (Moroberekan / CO 39)	Semi dwarf	135	India	South Asia / Africa
5	ARBN 138	*Oryza minuta* (Acc. 10114) / (WHD-IS-1-127) / (DM 360)	Dwarf	130	Philippines	South East Asia
6	ARBN 142	BL 142	Semi dwarf	130	Philippines	South East Asia
7	CB 98002	TNAU 89093 / ASD 5	Semi dwarf	135	India	South Asia
8	CB 98004	TNAU 89093 / ADT 40	Semi dwarf	138	India	South Asia
9	CB 98006	Ponni / CO 43	Semi dwarf	135	India	South Asia
10	CB 98013	CO 45 / IR 64	Semi dwarf	130	India	South Asia
11	Columbia – 2	Columbian *indica* cultivar	Semi dwarf	135	Columbia	Latin America
12	IR 64	IR 5657-3-3-3-1 / IR 2061-465-1	Semi dwarf	115-120	Philippines	South East Asia
13	Milyang 46	Doosan 8 / Sacheon 8	Dwarf	110	South Korea	South East Asia
14	Moroberekan	Guinean (West Africa) cultivar, *japonica*	Semi dwarf	130	Guinea (Africa)	Africa
15	Tadukan	Philippine *indica* cultivar (Luzon)	Semi dwarf	130-135	Philippines	South East Asia
16	Tetep	Vietnamese *indica* cultivar	Semi dwarf	130-135	Vietnam	South East Asia
17	BPT 5204	GEB-24 / T(N) 1 / Mahsuri	Semi dwarf	140-145	India	South Asia
18	IR 50	IR 2153-14 / IR 28 / IR 36	Dwarf	115	Philippines	South East Asia
19	TN 1	Chow-Woo-Gen / Tsai-Yuan-Chung.	Dwarf	120-125	Taiwan	South East Asia
20	White Ponni	Taichung 65/2 / Mayang Ebos- 80	Tall	125-130	Malaysia	South East Asia
21	ASD 16#	ADT 39 / CO 39	Semi dwarf	110-115	India	South Asia

#, Standard check used for comparing hybrids.

rapidly coalescing small, whitish, grayish or bluish lesions without distinct margins.

Individual plant in each entry was scored based on the leaf blast severity following standard evaluation system (SES, 2002) on a 0 to 9 scale as detailed at 25th day after sowing, when the susceptible check (Bharti) was fully infected. The potential disease incidence (PDI %) percent was worked out using the formula given by McKinney (1923) :

PDI % = (Sum of numerical rating / Number of leaves observed) x (100 / Maximum disease score).

Hybridization and biometric observations

Twenty genotypes with 16 rice blast resistant lines and four high yielding blast susceptible testers were raised in nursery beds with three staggered sowings at 10 to 15 days interval to ensure synchronized flowering to enable hybridization. Hybridization was carried out by wet cloth method or blowing method (Chaisang et al., 1967) and clipping method (Jennings et al., 1979). Crosses were effected between four female lines and sixteen male parents in a line x tester mating design and a total of 64 cross combinations were obtained. The 64 hybrids and 20 parents were raised along with the standard check ASD-16 in a randomized block design which was replicated five times by adopting a spacing of 20 x 20 cm between rows and plants in a single row of each 1.5 m length consisting of 10 plants per row. Single seedling per hill was planted. The recommended packages of practices and cultural operations were followed.

The following biometrical observations were recorded for the randomly selected hybrids, parents and the standard check. Days to 50% flowering (DFL), plant height (PH), number of tillers per plant (NOTP), number of productive tillers per plant (NOPTP), panicle length (PL), number of

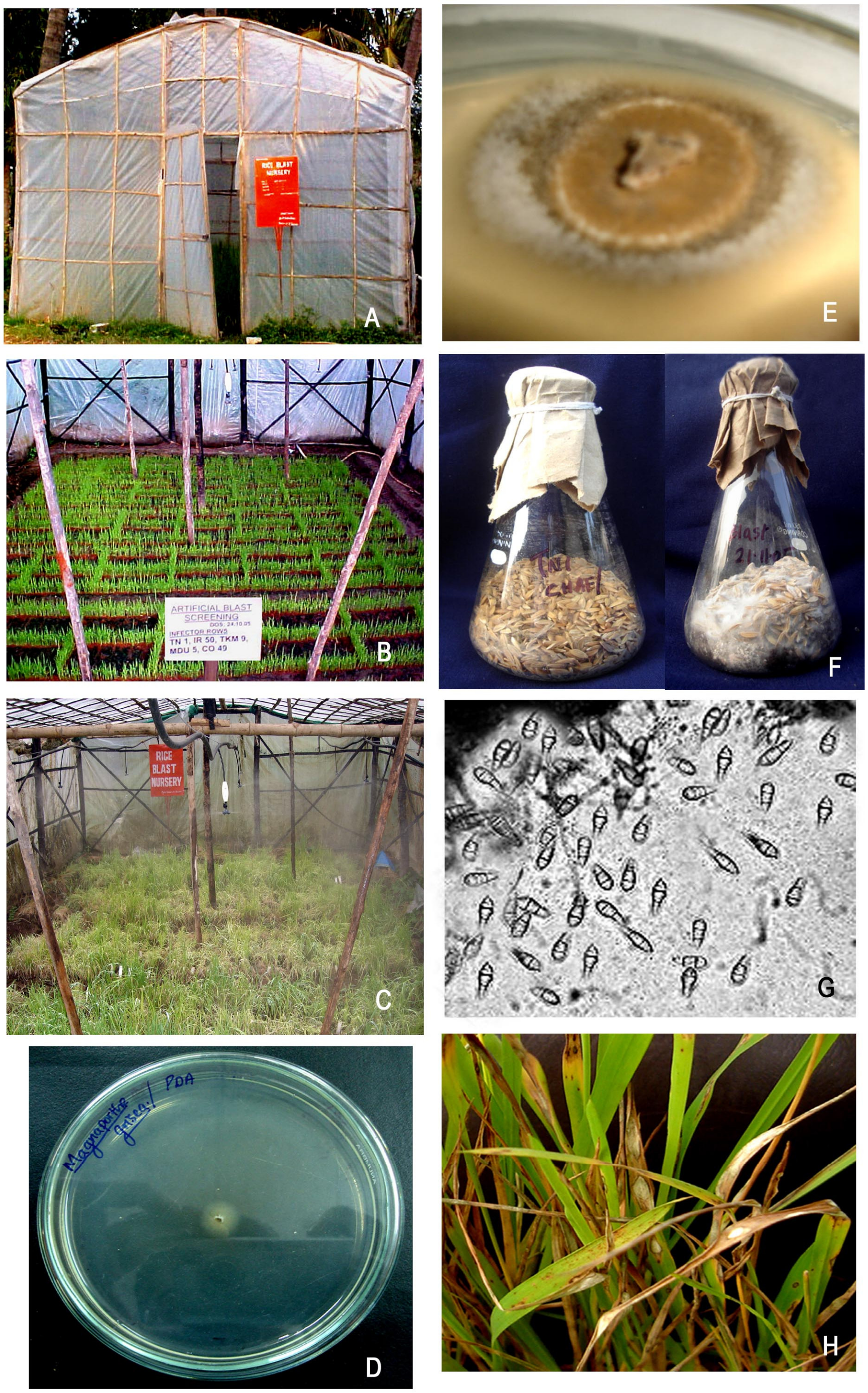

Figure 1. A, B. Well equipped artificial screen houses for rice blast screening with prepared trays beds. **C.** Artificial screen house equipped with mist blowers to maintain (RH) at 95% and leaf wetness. **D.** Five days after inoculation of the symptom, kept at 24-26 degrees celsius, immersed mycelial growth appears. **E.** An effused colony, thinly hairy, turning from olivaceous brown to greyish brown with immersed mycelium and wedge shaped centre was seen. **F**. Inoculated conical flasks maintained at 27 degree celsius at 90% RH inside fluorescent incubator for 15 days. **G.** Observation of rice blast spores at 15 - 20 days after inoculation in Leitz (Flovert FS) microscope under the magnification of 100x. **H.** Disease incidence after spraying of artificial rice blast sporulated inoculam with spore concentration adjusted to 50,000 conidia.ml–1 suspension with 0.5% gelatin spores (approx) 2 to 3 times inside the screen house for disease induction..

Table 2. Rice blast disease reaction at PBS, Coimbatore (artificial screening).

Genotype	Mean disease score	Mean PDI (%)	Blast disease reaction	Standard error	Standard deviation	Standard variance	Significance (5 % / 1 %)
ARBN 97	7.02**	78.07	S	0.547	2.678	7.712	1.131 / 1.535
ARBN 138	6.74**	74.95	MS	0.564	2.671	7.623	1.666 / 1.582
ARBN 139	6.76**	75.10	MS	0.506	2.479	6.382	1.047 / 1.421
ARBN 142	0.88**	9.77	R	0.253	1.239	1.536	0.532 / 0.710
ARBN 144	1.77*	19.71	R	0.564	3.203	5.610	1.353 / 1.836
ARBN 153	7.56**	83.99	S	0.311	1.523	2.391	0.643 / 0.873
IR 64	0.61*	6.81	R	0.233	1.142	1.304	0.482 / 0.654
CB 98002	1.82**	20.29	R	0.560	2.745	7.536	1.159 / 1.573
CB 98004	5.20**	57.77	MS	0.425	2.083	4.341	0.880 / 1.194
CB 98006	6.09**	67.55	MR	0.333	1.633	2.667	0.690 / 0.937
CB 98013	1.38**	15.40	R	0.342	1.676	2.810	0.708 / 0.961
Columbia 2	1.06**	11.25	R	0.225	1.110	1.210	0.465 / 0.630
Moroberekan	0.84**	9.33	R	0.175	0.859	0.737	0.363 / 0.492
Milyang 46	1.17*	13.03	R	0.381	1.865	3.478	0.788 / 1.069
Tadukan	0.81*	9.03	R	0.451	2.212	4.895	0.634 / 0.831
Tetep	1.62**	18.07	R	0.590	2.889	3.348	1.220 / 1.601
IR 50	6.92**	76.88	S	0.419	2.053	4.216	0.867 / 1.177
TN 1	8.60**	95.55	S	0.359	1.761	3.101	0.744 / 1.009
White Ponni	8.50**	94.50	S	0.465	2.278	5.188	0.962 / 1.305
BPT 5204	8.25**	91.70	S	0.567	2.823	7.971	1.192 / 1.618
ASD 16	7.21**	80.14	S	0.295	1.445	2.087	0.610 / 0.828

*Significant at 5 % level; **significant at 1% level (SES, 2002). Blast disease score, 1 to 3.0 = R, (resistant); 3.1 to 5.0 = MR (moderately resistant); 5.1 to 7.0 = MS (moderately susceptible); 7. 1 to 9.0 = S (susceptible).

filled grains per panicle (NOFLP), days to maturity (DM), test weight (TW) and grain yield per plant (GYP). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the method suggested by Singh and Chaudhary (1985). Heritability for the grain yield and yield components of hybrids were worked out in broad sense by adopting formula suggested by Hanson et al. (1956). Genetic advance (GA) was calculated by the method suggested by Johnson et al. (1955). Genotypic and phenotypic correlations were partitioned into path coefficient using the technique outlined by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Blast disease reaction

The 21 genotypes were subjected to the artificial screening at Paddy Breeding Station (PBS), Coimbatore. Highly significant, lower mean disease reaction score (0.84) and mean PDI per cent (9.33) was recorded by Moroberekan, followed by Columbia 2 (0.88 and 9.77%) and ARBN 142 (1.0688 and 11.255%). Significantly, lowest mean disease reaction scores and PDI per cent was recorded by IR 64 (0.61 and 6.81%) followed by Tadukan (0.81 and 9.03%). Highly significant, higher mean disease reaction scores was recorded by TN 1 (8.60 and 95.55%) followed by White ponni (8.50 and 94.50), BPT 5204 (8.25 and 91.70%), ARBN 153 (7.56 and 83.99%) and ASD 16 (7.21 and 80.14%) (Table 2).

The analysis of variance revealed significant difference among the genotypes for all the characters studied (Table 3). A wide range for all the traits indicates the existence of variation among genotypes for different traits. Coefficient of variation truly provides a relative measure of variance among the different traits. GCV (Table 4) was found to be highest for number of tillers per plant followed by number of productive tillers per plant, plant height and grain yield per plant. Similar trend was observed for PCV. Close relationship between GCV and PCV was found in all the characters and PCV values were slightly greater than GCV, revealing very little influence of environment for their expression. High variability recorded for number of tillers per plant followed by number of productive tillers per plant, plant height and grain yield per plant indicated that, the traits are governed by additive gene action. Similar results were obtained by Madhavilatha et al. (2005), Ananthi et al. (2006), Patra et al. (2006), Binodh et al. (2007), Sabesan et al. (2009) and Jayasudha and Sharma (2010).

Heritability and genetic advance

Heritability plays a vital role in deciding the suitability and strategy for selection of a particular character. All the nine characters under study exhibited high broad sense heritability of more than 95%, except panicle length which is

Table 3. Analysis of Variance (ANOVA) for grain yield and its attributing characters in rice.

Trait	Sources of variation	Degrees of freedom	Sum of squares	Mean sum of squares	F-value	Probability
Days to 50% flowering	Replicate	4	33.99*	8.50*	2.41	0.0493
	Treatment	83	62899.38**	757.82**	214.71	0.0000
	Error	332	1171.81	3.53	--	--
Plant height (cm)	Replicate	4	53.94	13.48	0.7169	0.5808
	Treatment	83	102069.45**	1229.75**	65.37	0.0000
	Error	332	6245.38	18.81	--	--
Number of tillers / plant	Replicate	4	66.77	16.69	1.72	0.1444
	Treatment	83	37184.17**	448.00**	46.24	0.0000
	Error	332	3216.02	9.68	--	--
No. of productive tillers / Plt	Replicate	4	66.17	16.54	1.66	0.1581
	Treatment	83	22440.86**	270.37**	27.18	0.0000
	Error	332	3301.43	9.94	--	--
Panicle length (cm)	Replicate	4	8.35	2.08	0.61	0.6487
	Treatment	83	1803.01**	21.72**	6.44	0.0000
	Error	332	1118.47	3.36	--	--
Number of filled grains / panicle	Replicate	4	468.419*	117.10**	2.66	0.0327
	Treatment	83	92005.55**	1108.50**	25.18	0.0000
	Error	332	14613.01	44.01	--	--
Days to maturity	Replicate	4	25.98	6.49	1.39	0.2354
	Treatment	83	55903.72**	673.53**	144.61	0.0000
	Error	332	1546.27	4.65	--	--
Test weight (gms)	Replicate	4	6.13	1.53	1.52	0.1945
	Treatment	83	1722.86**	20.75**	20.63	0.0000
	Error	332	334.04	1.00	--	--
Grain yield / plant (gms)	Replicate	4	33.00*	8.25*	2.4916	0.0430
	Treatment	83	12662.41**	152.55**	46.0798	0.0000
	Error	332	1099.17	3.31	--	--

*Significant at 0.05 level; **significant at 0.01 level.

less than 90%. Similar results have been reported by Bhandarkar et al. (2002), Kuldeep et al. (2004), Patra et al. (2006), Sabesan et al. (2009) and Jayasudha and Sharma (2010). Although, the presence of high heritability values indicates the effectiveness of selection on the basis of phenotypic performance, it does not show any indication to the amount of genetic progress for selecting the best individuals which is possible by using the estimates of genetic advance. High heritability coupled with high genetic advance and high GCV were observed for number of tillers per plant followed by number of productive tillers per plant, plant height and grain yield per plant. Hence, heritability with high genetic advance indicates the preponderance of additive gene action and such characters could be improved through selection. Johnson et al. (1955) also suggested that, high GCV along with high heritability and genetic advance gave better picture for the selection of the genotypes. Similar results were also reported by Singh and Singh (2005), Sarkar et al. (2007), Anbanandan et al. (2009), Sabesan et al. (2009) and Jayasudha and Sharma (2010).

Association analysis

Complete knowledge on interrelationship of plant character like grain yield with other characters is of paramount importance to the breeder for making improvement in complex quantitative character like grain yield for which direct selection is not much effective. Hence, association analysis was undertaken to determine the direction of selection and number of characters to be considered in improving grain yield. Phenotypic and genotypic correlation coefficients among the nine characters were assessed and are presented in Table 5. The present investigation indicated that, the genotypic correlation coefficients were higher than the phenotypic correlation coefficients demonstrating that, the observed relationships among the various characters were due to genetic causes. This is also in confirmation with the findings of Radhidevi et al. (2002), Najeeb and Wani (2004), Sarkar et al. (2007), Anbanandan et al. (2009), Sabesan et al. (2009) and Jayasudha and Sharma (2010). Plant height, number of tillers per plant, number of productive tillers

Table 4. Range, mean, coefficient of variation, heritability and genetic advance for grain yield and other attributes in rice.

Trait	Range	Mean ± SE	GCV#	PCV##	h^2 (%) (Broad sense)	Expected genetic advancement as % of mean 5%	Expected genetic advancement as % of mean 1%
Days to 50 % flowering	76.40 to 119.80	97.66 ± 0.83	12.58	12.61	99.50	25.84	33.12
Plant height (cm)	73.40 to 140.60	91.85 ± 1.93	16.94	17.07	98.50	34.63	44.38
Number of tillers / plant	17.00 to 56.00	28.29 ± 1.38	33.09	33.46	97.80	67.43	86.41
No. of productive tillers / Plt	14.40 to 42.60	23.46 ± 1.40	30.76	31.40	96.30	62.18	79.69
Panicle length (cm)	17.60 to 27.70	23.20 ± 0.81	8.25	8.98	84.50	15.63	20.03
Number of filled grains / panicle	94.00 to 162.40	123.58 ± 2.95	11.81	12.05	96.00	23.83	30.54
Days to maturity	96.00 to 146.00	128.07 ± 0.96	9.03	9.06	99.30	18.53	23.75
Test weight (gms)	15.70 to 23.80	19.72 ± 0.44	10.08	10.33	95.20	20.25	25.95
Grain yield / plant (gms)	15.30 to 46.40	27.13 ± 0.81	20.14	20.36	97.80	41.03	52.59

#Genetic coefficient of variation; ##phenotypic coefficient of variation.

per plant, panicle length, filled grains per panicle and test weight had significant positive association with grain yield both at the phenotypic and genotypic levels except productive tillers per plant which was associated only at genotypic level. A strong correlation of these traits with grain yield indicated that, simultaneous improvement of all the characters is possible. Days to 50% flowering and days to maturity has a negative correlation on tillers per plant, plant height and grain yield per plant. Hence, heritability with high genetic advance indicates the preponderance of additive gene action and such characters could be improved through selection. Johnson et al. (1955) also suggested that, high GCV along with high heritability and genetic advance gave better picture for the selection of the genotypes. Similar results were also reported by Singh and Singh (2005), Sarkar et al. (2007), Anbanandan et al. (2009), Sabesan et al. (2009) and Jayasudha and Sharma (2010).

Inter-correlation among the yield attributes

Days to 50% flowering had a strong and significant positive association with days to maturity (r = 0.923 and r = 0.931), filled grains per panicle (r = 0.301 and r = 0.307) both at phenotypic and genotypic levels. Days to 50% flowering exhibited negative significant association with 1000 grain weight (r = -0.225 and r = -0.227) at both levels (Table 5). This corroborates with the findings of Reddy et al. (2008), Babu et al. (2006) and Saravanan and Sabesan (2009) for days to maturity. The association expressed by plant height with number of tillers per plant (r = 0.385 and r = 0.393), number of productive tillers per plant (r = 0.333 and r = 0.341) and panicle length (r = 0.256 and r = 0.273) was significant and positive at both levels (Table 5). It suggests that, priority should be given to these traits while making selection for yield improvement. A similar result for plant height association with panicle length was reported by Eradasappa et al. (2007) and Jayasudha and Sharma (2010). The association of number of tillers per plant with number of productive tillers per plant (r = 0.951 and r = 0.965), panicle length (r = 0.298 and r = 0.320), filled grains per panicle (r = 0.359 and r = 0.367) and test weight (r = 0.374 and r = 0.381) was positive and significant at both levels. Similar results were reported by Madhavilatha et al. (2005) and Radhidevi et al. (2002). The correlation of number of productive tillers per plant exhibited positive and significant association with panicle length (r = 0.245 and r = 0.266), filled grains per panicle (r = 0.382 and r = 0.394) and test weight (r = 0.367 and r = 0.376). Similar results were reported by Surek and Beser (2003), Radhidevi et al. (2002) and Sabesan et al. (2009). The association of panicle length with test weight (r = 0.642 and r = 0.684) was positive and significant at both levels. The association of filled grains per panicle with days to maturity (r = 0.400 and r = 0.416), test weight (r = 0.333 and r = 0.334) was positive and significant at both levels. Positive and significant association of days to maturity with test weight (r = 0.647 and r = 0.674) was noticed at both levels as reported by Singh et al. (2000), Vinothini and Kumar (2008), Kumar and Vivekanandan (2009) and Priya and Joel (2009).

Path analysis

The estimates of correlation coefficients revealed only the relationship between yield and yield associated characters, but did not show the direct and indirect effects of different traits on yield *per se*. This is because the attributes which are in association do not exist by themselves, but are linked to other components. The path coefficient analysis suggested by Dewey and Lu (1959)

Table 5. Phenotypic and genotypic correlation coefficients among yield and its component traits in rice.

Characters	Days to 50% flower	Plant height	Number of tillers per plant	Number of productive tillers / plant	Panicle length	Filled grains per panicle	Days to maturity	Test weight	Grain Yield per plant
Days to 50% flower	1.000								
Plant height	0.052 (0.051)	1.000							
Number of tillers per plant	-0.134 (-0.138)	0.385 *** (0.393***)	1.000						
Productive tillers per plant	-0.065 (-0.064)	0.333 *** (0.341***)	0.951 *** (0.965***)	1.000					
Panicle length	0.086 (0.092)	0.256 ** (0.273**)	0.298 ** (0.320**)	0.245 * (0.266*)	1.000				
Filled grains per panicle	0.301 ** (0.307**)	0.023 (0.026)	0.359 *** (0.367***)	0.382 *** (0.394***)	-0.010 (0.004)	1.000			
Days to maturity	0.923 *** (0.931***)	0.045 (0.046)	0.057 (0.059)	0.133 (0.138)	0.004 (-0.002)	0.400 *** (0.416***)	1.000		
Test weight	-0.225 * (-0.227*)	0.167 (0.172)	0.374 *** (0.381***)	0.367 *** (0.376***)	0.642 *** (0.684***)	0.333 *** (0.334***)	-0.240* (-0.240*)	1.000	
Grain yield per plant	-0.041 (-0.042)	0.308 ** (0.330**)	0.228 * (0.254*)	0.180 (0.198*)	0.486 *** (0.525***)	0.373 *** (0.391***)	-0.097 (-0.102)	0.647 *** (0.674***)	1.000

Values inside parenthesis are genotypic correlation coefficients* - 5% level; significance levels 0.05, 0.01, 0.005 and 0.001; ** - 1 and 0.5% levels. If correlation r = 0.192, 0.250, 0.272 and0.317; *** - 0.1% levels.

specified the effective measure of direct and indirect causes of association and also depicts the relative importance of each factor involved in contributing to the final product that is, yield. In order to find out the cause and effect relationship between grain yield and its related characters, path analysis was taken up in the present investigation.

Direct effects

Path-coefficient analysis using grain yield as dependent variable and other characters as independent variables is presented in Table 6. The phenotypic and genotypic path diagrams are shown in Figures 2 and 3. Thousand grain weight exhibited maximum positive direct effect on grain yield per plant followed by filled grains per panicle, plant height, panicle length, number of tillers per plant and days to 50% flowering. Positive direct effects of these traits on grain yield indicated their importance in determining this complex character and therefore, should be kept in mind while practicing selection aimed at the improvement of grain yield. Similar results were also reported by Gawai et al. (2006) and Jayasudha and Sharma (2010) for days to 50% flowering, plant height, number of tillers per plant and filled grains per panicle. Number of productive tillers per plant and days to maturity expressed negative direct effect on grain yield per plant. Similar results were also reported by Gawai et al. (2006), Vinothini and Kumar (2008), Priya and Joel (2009) and Jayasudha and Sharma (2010).

Indirect effects

Days to 50% flowering had indirect positive effect on grain yield through plant height, panicle length, filled grains per panicle and days to maturity.

Table 6. Direct (diagonal) and indirect (off-diagonal) effect of 8 traits on grain yield in rice.

Character	Days to 50% flower	Plant height	Number of tillers per plant	Number of productive tillers / plant	Panicle length	Filled grains per panicle	Days to maturity	Test weight
Days to 50% flower	**0.157** **(0.306)**	0.008 (0.016)	-0.021 (-0.042)	-0.001 (-0.019)	0.013 (0.028)	0.047 (0.094)	0.145 (0.284)	-0.036 (-0.069)
Plant height	0.012 (0.0119)	**0.242** **(0.231)**	0.093 (0.417)	0.081 (0.079)	0.062 (0.063)	0.006 (0.006)	0.011 (0.011)	0.040 (0.040)
Number of tillers per plant	-0.016 (-0.058)	0.045 (0.164)	**0.118** **(0.090)**	0.112 (0.402)	0.035 (0.133)	0.042 (0.153)	0.007 (0.024)	0.044 (0.159)
Number of productive tillers per plant	0.019 (0.0357)	-0.101 (-0.191)	-0.288 (-0.539)	**-0.303** **(-0.559)**	-0.074 (-0.148)	-0.116 (-0.220)	-0.040 (-0.077)	-0.111 (-0.210)
Panicle length	0.018 (0.015)	0.054 (0.045)	0.063 (0.052)	0.052 (0.043)	**0.212** **(0.163)**	-0.002 (-0.001)	0.001 (-0.001)	0.136 (0.112)
Filled grains per panicle	0.116 (0.118)	0.009 (0.009)	0.138 (0.141)	0.147 (0.152)	0.004 (0.002)	**0.385** **(0.385)**	0.154 (0.160)	0.128 (0.131)
Days to maturity	-0.263 (-0.376)	-0.013 (-0.019)	-0.016 (0.024)	-0.038 (-0.056)	-0.001 (0.001)	-0.114 (-0.168)	**-0.284** **(-0.404)**	0.068 (0.097)
Test weight	-0.085 (-0.094)	0.063 (0.072)	0.141 (0.158)	0.139 (0.156)	0.242 (0.284)	0.126 (0.141)	-0.090 (-0.100)	**0.377** **(0.415)**
Grain yield per plant	-0.041 (-0.042)	0.308 (0.330)	0.228 (0.254)	0.180 (0.198)	0.486 (0.525)	0.374 (0.391)	-0.097 (-0.102)	0.647 (0.673)
Partial R^2	-0.006 (-0.013)	0.075 (0.075)	0.027 (0.106)	-0.054 (-0.112)	0.103 (0.086)	0.144 (0.150)	0.028 (0.041)	0.244 (0.279)

Phenotypic path (R^2 = 0.5586 residual effect = 0.6643); values inside parenthesis are genotypic path values. Genotypic path (R^2 = 0.6147 residual effect = 0.6207).

Plant height expressed indirect positive effect on grain yield per plant through days to 50% flowering, panicle length, number of tillers, number of productive tillers, panicle length, filled grains per panicle, days to maturity and 1000 grain weight. The indirect expression of number of tillers per plant on grain yield through all the foresaid characters were positive except days to 50% flowering which was negative. The indirect expression of number of productive tillers per plant on grain yield through all the characters studied was negative except days to fifty per cent flowering which were positive. Panicle length expressed indirect positive effect on yield per plant through all characters except filled grains per panicle. The indirect expression of filled grains per panicle on yield per plant through all characters was positive. The indirect expression

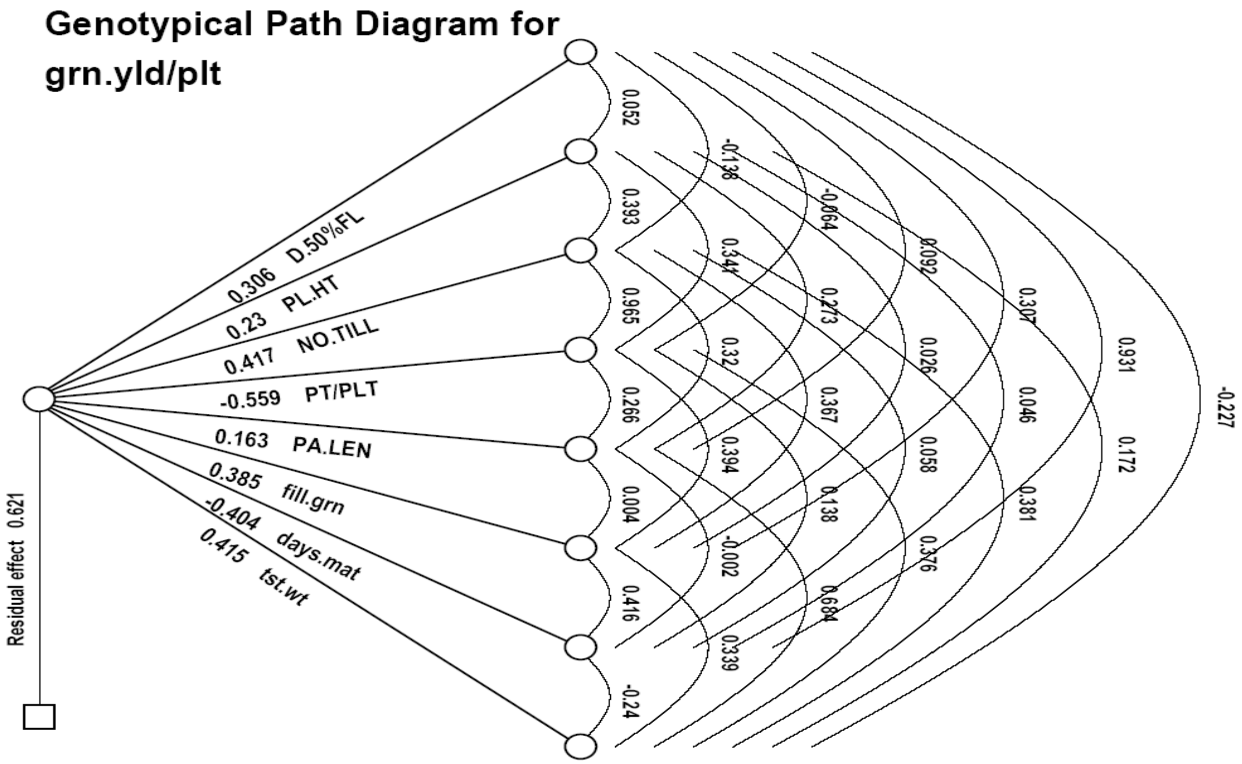

Figure 2. Genotypic path diagram for grain yield per plant in rice.

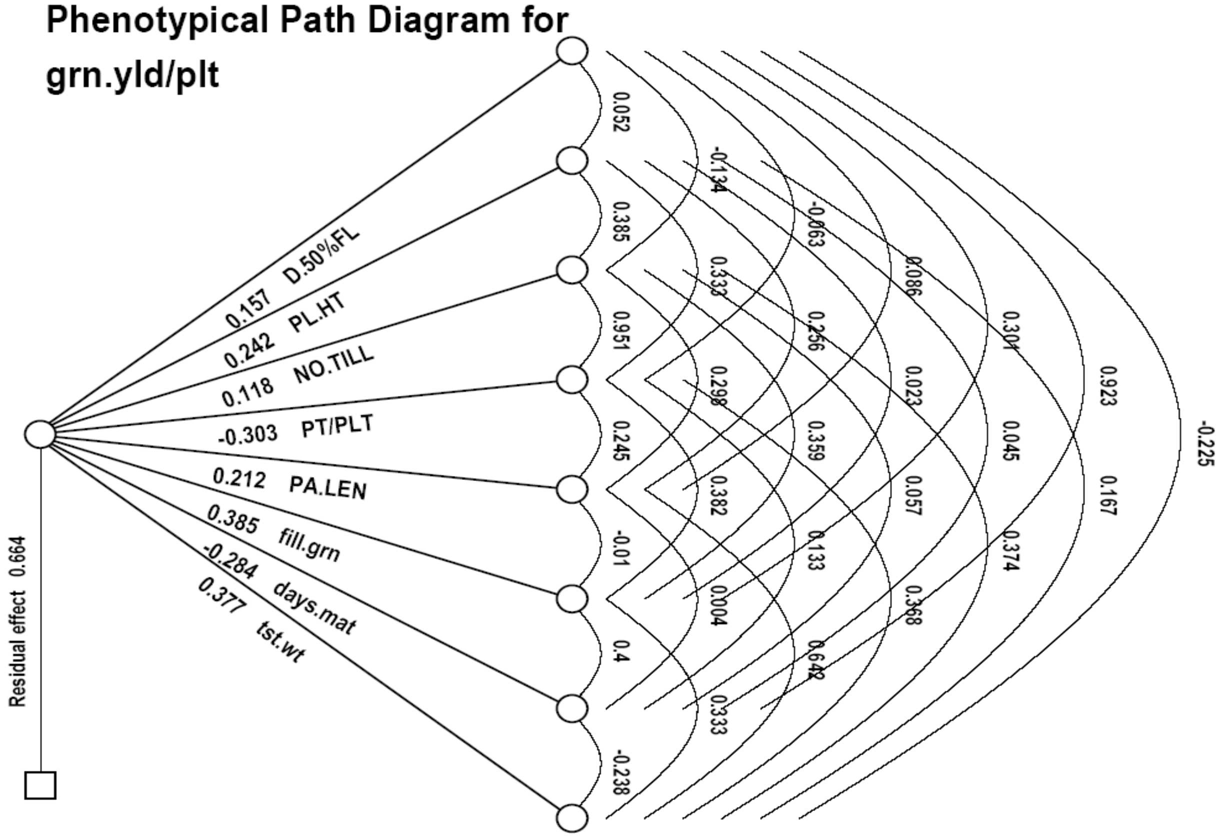

Figure 3. Phenotypic path diagram for grain yield per plant in rice.

of days to maturity on grain yield per plant through test weight had a positive effect. 1000 grain weight expressed positive indirect effect on yield per plant through plant height, number of tillers, number of productive tillers, panicle length and filled grains per panicle.

Conclusion

The genetic architecture of grain yield is based on the balance or overall net effect produced by various yield components interacting with one another. Based on the studies on genetic variability and correlation analysis, it may be concluded that, thousand grain weight exhibited maximum positive direct effect on grain yield per plant followed by filled grains per panicle, plant height and panicle length seems to be primary yield contributing characters and could be relied upon for selection of genotypes to improve genetic yield potential of rice. Hence, utmost importance should be given to these characters during selection for single plant yield improvement. Similar results had been reported by Radhidevi et al. (2002), Oad et al. (2002), Priya and Joel (2009) Govindaraj et al. (2009) and Anbanandan et al. (2009). Selection of plants on the basis of these traits would certainly lead to improvement in grain yield.

Abbreviations

G, Genotype; **E,** environment; **RH,** relative humidity; **DFL,** days to 50% flowering; **PH,** plant height; **NOTP,** number of tillers per plant; **NOPTP,** number of productive tillers per plant; **PL,** panicle length; **NOFLP,** number of filled grains per panicle; **DM,** days to maturity; **TW,** test weight; **GYP,** grain yield per plant; **GCV,** genotypic coefficient of variation; **PCV,** phenotypic coefficient of variation; **GA,** genetic advance; **PBS,** Paddy Breeding Station.

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