VOL. 8, NO. 2, FEBRUARY 2013 ISSN 1990-6145
ARPN Journal of Agricultural and Biological Science


www.arpnjournals.com

IDENTIFICATION OF SLOW-BLASTING RICE GENOTYPES THROUGH MULTIVARIATE ANALYSIS OF COMPONENTS OF RESISTANCE

A. K. Mukherjee, N. K. Mohapatra and P. Nayak
Central Rice Research Institute, Cuttack, Orissa, India
E-Mail: nparsuramata@yahoo.co.in

ABSTRACT

Slow-blasting resistance in rice, caused by *Magnaporthe grisea* (Hebert) Barr, characterized by longer incubation period and latent period, shorter infectious period, lower infection efficiency, number of lesions per leaf, necrotic zone area, chlorotic zone area, mean lesion area, lesion cover, sporulation capacity and finally lower area under disease progress curve; was recognized in 13 rice genotypes. There was a strong association among all the components, except infection frequency in terms of the number of penetration points which was not correlated with any of the 13 components. The basic data on the dynamics of components of slow-blasting resistance was analyzed by means of the methods of multi-variate analyses like the principal component analysis (PCA), the factor analysis and the cluster analysis. The factor analysis recognized three factors, each explaining distinct phases of the pathogen like establishment, growth and reproduction, while nine principal components (PC) were identified through PCA; PC-1 alone accounting for the largest amount (96.3 %) of the total variability. The cluster analysis recognized groups of genotypes possessing distinct slow-blasting and fast-blasting characteristics. Super-imposition of the clustering pattern on to the figure on ordination of the genotype-scores on the planes of PC-1 and PC-2, clearly displayed the positioning of the slow-blasting genotype-clusters nearer to the point of intersection between the two ordinates and the fast-blasting genotype-clusters away from it. Thus, the genotypes could be arrayed in a spectrum ranging from slow-blasting resistance to those possessing fast-blasting attributes. The confirmation of the field reactions of these genotype-clusters through estimation of cluster means in respect of 12 parameters and comparison of the respective average disease progress curves, explores the possibility of practical utility of the methods of multivariate analyses for easy and quick identification of genotypes possessing slow-blasting resistance.

Keywords: rice genotypes, *Magnaporthe grisea,* dendrogram, partial resistance, principal component analysis, rate-reducing resistance.

INTRODUCTION

Blast disease of rice (*Oryza sativa* L.) incited by the fungus *Magnaporthe grisea* (Hebert) Barr (*Pyricularia grisea* Sacc. = *Pyricularia oryzae* Cav.), still remains as the number one, most wide spread and devastating disease, causing huge yield losses, especially in endemic areas of tropics and sub-tropics. Although successful chemical control measures have been evolved, these are too expensive and hence, host resistance is given priority in disease control strategy. It is also considered as no-cost technology, especially for poor and marginal farmers as well as an important component of eco-friendly technology in an integrated disease management program. Genetic analysis resulted in identification of several major genes governing resistance (Chaudhary and Nayak, 1987; Kiyosawa, 1981; Manibhushan Rao, 1994; Ou, 1985), which function in a race-specific vertical manner. Widespread cultivation of cultivars possessing such vertical resistance led to breakdown of resistance in several occasions in the past, which have been well documented (Crill *et al.* 1982; Kiyosawa and Shiyomi, 1976; Ryu *et al.,* 1987; Yamada, 1965 and 1979).

Consequent upon the frequent breakdown of vertical resistance in several plant-pathosystems, plant pathologists and breeders have developed renewed interest in development of varieties possessing rate-reducing resistance. This type of resistance allows some disease to develop; resulting in reduced selection pressure for the preferential development of undetected virulent strains and hence remains effective for a longer time. Such types of resistance have the effects of slowing down the development of an epidemic. Rate reducing resistance is attributed to different components, which are responsible individually or jointly for expression of the total disease in the host plant. Several such components have been identified in different plant-pathosystems (Parlevliet, 1979). In rice-blast pathosystem, some such components of resistance viz; lesion number (LN), lesion size (LS) and sporulation capacity (SC) (Chou *et al.,* 1979); disease efficiency (DE), LS and SC (Villareal *et al.,* 1981); latent period (LP), LN and SC (Brondy *et al.,* 1988); DE, LP and SC (Castano *et al.*, 1989); incubation period (ICP) lesion cover (LC), LN and SC (Nomura and Ishi, 1989); hypal growth, dwarfing index, LN and SC (Ryu *et al.*, 1990); relative infection efficiency (RIE), DE, SC, LS and ICP (Sun *et al.,* 1990); diseased leaf area, area under disease progress curve (AUDPC), LS and SC (Wang and Wang, 1991) have been identified. Mukherjee (1994) and Mukherjee and Nayak (1997a) identified ICP, LP, infectious period (IP), infection frequency (IF), infection efficiency (IE), LN, necrotic zone area (NZA), chlorotic zone area (CZA) and SP as important components of slow-blasting resistance. These components are genetic and heritable in nature and maximum correlated response and relative selection efficiency could be expected through selection for LN, followed by LN+NZA (Mukherjee *et al.,* 1996). Partial resistance to *M. grisea* was recognized in two tall fescue genotypes by longer ICP and LP, reduced rate of disease progress and lesion expansion, lower final disease incidence (FDI), final foliar blight incidence, final

mean lesion length (FLL) and AUDPC (Tredway *et al.,* 2003). According to them, measurement of ICP, LP, FDI and FLL were the most effective and efficient methods for detecting *M. grisea* resistance in tall fescue.

These components interact among themselves and their effects are cumulative during the course of an epidemic development. Hence, it becomes very difficult to recognize host genotypes possessing such type of resistance, especially from among a large number of test materials, each with several components of resistance. The application of multivariate analysis has special advantage of simplifying such complexities, since the host genotypes under study could be distinctly separated into groups of specific levels of resistance through clustering and ordination. Similar successful numerical classification of the host genotypes on the basis of their attributes of disease assessments at different dates have been made for slow stem rusting in wheat (Rees *et al.,* 1979a and b; Thompson and Rees, 1979), slow-mildewing in lettuce (Lebeda and Jendrulek, 1988), and early blight resistance intomato (Madden and Pennypacker, 1979). However, no attempt has so far been made to simplify the complexity of genotype x components interactions and classify rice genotypes on the basis of different components of slow-blasting resistance. The present investigation was aimed at (i) identification important components of slow-blasting resistance and estimation of associated variation among them, (ii) grouping of host genotypes based on their levels of resistance to different components and (iii) comparison of such groups of host genotypes with those based on different parameters for evaluation of resistance.

MATERIALS AND METHODS

Source of materials and cultural conditions

The seeds of 15 rice genotypes were collected from the list of donors for various biotic and abiotic stresses, being maintained at the International Rice Research Institute, Philippines through the National Bureau of Plant Genetic Resources, New Delhi, India and the National Rice Germplasm collections being maintained at the Central Rice Research Institute, Cuttack, India. These rice genotypes possessed a predetermined level of resistance to rice blast disease ranging from 1 to 5 in the SES scoring system assessed through multi-location trials at different testing centers all over the world. The rice genotype Karuna was used as the susceptible check. Seeds of these rice genotypes were sown in 60 x 40 x 10 cm^3 zinc trays in a randomized complete block design with two replications. Fertilizer was applied in the form of ammonium sulphate at the rate 100 kg N/ha in split doses.

Inoculation and observation

Trays containing 25 day-old healthy seedlings were transferred into the inoculation chamber. The plants were spray-inoculated with the inoculum prepared from a profusely sporulating culture of a highly virulent local strain of *Magnaporthe grisea*, grown on rice leaf extract sucrose agar medium. The number of conidia applied per cm^2 of leaf area was counted at 10 x 10*X* with a 6 x 6 square grid in the microscope, from the glass slides placed in the plant canopy at the time of inoculation.

Critical observations were recorded in order to facilitate computation of different estimates of 14 individual components of slow-blasting resistance. The components were: (i) Incubation period (ICP) - the number of days from inoculation to the first appearance of the visible disease symptoms, (ii) Latent period (LP) - the number of days from inoculation till the beginning of spore production, (iii) Infectious period (IP) - the number of days from initial sporulation till the lesion ceased to produce spores, (iv) Infection frequency (IF) - the number of penetration points observed per unit leaf area from a given amount of inoculum load, (v) Infection efficiency (IE) - the ratio of the number of sporulating lesions developed per unit leaf area after 10 days of inoculation to the number of penetration points per unit leaf area expressed as percentage, (vi) Lesion number (LN) - the total number of sporulating lesions per leaf, (vii) Lesion area (LA) - mean lesion area of 50 lesions selected randomly, (viii) Necrotic zone area (NZA) - the estimated necrotic zone area of the lesion, (ix) Chlorotic zone area (CZA) - the estimated chlorotic zone area around the NZA, (x) The lesion cover (LC) - sum of NZA and CZA, (xi) Sporulation capacity (SC) - the total number of conidia produced by a lesion during the entire infectious period (SP/L), (xii) Spores produced per lesion per day (SP/L/D), (xiii) Spores produced per leaf per day (SP/Lf/D) by multiplying SP/L with the LN/Lf and finally, (xiv) Area under disease progress curve(AUDPC).

The infection frequency and infection efficiency were determined following the methods suggested by Mukherjee *et al*. (1998). The necrotic zone area was determined by using the formula developed by Mukherjee *et al.* (1997), which is given by NZA = 0.61 LB, L and B being the length and maximum width of the lesion, respectively. The chlorotic zone area was determined using the formula, CZA = 1.40+0.88 LB, as suggested by Mukherjee and Nayak (1997b). The number of conidia discharged by a lesion was determined as per the methods described by Mukherjee and Nayak (1998). The area under disease progress curve, although not a component, was the net result of the cumulative effect of all these components, and hence was considered as the resultant component in the present context, which was estimated following the methods suggested by Shaner and Finney (1977). Thus a total of 14 components of resistance were measured over two replicates for 15 rice genotypes and the significant differences among the genotypes with regard to the components were calculated through analysis of variance. The association among the components over the 15 rice genotypes was also estimated.

Different parameters of slow-blasting resistance like (i) FDS - final disease severity percentage, (ii) SES - severity scores following standard evaluation system (IRRI, 1988), (iii) AUDPC - the area under disease progress curve (Shaner and Finney, 1977), (iv) RAUDPC - relative area under disease progress curve (Fry, 1978), (v)

r -apparent infection rate following logistic model (van der Plank, 1963), (vi) k - Gompertz model (Berger, 1981), (vii) T_{50} the time required to reach 50% severity (Shaner and Finney, 1977) in logistic (T_{50r}) and Gompertz models (T_{50k}), (viii) IS - index scores following the single component index 6.41LN and the two-component index 5.61LN + 14.67NZA (Mukherjee, 1994; Mukherjee *et al.*, 1996) were estimated. The genotype-scores on PC-1 and PC-2, estimated through principal component analysis (PCA) of the 14 components of resistance, were also considered as two parameters. The field performance of the genotype clusters was verified by estimation and comparison of the cluster means in respect of 12 parameters and the respective average disease progress curves.

Statistical analyses

The significant differences among genotypes in respect of each of the 14 components of resistance were tested through analysis of variance and the associated variation among them was analyzed by applying multiple correlation analysis. The data on 14 component of resistance in respect of 15 genotypes were subjected to multivariate analyses like (i) factor-analysis, (ii) cluster-analysis and (iii) principal component analysis.

The factor analysis was performed by considering each of the 14 components of resistance as the entities and 15 genotypes as the variables following the methods suggested by Kendall and Stuart (1968). The analysis extracted eigen vectors and factor matrix showing inter-correlation among the components. Thus, the main value of the analysis in the present study was that the complexity of interaction between 15 host genotypes and 14 components of resistance was simplified and the dimensionality reduced.

The hierarchical agglomerative method of cluster analysis was based on the N x P matrix, where there were N (=15) individual genotypes and P (=14) components of resistance. The main objective of such an analysis was to find out the groups of genotypes on the basis of similarity in their response to 14 components of resistance and to compare with those exhibiting susceptible reactions. The analysis performed by this method could be illustrated in a dendrogram on the basis of similarity coefficients and Euclidian distance between groups.

The cluster analysis was followed by the principal component analysis, which produces independent linear combinations of the original variables. For this purpose, the genotypes were considered as the entities and the components as the variates. The principal component analysis breaks down the covariance matrix into a set of orthogonal components, equal in number to the number of variates, irrespective of the distribution of the variates or even their randomness. The main value of the principal component analysis in the present investigation is that, because the dimensionality is maintained, it is possible to obtain genotype-scores on each principal component. The principal component analysis extracted the data Tables on correlation matrix, latent roots and vectors, per cent variation explained by each root and finally the genotype-scores on first few principal components contributing more than 90% of the variation in the communality. The first two principal components contributing more than 80 to 90% of the variation in the communality were identified and the corresponding genotype-scores were plotted on to the ordinates of PC-1 and PC-2. The clustering pattern obtained from the dendrogram drawn through cluster analysis, was super-imposed on to the ordination Figure to locate the position of the clusters of genotypes, which could lead to a definite conclusion on positioning and identification of resistant/susceptible genotype-clusters.

The relative importance of the parameters for evaluation of resistance was determined by subjecting the data to principal component and factor analyses, considering each of the 12 parameters as entities and 15 genotypes as variables. The top ranking parameters were identified by comparison of the degree of variability and inter-correlations among them on the basis of which these parameters are included into factors.

The entire set of multivariate analyses was performed with the help of statistical package developed by INDOSTAT Services, Hyderabad, India. The field reaction of the groups of genotypes under each cluster was verified through estimation of the cluster means in respect of 12 parameters for evaluation of resistance and comparison of the average disease progress curves for respective groups of genotypes.

RESULTS

Components of resistance

The analysis of variance revealed highly significant differences among the genotypes in respect of all the component characters (Table-1). Significantly longer ICP, LP and shorter IP was observed in genotypes with lower AUDPC values, compared with the susceptible check Karuna and a few other genotypes with high values of AUDPC. The genotypes with lower AUDPC exhibited significantly lower IF, IE, LN, NZA, CZA, SP/L, SP/L/D and SP/Lf/D. The only exceptions of high IF for Lien-Tsang-50, N-22, CR-570 and high NZA for Surjamukhi were compensated by their corresponding low IE and LN, which ultimately resulted in significantly low AUDPC values over the susceptible check Karuna. Thus slow-blasting resistance was characterized by longer ICP and LP, shorter IP, lower IE, LN, NZA, CZA, SP/L, SP/L/D and SP/Lf/D and finally lowers estimates of AUDPC values.

Table-1. Components of resistance to *M. grisea* in 15 rice genotypes.

Genotypes	ICP	LP	IP	IF	IE	LN	LA	NZA	CZA	TAT	SP/L ($x10^3$)	SP/L/D ($x10^3$)	SP/Lf/D ($x10^3$)	AUDPC
Sakai	5^{b}	7.0^{bc}	5^{e}	0.48^{cd}	0.65^{f}	0.02^{e}	3.20^{d}	0.95^{fgh}	2.64^{gh}	3.59^{c}	1.03^{e}	0.209^{ef}	0.0042^{d}	8.07^{k}
DJ-8	6^{a}	9.0^{a}	2^{f}	0.43^{de}	0.66^{f}	0.03^{e}	1.46^{d}	1.21^{fg}	1.88^{ij}	3.09^{c}	0.01^{e}	0.003^{h}	0.0001^{d}	12.27^{j}
DM-27	5^{b}	7.5^{bc}	6^{e}	0.39^{e}	1.76^{d}	0.05^{e}	2.44^{d}	1.37^{g}	3.20^{f}	4.57^{c}	0.19^{e}	0.031^{gh}	0.0016^{d}	14.04^{j}
Dahanala	5^{b}	7.5^{bc}	4^{ef}	0.48^{cd}	1.09^{e}	0.04^{e}	1.86^{d}	0.84^{ghi}	1.26^{j}	2.10^{c}	0.32^{e}	0.080^{fgh}	0.0029^{d}	24.80^{h}
Laurent-Tc	5^{b}	7.5^{bc}	9^{d}	0.67^{b}	0.81^{ef}	0.54^{e}	1.83^{d}	0.47^{i}	1.57^{ij}	2.04^{c}	0.39^{e}	0.043^{gh}	0.0235^{d}	32.41^{g}
Ch. Ts. Tao	4^{c}	7.0^{bc}	2^{f}	0.65^{b}	0.70^{f}	0.06^{e}	1.25^{d}	1.11^{fg}	1.98^{hi}	3.09^{c}	0.02^{e}	0.008^{h}	0.0005^{d}	19.87^{i}
Li.Ts-50	6^{a}	8.0^{ab}	5^{e}	0.83^{a}	0.15^{g}	0.03^{e}	0.92^{d}	0.58^{hi}	3.29^{f}	3.87^{c}	0.18^{e}	0.037^{gh}	0.0011^{d}	21.61^{hi}
Surjamukhi	5^{b}	7.0^{bc}	15^{b}	0.54^{c}	0.74^{f}	0.78^{e}	28.21^{b}	5.74^{a}	8.66^{c}	14.40^{a}	11.10^{c}	0.740^{c}	$.5772^{bc}$	34.95^{g}
E-425	4^{c}	5.5^{de}	11^{cd}	0.28^{f}	4.80^{b}	2.70^{de}	15.25^{c}	4.34^{c}	7.64^{de}	11.98^{b}	17.08^{b}	1.552^{b}	4.2001^{bc}	39.07^{f}
DNJ-155	5^{b}	7.0^{bc}	4^{ef}	0.65^{b}	0.86^{ef}	0.04^{e}	2.82^{d}	1.23^{fg}	1.70^{ij}	2.93^{c}	0.65^{e}	0.162^{fg}	0.0062^{d}	34.70^{g}
DZ-192	5^{b}	6.5^{ad}	5^{e}	0.49^{c}	1.10^{e}	0.03^{e}	3.52^{d}	1.15^{fg}	1.56^{ij}	2.71^{c}	1.62^{e}	0.325^{e}	0.0110^{d}	44.70^{e}
N-22	4^{c}	5.5^{de}	12^{c}	0.80^{a}	3.34^{c}	5.08^{d}	27.45^{b}	3.65^{d}	8.13^{cd}	11.77^{b}	2.45^{e}	0.204^{ef}	1.0381^{bc}	59.92^{d}
CR-570	3^{d}	4.5^{ef}	11^{cd}	0.81^{a}	3.32^{c}	12.36^{c}	4.56^{d}	3.20^{e}	6.95^{e}	10.15^{b}	5.62^{d}	0.511^{d}	6.3050^{b}	103.50^{c}
CR-289-1045	4^{c}	5.5^{de}	12^{c}	0.80^{a}	3.55^{c}	19.06^{b}	30.50^{b}	6.06^{a}	10.03^{b}	16.09^{a}	3.77^{e}	0.314^{e}	5.9848^{bc}	329.21^{b}
Karuna	3^{d}	4.0^{f}	19^{a}	0.76^{a}	17.24^{a}	77.45^{a}	36.60^{a}	5.27^{b}	13.42^{a}	18.69^{a}	44.56^{a}	2.345^{a}	181.6700^{a}	491.80^{a}

Figures in a column super-scribed by the same letter do not differ significant at P = 0.05 according to Fisher's least significant test.

Association among the components

The correlation between the components of resistance revealed strong association among them (Table-2), with the only exception of IF in term of the number of penetration points, which was not correlated with any of the 13 components, while IE in terms of the proportion of productive lesions was correlated with all the components. The ICP and LP were negatively correlated with rest of the components, which indicated their adverse effect on the process of disease development. Rest of the components was significantly correlated with each other as well as AUDPC, thus signifying their inter-dependency in disease development.

Table 2. Association among 14 components of resistance to *M. grisea* in 15 rice genotypes.

Components	LP	IP	IF	IE	LN/Lf	LA	NZA	CZA	TAT	SP/L	SP/L/D	SP/Lf/D	AUDPC
ICP	0.93**	-0.64*	-0.35	-0.67*	-0.62*	-0.54	-0.60*	-0.69*	-0.67*	-0.59	-0.61*	-0.52	-0.62*
LP		-0.76**	-0.39	-0.73*	-0.67*	-0.65*	-0.69*	- 0.79**	-0.76**	-0.66*	-0.70*	-0.56	-0.69*
IP			0.33	0.72*	0.70*	0.88**	0.86**	0.93**	0.92**	0.77**	0.76**	0.62*	0.70*
IF				0.23	0.37	0.31	0.21	0.36	0.31	0.10	-0.02	0.26	0.46
IE					0.97**	0.67*	0.56	0.76**	0.70*	0.95**	0.88**	0.96**	0.87**
LN/Lf						0.66*	0.54	0.74**	0.68*	0.90**	0.80**	0.97**	0.93**
LA							0.92**	0.93**	0.94**	0.68*	0.66*	0.57	0.74**
NZA								0.93**	0.97**	0.62*	0.65*	0.41	0.66*
CZA									0.99**	0.77**	0.77**	0.64*	0.79**
TAT										0.73**	0.74**	0.57	0.75**
SP/L											0.97**	0.92**	0.77**
SP/L/D												0.81**	0.69*
SP/Lf/D													0.84**

*and **: Significant at P=0.05 and 0.01, respectively

Principal components and factors

The principal component (PC) analysis could recognize nine principal components (Figure-1) the first principal component (PC-1) alone accounting for 96.3% of the total variation in the communality and was dominated by high positive weights for AUDPC. A low positive score on PC-1 indicated high level of resistance and *vice versa* and hence this PC distinguished genotypes possessing slow-blasting resistance. The second principal component (PC-2) accounted for 3.1% of the total variation and was dominated by positive weights for SP/Lf/D, which is a reproductive phase of the pathogen. It distinguished genotypes with low sporulation capacity. The third, fourth and fifth PCs were dominated by high positive weights for LA, SP/L and LN; while the sixth and seventh were dominated by high negative weights for IP and IE, respectively. The eighth and ninth PCs were dominated by high positive weights for IE and LN, respectively. The PC-3 to PC-9 together accounted for less than 1 % of the total variation in the communality.

The factor analysis notably reduced the dimensionality and recognized three factors with eigen values greater than unity, which accounted for 72.1, 10.6 and 8.2% of the variability. These three factors were readily interpretable (Figure-1). Factor-2 was dominated by high positive weights for AUDPC, IE, LN, SP/L, SP/L/D and SP/Lf/D. Among these component characters, the first three were related to growth and the last three related to production phase of the pathogen. Factor-2 was, therefore interpreted as growth and reproductive factor. Factor-1 was dominated by high positive weights for the IP, LA, NZA, CZA and LC and high negative weights for ICP and LP; all of which are related to growth phase of the pathogen and hence it was interpreted as the growth factor. Factor-3 was dominated by high positive weight for IF. Since this component is responsible for pathogen establishment rather than growth, factor-3 was interpreted as establishment factor.

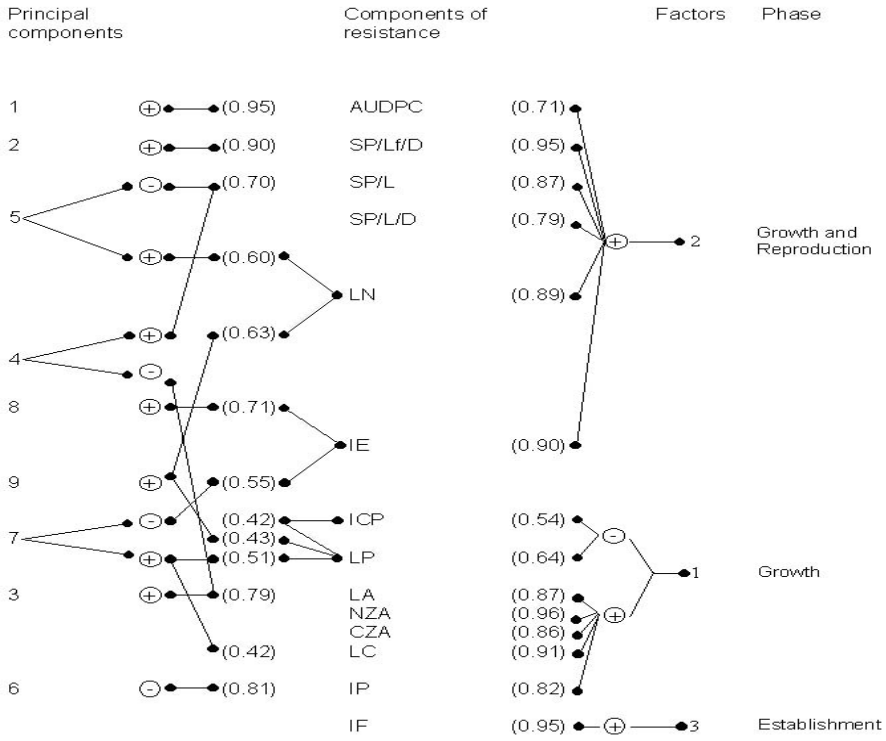

Figure-1. Diagram showing the relationship between the components of resistance and the principal components as well as factors. The signs of the coefficients dominating the latent vectors are shown as positive (+) or negative (-) and the corresponding vectors in brackets.

Clustering pattern

The dendrogram showing the clustering of genotypes based on their variability in respect of the 14 components of resistance (Figure-2) revealed a clear classification of the genotypes into groups of slow-blasting and fast-blasting clusters. The 9 genotypes namely; DJ-88, DM-27, Sakai, Chiang Tsene Tao, Lien Tsan-50, Dahanala-2014, Laurent TC, DNJ-155 and DZ-192; with little variation in respect of all the components; truncated into a sub-cluster (C-I) and merged with another sub-cluster (C-II) constituting of three genotypes Surjamukhi, E-425 and N-22; all of which differed from the 1st sub-cluster in terms of higher values of most of the components. These two sub-clusters, after forming a

cluster, again merged with the genotype CR-570, which differed from these genotypes in terms of LN, SP/L and SP/Lf/D and also AUDPC. The two fast-blasting genotypes namely; CR-289-1045-16 and Karuna, differing from each other by way of appreciably higher values of IP, IE, LN, SP/L, SP/L/D, SP/Lf/D and AUDPC in the later than the former; maintained their identity as two independent clusters. Thus, the cluster analysis distinguished three groups of genotypes of clusters-A and B possessing fast-blasting and cluster-C possessing slow-blasting characters.

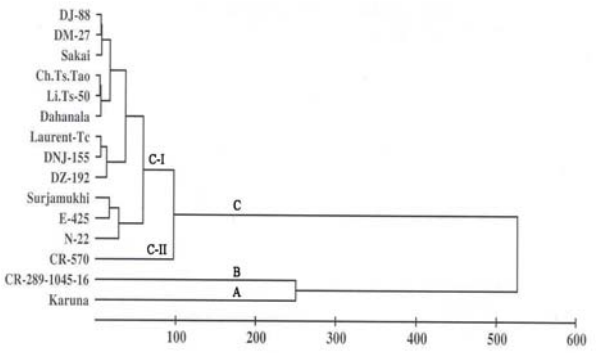

Figure-2. A dendrogram showing the similarity and successive clustering of 15 rice genotypes based on 14 components of resistance to blast disease.

The composition of the clusters and the geographical origin of the constituent genotypes (Table-3) revealed that cluster-C constituting of 13 genotypes, possessed slow-blasting characters expressed by longer ICP and LP; shorter IP and lower estimates of IF, IE, LN, LA, NZA, CZA, LC, SP/L, SP/L/D, SP/Lf/D and ultimately lower values of AUDPC. Thus, cluster-C was characterized as constituent of genotypes possessing slow-blasting resistance. Clusters-A and B on the other hand, constituted of two genotypes namely; the susceptible check Karuna and CR 289-1045-16, both of which exhibited shorter ICP and LP, longer IP and higher estimates of rest of the components. Thus, these two clusters constituted of genotypes characteristics of fast-blasting nature. An insight into the data on geographical origin revealed no relationship between slow-blasting resistance and geographical origin of the genotypes.

Table-3. Composition of each cluster and geographical origin of the constituent genotypes.

Cluster	**Number of genotypes**	**Genotypes** (origin)
A	1	Karuna (India)
B	1	CR 289 - 1045 -16 (India)
C	13	Sakai (Malaysia)
		DJ - 88 (Bangladesh)
		DM - 27 (Bangladesh)
		Dahanala (Sri Lanka)
		Laurent TC (Philippines)
		Chiang Tsene Tao (Brazil)
		Lien Tsan - 50 (China)
		Surjamukhi (Bangladesh)
		E - 425 (West Africa)
		DNJ - 155 (Bangladesh)
		DZ - 192 (Bangladesh)
		N - 22 (India)
		CR - 570 (India)

Cluster mean

The cluster means in respect of individual components (Table-4) revealed that the genotypes under clusters-A and B were dominated by lower values of ICP and L*P* and comparatively higher values for rest of the components, which have ultimately resulted in AUDPC value of 11.9 times greater than those for cluster-C. The most interesting part was production of 6.8 times greater IE leading to 28.8 times higher LN and 100.2 times more SP/Lf/D in the former than the later. There was, however, a distinct difference between the maximum range values of the cluster-*C* and minimum range value of clusters-A and B, only with regard to the components LN, LA, CZA, LC and the net result AUDPC (data not presented). There was an overlapping between the fast-blasting clusters and the slow-blasting cluster-C, specifically due to some genotypes in a cluster, which were responsible for such type of disease reaction in respect of certain individual components. There was no appreciable difference in IF between the two clusters, and the range values of the susceptible genotype-clusters-A and B, which were within the range value of the resistant genotype-cluster C. This fact has also been reflected in Table-2, that IF exhibiting no correlation with any of the 13 components of resistance.

Table-4. Cluster mean for 14 components of resistance.

Components	Cluster-A	Cluster-B	Cluster-C
ICP (days)	3.00	4.00	4.77
LP (days)	4.00	5.50	6.88
IP (days)	19.00	12.00	7.00
IF (No.)	0.76	0.80	0.58
IE (No.)	17.24	3.55	1.54
LN (No.)	77.45	19.06	1.67
LA (mm^2)	36.60	30.50	7.29
NZA (mm^2)	5.27	6.06	1.99
CZA (mm^2)	13.42	10.03	3.83
LC (mm^2)	18.69	16.09	5.87
SP/L ($x10^3$)	44.56	3.77	3.13
SP/L/D ($x10^3$)	2.35	0.31	0.30
SP/Lf/D ($x10^3$)	181.67	5.98	0.94
AUDPC	491.80	329.21	34.59

The principal component analysis (PCA) revealed that PC-1 alone explained 72.0% of the total variability, next being 10.6% by PC-2, both totaling to 82.6%. Ordination of the genotype-scores on to the planes of PC-1 and PC-2 (Figure-3) and super-imposition of the clustering pattern obtained from the dendrogram (Figure-2) on to the ordination Figure, revealed that both the susceptible genotypes Karuna (cluster-A) and CR-289-1045-16 (cluster-B) were located away from the point of intersection of both the ordinates, in the negative direction of PC-1, while rest of the genotypes in cluster-C were located in two sub-groups C-I and C-II, very closer to the point of intersection, C-I on the positive side and C-II on negative side of PC-1. Thus, super-imposition of the clustering pattern obtained from the dendrogram on to the scattered diagram obtained through the ordination of genotype-scores on to the PC-1 and PC-2, confirmed the expression of disease reaction of the genotype clusters with regard to 14 components of resistance.

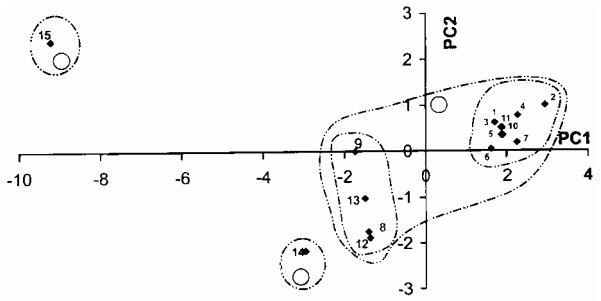

Figure-3. Ordination of 15 rice genotypes on to the planes of vector 1 and 2 from principal component analysis. The groups of genotypes encircled are the main clusters obtained from the dendrogram (Figure-2).

Parameters for evaluation of resistance

Classification of a large number of genotypes into different groups of resistance/ susceptibility on the basis of different components, although most reliable; is tedious, time consuming and difficult in estimation of each of the components. Attempts were, therefore, made to classify these genotypes into different groups of resistance/ susceptibility by estimation of various parameters, to identify the best parameter, and to check the field reaction of these genotype-clusters. The estimate of 12 different parameters in respect of the 15 rice genotypes (Table-5) clearly revealed the existence of a wide range of variation among the genotypes in respect of all the parameters. The estimates of all the parameters, except T_{50r}, T_{50k}, genotype-score on PC-1 and PC-2 were significantly higher in two susceptible genotype-clusters Karuna and CR 289-1045-16, compared to rest of the genotypes. The estimates of T_{50r} and T_{50k} were significantly lower in these susceptible genotype-clusters than those for rest of the genotypes, which was not unexpected, because the lower the rate of disease progress, higher is the time required for the disease to reach 50% severity and vice versa. In general, the apparent infection rates in logistic model were 1.7 to 6.2 times higher than those in Gompertz model, which resulted in lower T_{50} values in the former than in the later model.

Table-5. Estimates of 12 parameters for evaluation of slow-blasting resistance in 15 rice genotypes.

Genotypes	FDS %	SES	AUDPC	RAU DPC	r	k	T_{50r}	T_{50k}	IS_{LN}	IS_{LN+NZA}	PC-1	PC-2
1. Sakai	1.95	1.00	21.30	0.78	0.082	0.014	63.91	117.73	0.13	14.05	1.87	0.51
2. DJ-88	4.18	1.00	38.35	1.39	0.101	0.002	60.51	94.18	0.19	17.92	1.61	0.05
3. DM-27	3.13	1.25	38.04	1.34	0.103	0.023	71.83	112.83	0.32	20.38	1.89	0.35
4. Dahanala	3.13	1.00	32.15	1.13	0.103	0.021	61.46	97.74	0.23	12.53	1.85	0.51
5. Laurent-TC	4.59	1.25	44.47	1.67	0.073	0.022	65.52	98.02	3.46	9.92	2.24	0.19
6. Ch. Ts. Tao	4.60	1.25	41.70	1.51	0.088	0.021	71.86	99.98	0.38	16.62	-1.41	-1.74
7. Li.Ts.50	3.75	1.50	40.45	1.45	0.098	0.019	61.58	98.74	0.19	8.68	-1.74	0.01
8. Surjamukhi	10.00	2.70	91.04	3.27	0.173	0.044	39.57	46.59	5.00	88.59	-1.37	-1.87
9. E-425	8.33	2.00	75.60	2.77	0.124	0.031	59.08	64.82	17.33	78.84	1.70	0.62
10. DNJ-155	2.60	1.00	30.44	1.09	0.093	0.018	63.40	95.27	0.24	18.26	2.26	0.78
11. DZ-192	2.19	1.00	32.15	1.08	0.136	0.015	63.56	109.01	0.21	17.06	2.93	1.00
12. N-22	17.09	3.75	177.50	6.31	0.146	0.046	44.86	61.02	32.55	82.04	-1.50	-1.01
13. CR-570	6.67	2.00	78.20	2.88	0.160	0.044	30.78	49.28	79.22	116.29	1.86	0.35
14. CR-289	56.64	6.80	334.75	22.80	0.368	0.181	27.66	30.46	122.14	195.82	-2.97	-2.15
15. Karuna	98.62	9.00	483.38	26.33	0.677	0.384	12.42	11.31	496.30	511.76	-9.22	2.42
LSD at P=0.05	15.04	2.20	69.74	2.49	0.173	0.038	15.26	23.55	35.36	73.23	--	--

Association among the parameters

The correlation matrix between all possible pairs of parameters (Table-6) revealed the existence of a strong significant positive correlation among all the parameters, except T_{50r} and T_{50k}, both of which were negatively correlated with rest of the parameters. This was due to the fact that faster the rate of disease progress, quicker it takes to reach specific level (50%) of severity and vice versa. However, the genotype-score on PC-2 was not correlated with any of the 11 parameters.

Table-6. Association among the parameters for evaluation of slow-blasting resistance in rice.

	FDS	SES	AUDPC	RAUDPC	r	k	T_{50r}	T_{50k}	IS_{LN}	IS_{LN+NZA}	PC-1
SES	0.958**										
AUDPC	0.988**	0.990**									
RAUDPC	0.969**	0.982**	0.989**								
r	0.987**	0.953**	0.978**	0.945**							
k	0.993**	0.950**	0.978**	0.946**	0.993**						
T_{50r}	-0.832**	-0.902**	-0.881**	-0.852**	-0.865**	-0.834**					
T_{50k}	-0.774**	-0.866**	-0.837**	-0.807**	-0.801**	-0.773**	0.970**				
IS_{LN}	0.947**	0.883**	0.920**	0.864**	0.967**	0.976**	-0.799**	-0.729**			
IS_{LN+NZA}	0.926**	0.890**	0.908**	0.862**	0.940**	0.945**	-0.834**	-0.735**	0.952**		
PC-1	-0.872**	-0.887**	-0.876**	-0.840**	-0.870**	-0.882**	0.722**	0.728**	-0.843**	0.982**	
PC-2	0.216	0.039	0.120	0.043	0.264	0.276	-0.030	0.093	0.426	0.306	0.001

** Significant at P = 0.01

Clustering of host genotypes

Classifications of the genotypes (entities) on the basis of their attributes of the 12 parameters (variables), through hierarchical method of cluster analysis and the resulting dendrogram (Figure-4); clearly showed that the nine genotypes namely; DJ-88, Laurent-TC, Sakai, DM-

27, Dahanala-2014, Chiang Tsene Tao, Lien Tsan-50, E-425 and Surjamukhi; with lowest values of FDS, SES, AUDPC, RAUDPC, r, k, IS_{LN}, $IS_{LN+NZA,}$ genotype-score on PC-1 and PC-2 and highest values of T_{50r} and T_{50k}; truncated into one sub-group (C-I), which merged into another sub-group (C-II) of four genotypes namely; DZ-192, N-22, CR-570, and DNJ-155, with comparatively higher values of all these parameters. These 13 genotypes together constituted of cluster-C, characterized as slow-blasting in nature. The genotypes Karuna and CR-289-1045-16, both exhibiting susceptible reactions, the former exhibiting higher level of susceptibility than the later, formed two individual clusters of A and B, similar to that in dendrogram drawn on the basis of the data on 14 components of resistance.

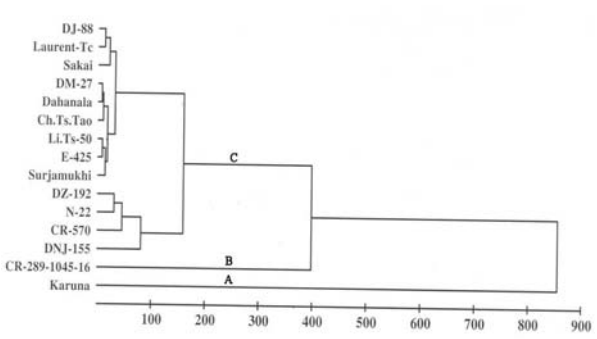

Figure-4. A dendrogram showing the similarity and successive clustering of 15 rice genotypes based on 12 parameters for evaluation of resistance to blast disease.

Clustering pattern

The clustering patterns of the genotypes extracted from the dendrogram (Figure-4) revealed that the group of 13 slow-blasting resistant genotypes namely; Sakai, DJ-88, DM-27, Dahanala-2014, Laurent-TC, Chiang Tsene Tao, Lien Tsan-50, Surjamukhi, E-425, DNJ-155, DZ-192, N-22 and CR-570, grouped under cluster-C as per the classifications based on 14 components of resistance, also formed one cluster (cluster-C). The susceptible genotype-clusters A and B on the basis of 14 components of resistance have maintained their identity as two clusters consisting of the susceptible genotype CR-289-11045-16 into cluster-B and the highly susceptible check Karuna into cluster-A, although both these genotypes belong to the susceptible category. Thus, the clustering pattern based on the 14 components of resistance was confirmed with that of 12 parameters for evaluation of resistance, and hence the compositions of the clusters are similar to those presented in Table-3.

Cluster mean

The trend of the data on the cluster means estimated for each parameter (Table-7) are almost the same for those estimated by clustering of the genotypes on the basis of 14 components. The cluster means, for the slow-blasting resistance cluster-C, were low in respect of the parameters FDS, SES, AUDPC, RAUDPC, r, k, IS_{LN} and IS_{LN+NZA} and high for $T_{50r,}$ T_{50k}, genotype-score on PC-1 and PC-2 in comparison with those for two susceptible genotype-clusters A and B.

Table-7. Cluster means of 12 parameters for evaluation of slow-blasting resistance in rice.

Parameter	Cluster means		
	Cluster-A	Cluster-B	Cluster-C
FDS	98.62	56.64	5.55
SES	9.00	6.80	1.59
AUDPC	483.38	334.75	57.03
RAUDPC	26.33	14.33	2.05
r	0.68	0.37	0.11
k	0.38	0.18	0.03
T_{50r}	12.42	27.66	58.09
T_{50k}	11.31	30.46	88.09
IS_{LN}	496.30	122.14	10.13
IS_{LN+NZA}	511.76	195.82	38.55
PC-1	-9.22	-2.97	1.15
PC-2	2.42	-2.15	0.14

Relative importance of parameters

The relative importance of the parameters for identification of slow-blasting rice genotypes, was determined by comparison of the degree of variability and inter-correlations among them, estimated through the principal component and factor analyses, considering the parameters as entities and the genotypes as variables. The principal component analysis extracted eigen vectors equal in number to the number of variables. The first three vectors accounted for 97.4% of variation present in the communality (Table-8). The factor analysis extracted two factors from rotated correlation matrix, both together accounting for 100% of the variation in the communality. The most interesting inter-correlations were in factor-1, which proves high positive inter-correlations for FDS, SES, AUDPC, RAUDPC, r, k., IS_{LN}, IS_{LN+NZA} and high negative inter-correlations for $T_{50r,}$ T_{50k} and genotype-score on PC-1. The factor-2 proves high positive inter-correlation for genotype-score on PC-2. Thus the parameters, except the genotype-score on PC-2, were identified as the top ranking for evaluation of slow-blasting resistance in rice.

Table-8. Eigen values and vectors, factor matrix of 12 parameters for evaluation of blast disease resistance in respect of 15 rice genotypes.

Parameters	Eigen values and vectors			Factors	
	Vector-1	Vector-2	Vector-3	Factor-1	Factor-2
FDS	0.31	0.06	0.19	**0.96**	0.21
SES	0.31	-0.12	0.08	**0.99**	0.01
AUDPC	0.31	-0.04	0.11	**0.99**	0.10
RAUDPC	0.30	-0.10	0.18	**0.97**	0.03
r	0.31	0.09	0.06	**0.96**	0.24
k	0.31	0.11	0.14	**0.96**	0.27
T_{50r}	-0.28	0.17	0.59	**-0.90**	0.06
T_{50k}	-0.27	0.28	0.55	**-0.90**	0.19
IS_{LN}	0.30	0.25	0.02	**0.90**	0.41
IS_{LN+NZA}	0.31	0.12	-0.09	**0.95**	0.27
PC-1	-0.28	0.11	-0.41	**-0.90**	-0.01
PC-2	0.06	0.87	-0.24	0.03	**0.98**
Root	10.01	1.25	0.44	9.82	1.43
σ^2 % explained	85.58	10.68	3.74	87.26	12.74
$\Sigma\sigma^2$ explained	85.58	96.26	100.00	87.26	100.00

Average disease progress curves

The field reactions of each group of genotypes were compared through average disease progress curves for each cluster, drawn on the basis of mean percentage disease severity for each day of observation for each group of genotypes (Figure-5). The distinct difference in disease progress curves between slow-blasting resistant group and fast-blasting group could be visualized from these curves. The clustering patterns on the basis of 14 components as well as 12 parameters being similar, the average disease progress curves have been presented in the same Figure (Figure-5).

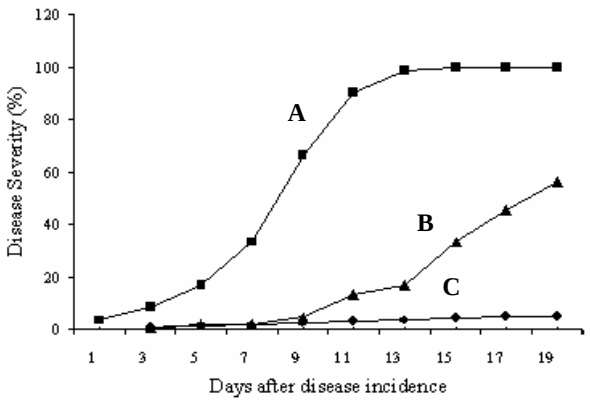

Figure-5. Average disease progress curves for each cluster of rice genotypes as evidenced from Figure 2 & 4

Thus, the grouping of the genotypes on the basis of the 14 components of resistance was confirmed through the field reaction of these genotypes by estimation of 12 parameters for evaluation of the disease progress curves. In view of the difficulty in collection of accurate data on individual components of resistance on several genotypes; the later method of estimation of parameters of resistance by analysis of disease progress curves and grouping of genotypes into different clusters would be preferred.

DISCUSSIONS

Slow-blasting resistance is known to function through different components, which are jointly responsible for limiting the rate of disease development at various stages. The 15 genotypes included in the present investigation exhibited significant differences in their response to the 14 components of resistance. Although slow-blasting resistance could be characterized by longer ICP and LP, shorter IP, lower IF, IE, LN, LA, NZA, CZA, LC and SC in terms of SP/L, SP/L/D, SP/Lf/D and AUDPC; it is difficult to distinctly categorize large number of genotypes on the basis of their response to all the components, because they interact among themselves and their effects are cumulative during the course of disease development (Mukherjee, 1994; Mukherjee and Nayak, 1997a). Longer ICP and LP delays the onset of epidemic, while shorter IP reduces the total sporulation capacity, which ultimately reduces the IF, IE, LN and AUDPC. Lower IF and IE reduce the chances of colonization by the pathogen through reduced LN, LC, SC

and AUDPC. These observations have been well reflected in the present investigation (Tables 1 and 2).

Certain specific genotypes, however, need special mention on their response in respect of few components of resistance. The genotype Surjamukhi with high IP and CZA and highest NZA, exhibited lower estimate of AUDPC, probably due to lower IE, SP/L/D and LN. The estimates of AUDPC for Lien Tsan-50 was low in spite of its IF being similar to that of the susceptible check Karuna, because of the low IP, IE, LN, NZA and SP/L/D. Similarly, E-425 exhibited AUDPC values within the range of recognizing it as a slow-blasting genotype due to its lowest IF and low LN, in spite of its possessing longer IP, higher IE and SP/L/D. Although the genotypes N-22 and CR-570 exhibited IF equivalent to that of the susceptible check Karuna, in addition to higher IE, longer IP, shorter ICP and LP; their AUDPC estimates were low due to moderately low NZA, LN as well as low SP/L/D. These critical observations demonstrate the practical difficulty in precise comparison among genotypes on the basis of their response to different components and grouping them according to their levels of expression. Such complexities could be easily overcome by application of the methods of multivariate analyses like principal component analysis, factor analysis and cluster analysis.

The factor analysis is a different model of multivariate analysis, which follows the hypothesis that the variables being measured are manifestations of a lesser number of factors thereby simplifying the complexity by way of reduced dimensionality. The factor analysis identified three factors, each constituting distinct variables related to specific phases of host-pathogen interactions like factor-3 for establishment, factor-1 for growth and factor-2 for growth and reproduction phase of the pathogen in the host tissue. Although no such characterization of the components of slow-blasting resistance in rice has been made in the past, Parlevliet (1979) classified the components of partial resistance into (i) resistance to infection (ii) resistance to colonization and (iii) resistance to reproduction; corresponding to the establishment (factor-iv), growth (factor-iii) and reproduction (factor-ii) phase of *Septoria nodorum* in wheat seedlings reported by Jeger *et al.* (1983). These distinct phases corroborate with the establishment (factor-3) and growth (factor-1) phase observed through the present investigation, with the only difference that existed in factor-2 involving both growth and reproduction phase of the pathogen.

The technique of cluster analysis could be applied for natural data clustering by simplifying description of vast multivariate data sets. The 15 genotypes included in the present investigation could be grouped into three distinct clusters by cluster analysis following a series of successive fusions on the basis of similarity in their response to 14 components of slow-blasting resistance. The practical utility of such a method of clustering in identification of slow-blasting genotypes was convincingly demonstrated by grouping all the 13 slow-blasting genotypes into cluster-C and the fast-blasting genotypes into cluster- A and B. This technique has been successfully used in the past for micro-evolutionary studies, inter-organism genetics, studies on genetic variability in phytopathogenic fungi, bacteria etc., pathogenic variability in *Xanthomonas campestris* pv. *Oryzae* (Nayak, 1996), grouping of rice genotypes for resistance to blast disease (Seshu *et al*., 1986), identification of slow-rusting wheat cultivars against stem rust caused by *Puccinia graminis* f. sp. *tritici* (Rees *et al.,* 1979a) and leaf rust caused by *Puccinia recondita* f.sp. *tritici* (Rees *et al.,* 1979b), yellow rust resistance in wheat caused by *Puccinia striiformis* (Priestley *et al.,* 1984) and field resistance to lettuce downy mildew caused by *Bremia lactucai* (Lebeda and Jendrulek, 1988)). All of them have used physiological, morphological, biochemical, virulence pattern or epidemiological components as operational taxonomic units (OTU). The successful use of the components of resistance as the OTUs for clustering genotypes through the present investigation has opened up a new dimension to the utility of this method in rice pathology in particular and plant pathology in general.

The country of origin of the genotypes sometimes play a vital role in their response to resistance, because they might be carrying genes for resistance to specific races while being screened under specific eco-geographical situation. A critical insight into the clustering pattern of the 15 genotypes revealed that the 13 genotypes grouped under cluster-C had their origin from eight countries of widely different agro-ecological regions of the world (Table-3). On the other hand, the genotypes of Indian origin were distributed into all the three clusters, thus indicating non-parallelism between geographical origin and the clustering pattern of these genotypes, Although similar findings of non-parallelism between the two were observed through D^2 analysis following Mahalanobis' generalized distance (Mukherjee, 1994; Mukherjee *et al.,* 1999), the identification of distinct clusters possessing slow-blasting genotypes through the present set of analyses has greater advantage.

The principal component analysis extracts eigen values and vectors from the correlation matrix of the components of resistance. The eigen vectors are composed of weights for the resistance components contributing to each eigen vector. The principal component (PC) has associated with it an eigen value representing the total variation that the PC accounted for. The PCA produces independent linear combinations of the original variables without reduction in the dimensionality of the complex under study, the number of PCs being equal to the number of variables, although there is criteria for disregarding some less important PCs with latent roots less than unity. Because the dimensionality is maintained, it is also possible to obtain genotype-scores on each PC. In the present investigation, PC-1 alone accounted for 96.3% of the total variation in the communality and was dominated by high positive weights for AUDPC. The strong association of the genotype-score on PC-1 with the field performance of the genotypes expressed in terms of

different parameters like FDS, SES, AUDPC, RAUDPC, r, k, $T_{50r,}$ T_{50k}, IS_{LN} and IS_{LN+NZA} (Table-6), further suggested the ranking of the genotypes on PC-1 to be continuous. The ordination on to the planes of PC-1 and PC-2 based on the 14 components of resistance reveals that the 15 genotypes are arrayed in a spectrum of resistance from the slow-blasting genotypes positioned at the center of the plane i.e., nearer to the point of intersection between the two ordinates, to the fast-blasting genotypes positioned away from it. The super-imposition of the clustering pattern obtained from the dendrogram on to the ordination diagram clearly displayed the ranking of the genotypes and distinguished the slow-blasting genotype cluster from the fast-blasting clusters (Figure-3).

Kranz (1974) first used cluster analysis to express the variability among curve models of 40 host-pathogen combinations. Following the suggestion on the possible use of pattern analysis (Thompson and Rees, 1979) consisting of the methods of joint numerical classification and ordination, different group of workers demonstrated the epidemiological evaluation of wheat resistance to leaf and stem rust (Rees *et al.*, 1979a, b) and lettuce resistance to downy mildew (Lebeda and Jendrulek, 1988). Jeger *et al*., (1983) for the first time applied the method of PCA in studies on seven components of glume blotch resistance in wheat. The results of the present investigation is the first report on the use of multivariate analyses in grouping of rice genotypes on the basis of different components of resistance to rice blast disease.

It is essential to check the field reaction of each group of genotypes through comparison of different parameters of resistance. The conclusions drawn from the PCA were strongly supported by the field reaction of the genotype-clusters through comparison of the cluster means in respect of 12 parameters (Table-7) as well as average disease progress curves for the respective genotype clusters (Figure-5), which convincingly demonstrated the superiority of the cluster-C over the other two clusters. The similarity in clustering of the genotypes based on 14 components as well as 12 parameters for evaluation of resistance, further suggests that any of these two methods could be adopted for the purpose. Although the former method is scientifically more sound and accurate; it is difficult, tedious, labor intensive and time consuming to estimate all these components while testing a large number of genotypes. Hence one can opt for the later method, which is easy to estimate different parameters from a set of data on disease progress curves recorded at frequent intervals. The question now arises as to which of these parameters are important in identification of slow-blasting resistance. Comparison of the degree of variability and correlations among the entities (parameters), estimated through the principal component and factor analyses revealed all the parameters, except genotype-score on PC-2 to be top ranking by way of their inclusion into factor-1, accounting for 87.3% variability present in the communality. Mohapatra (2002) and the authors (unpublished) identified FDS, MDS, AUDPC, RAUDPC, r, k, and genotype-score on PC-1 as top ranking parameters due to their constant inclusion into factor-1 over nine seasons of repeated testing of 42 rice genotypes. Hence, one can prefer any of these parameters from amongst AUDPC, RAUDPC, r, k or genotype-score on PC-1.

The two methods of multivariate analyses i.e., principal component and factor analyses, supplemented by the cluster analysis, provided the most appropriate measures for identification of slow-blasting resistance in rice. The application of multivariate analysis is relatively new to plant pathology, especially rice pathology, compared with the most familiar methods of multiple regression analysis. In view of the present findings on the distinct grouping of slow-blasting genotype-cluster and the fast-blasting genotypes through multivariate analyses involving the different components and parameters, and with the easy access to computer facilities as well as developed packages; the future application of such unique techniques is expected to increase and yield desired results.

ACKNOWLEDGEMENT

Financial support received from the Indian Council of Agricultural Research, New Delhi, India and the facilities provided by the Director, Central Rice Research Institute, Cuttack, India, are thankfully acknowledged.

REFERENCES

Berger R.D. 1981. Comparison of the Gompertz and logistic equations to describe plant disease progress. Phytopathology. 71: 716-719.

Brondy U., J.C. Zapata and R.R. Nelson. 1988. Evaluation of rate-limiting resistance of blast disease in rice cultivars using sub-lethal concentration of a systemic fungicide. J. Phytopathol. 122: 174-180.

Castano J., D.R. MacKenzie and R.R. Nelson. 1989. Component analysis of race non-specific resistance to blast disease of rice caused by *Pyricularia oryzae*. J. Phytopathol. 127: 89-99.

Chaudhary R.C. and P. Nayak. 1987. Genetics and breeding for blast and bacterial blight resistance in rice. S. Kannaiyan (Ed.). Advances in Rice Pathology, TNAU, Coimbatore, India. pp. 1-35.

Chou L.K., F.L. Nuque and J.P. Crill. 1979. Varietal resistance and possible components of horizontal resistance to blast. Int. Rice Res. Newsl. 4: 9-10.

Crill J.P., Y.S. Ham and H.M. Beachell. 1982. The rice blast disease in Korea and its control with race prediction and gene rotation. In: Evaluation of the Gene Rotation Concept for Rice Blast Control, International Rice Research Institute, Manila, Philippines. pp. 123-130.

Fry W.E. 1978. Quantification of general resistance of potato cultivars and fungicide effects for integrated control of potato late blight. Phytopathology. 68: 1650-1655.

IRRI (International Rice Research Institute). 1988. Standard Evaluation System for Rice. Manila, Philippines, 3rd Ed.

Jeger M.J., D.G. Jones and E. Griffiths. 1983. Components of partial resistance of wheat seedlings to *Septoria nodorum*. Euphytica. 32: 575-584.

Kendall M.G. and A. Stuart. 1968. The Advanced Theory of Statistics. Vol.3, 2nd Edn. London, Charles Griffin and Co. Ltd.

Kiyosawa S. 1981. Gene analysis for blast resistance. Oryza. 18: 196-203.

Kiyosawa S. and M. Shiyomi. 1976. Simulation of the process of breakdown of disease resistant varieties. Japan. J. Breed. 26: 339-352.

Kranz J. 1974. Comparison of epidemics. Annu. Rev. Phytopathol. 12: 355 -374.

Lebeda A. and T. Jendrulek. 1988. Application of methods of multi-variate analysis in comparative epidemiology and research into field resistance. Zeitschrift. Fur Pflanzenkrankheiten and Pflanzenschutz. 95: 495-505.

Madden L. and S.P. Pennypacker. 1979. Principal component analysis of tomato early blight epidemics. J. Phytopathol. 95: 364-369.

Manibhushan Rao K. 1994. Rice Blast Disease. Daya Publishing House, New Delhi, India.

Mohapatra N.K. 2002. Studies on Durable Resistance to Blast Disease of Rice. PhD thesis, Utkal University, Bhubaneswar, Orissa, India.

Mukherjee A.K. 1994. Components of Slow-blasting Resistance in Rice. PhD thesis, Utkal University, Bhubaneswar, Orissa, India.

Mukherjee A.K. and P. Nayak. 1997a. Association among the components of slow-blasting resistance in rice. J. Mycol. Plant Pathol. 27: 175-183.

Mukherjee A.K. and P. Nayak. 1997b. Method of estimating chlorotic area from the linear measurements of necrotic area of rice blast lesions. Int. J. Tropical Plant Dis. 15: 177-181.

Mukherjee A.K. and P. Nayak. 1998. Sporulation capacity as a component of slow-blasting resistance in rice. Oryza. 35: 82-85.

Mukherjee A.K., B.K. Mohapatra and P. Nayak. 1996. The use of selection indices for identification of slow-blasting rice genotypes. Int. J. Tropical Plant Dis. 14: 179-187.

Mukherjee A.K., N.K. Mahana and P. Nayak. 1997. *In situ* estimation of lesion area of rice blast disease using linear measurements. Indian Phytopathol. 50: 431- 433.

Mukherjee A.K., N.K. Mohapatra and P. Nayak. 1998. Technique for determination of infection frequency and infection efficiency as components of slow-blasting resistance in rice. Oryza. 35: 184-185.

Mukherjee A.K., A.V. Suriya Rao, R.N. De and P. Nayak. 1999. Genetic diversity among slow-blasting rice genotypes. Oryza. 36: 70-73.

Nayak D. 1996. Variability in *Xanthomonas campestris* pv. *oryzae*, the causal organism of bacterial blight disease of rice. PhD thesis, Utkal University, Bhubaneswar, Orissa, India.

Nomura K., K. Ishi. 1989. Effects of the components of field resistance to *Pyricularia oryzae* in rice on disease development and relationship between the components. Bulletin of the College of Agriculture and Veterinary Medicine, Nihon University. 46: 40-47.

Ou S.H. 1985. Rice Diseases, 2nd ed. Wallingford, UK: CAB International.

Parlevliet J.E. 1979. Components of resistance that reduce the rate of epidemic development. Annu. Rev. Phytopathol. 17: 203-222.

Priestley R.H., R.A. Bayles and J. Ryall. 1984. Identification of specific resistance against *Puccinia striiformis* (Yellow rust) in winter wheat varieties. II. Use of cluster analysis. J. Natl. Inst. Agril. Botany. 16: 477-485.

Rees R.G., J.P. Thompson and R.J. Mayer. 1979a. Slow rusting and tolerance to rust in wheat. I. The progress and effect of epidemics of *Puccinia graminis tritici* in selected wheat cultivars. Australian J. Agric. Res. 30: 403-419.

Rees R.G., J.P. Thompson and E.A. Goward. 1979b. Slow rusting and tolerance to rust in wheat. II. The progress and effect of epidemics of *Puccinia recondita tritici* in selected wheat cultivars. Australian J. Agric. Res. 30: 421- 432.

Ryu J.D., E.J. Lee and J.H. Oh. 1990. The factors associated with race nonspecific resistance of seomycinbyeo to rice blast (*Pyricularia oryzae* Cav.). Crop Prot. 32: 73-81.

Ryu J.D., W.H. Yeh, S.S. Han, Y.H. Lee and E.J Lee. 1987. Regional and annual fluctuation of races of

Pyricularia oryzae during 1978-1985 in Korea. Korean J. Plant Patholol. 3: 174-179.

Seshu D.V., T.S. Kwak and D.J. Mackill. 1986. Global evaluation of rice varietal reactions to blast disease. In: Progress in Upland Rice Research. International Rice Research Institute, Manila, Philippines. pp. 335-352.

Shaner G. and R.E. Finney. 1977. The effect of nitrogen fertilization on the expression of slow-mildewing resistance in Knox wheat. Phytopathology. 67: 1051-1056.

Sun G.C., D. Shi, G.Z. Zhuge and S.Y. Sun. 1990. Some components of partial resistance to blast in *indica rices*. Int. Rice Res. Newsl. 15: 11-12.

Thompson J.P. and R.G. Rees. 1979. Pattern analysis in epidemiological evaluation of cultivar resistance. Phytopathology. 69: 545-549.

Tredway L.P., K.L. Stevenson and L.L. Burpee. 2003. Components of resistance to *Magnaporthe grisea* in 'Coyote' and 'Coronado' tall fescue. Plant Disease. 87: 906-912.

Van der Plank and J.E. 1963. Plant Diseases: Epidemics and Control, Academic Press, New York, USA.

Villareal R.L., R.R. Nelson, D.R. MacKenzie and W.R. Coffman. 1981. Some components of slow- blasting resistance in rice. Phytopathology. 71: 608-611.

Wang Q.F. and Q.M. Wang. 1991. Study on slow-blasting resistance of rice to *Pyricularia oryzae* Cav. Acta Phytopathologica Sinica. 13: 97-102.

Yamada M. 1965. Breakdown of blast resistance in highly resistant rice varieties derived from foreign varieties. Shokobutsu Boeki. 19: 231-234.

Yamada M. 1979. Changes in population of *P. oryzae* races and varietal resistance to blast disease in Japan. In: Lecture Meeting on Rice Blast Disease, Suweon, Korea, ASPAC/FRTC and ORD. pp. 75-108.