

Interpretation of Varietal Response to Rice Leaf Blast by $G \times E$ Analysis with Reduced Number of Nursery Test Sites

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ABSTRACT : Blast severity data of 39 rice varieties at 11 sites in Korea from 1997 to 1999 were analyzed using AMMI model and pattern analysis. Genotype \times Environment ($G \times E$) interaction sum of squares (SS) accounted for 12% of the total SS. Eight genotype groups and seven location groups were identified based on blast reaction pattern. The data obtained from over 21 sites with 44 test varieties from 1981 to 1996 were also considered. These were compared with the 1997-1999 data using the $G \times E$ analysis results. Majority of the variability in the Korean Rice Blast Nursery (KRBN) were attributable to variations due to genotypes. Variations of $G \times E$ interaction were maintained though test sites were reduced from 21 to 11 sites. Broadly compatible biological discriminative varieties identified were Nagdongbyeo and Akibare while broadly incompatible biological discriminative varieties identified were Hangangchalbyeo and Seogwangbyeo. Key sites for future evaluation work could be selected from location groups. Each location group should be represented by the site with the strongest interaction pattern. Blast responses in Cheolwon, Gyehwa, Suwon, Iksan, and Icheon showed different patterns from other locations.

Keywords : AMMI, Pattern analysis, $G \times E$ Interaction, Korean Rice Blast Nursery, discriminative Variety, Key site

For the breeding of highly durable blast-resistant rice variety (Kim and Ahn, 1991), blast nursery test has been being done as a first step of series of blast evaluation. Information of population dynamics of the blast pathogen over spatial and temporal interaction with rice cultivars under diverse environments is essential for the strategic and effective use of genetic resistance (Ahn, 1998). At the same time, we study the blast pathogen that is continuously changing and work on accumulating blast resistance genes using molecular techniques. On the other hand, the chemical industry and institute are investigating chemical control for rice blast. There are clear relationships between many of the

analytical methodologies used for studying genotypic variation and $G \times E$ interaction (Westcott, 1986) in plant breeding experiments (Cooper and Delacy, 1994). The KRBN is a multilocation trial observing genotypes change across test environments. Blast reaction data over locations and years of several varieties in the nursery can be examined to understand $G \times E$ interaction in rice blast screening. $G \times E$ interaction can be evaluated using the Additive Main Effects and Multiplicative Interaction (AMMI) model (Gauch and Zobel, 1990) and pattern analysis (Abdalla *et al.*, 1996). The AMMI model is fit by carrying out a mean polish on the raw $G \times E$ matrix and then fitting a few interaction principal component axes (IPCA) to the matrix of residuals using a singular value decomposition or SVD. Furthermore the mean polish fits the additive main effects for genotypes and environments by least squares.

Pattern Analysis (PA) is a combination of cluster analysis and ordination used to analyze interaction of two factors on a response variable. PA also performs a two-way hierarchical agglomerative clustering using Wards method of minimum incremental sum of squares and principal component analysis on the environment standardized $G \times E$ matrix. PCA ordination is essentially used to display relationships between genotypes and environments or between genotype and environment group in the form of biplots (Kempton, 1984).

The KRBN was conducted in 21 locations from 1981 to 1996. Since 1997, it has been being conducted in 11 sites. The number of testing sites has been reduced for administrative reasons. This reduction in the number of testing sites affected the blast response pattern. Thus, there is a need to evaluate the $G \times E$ interaction for blast reaction in the KRBN conducted from 1997 to 1998 to erudite shift of blast response and to come up with a recommendation on testing sites and probe genotypes even though approach of host resistant gene and pathogen gene are in progress. The specific objectives of this study were: 1) to understand the $G \times E$ interaction using AMMI model and pattern analysis; 2) to identify environmental factors contributing to $G \times E$ interaction; 3) to compare the genotypic and regional groups gener-

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ated from the pattern analysis of blast nursery result from 1981 to 1996 (Roh *et al.*, 1998) with the groups from 1997 to 1999; 4) to identify the test sites to be used in future trials; and 5) to identify discriminative genotypes for varietal evaluation for blast resistance.

MATERIALS AND METHODS

Rice plants of each varieties were grown in single, 30 cm long rows spaced 10 cm apart. Two susceptible varieties, Nagdongbyeo (Japonica) and Yushin (Indica), were used as spreaders. They were sown in the borders and after every two test entries. Every year, sowing was done in late June. Fertilizers were applied at the rate of 12 g N-10 g P₂O₅-10 g K₂O/m. Blast severity was scored following the standard evaluation system for rice. Data for 39 varieties (Table 1) evaluated from 1997 to 1999 in 11 sites (Table 2), hereafter referred to Data Set II, were used in this study. Evaluation was done using the Standard Evaluation System (SES) base on 0 to 9 scale (International Rice Testing Program, 1988). Reaction scores of 0~3 indicate the absence of compatible type lesions and scores of 4~9 indicate the presence of compatible races including different levels of quantitative resistance. The test varieties included 3 Korean inbred lines and several rice varieties from Korea, Japan and other countries. The test sites represented varied agroecological zones in Korea. Variety means across years were subjected to AMMI

and pattern analyses. Correlation analysis between IPCA scores and environmental variables averaged over years representing elevation, latitude, longitude, precipitation, temperature and sunshine duration was done. Location groups and genotype groups formed were compared to those generated in the analysis of data for 44 varieties evaluated from 1981 to 1996 in 21 sites (Data Set I). The 11 sites in Data Set II were included in 21 sites in Data Set I. The 39 varieties in Data Set II were among the 44 varieties included in Data Set I.

RESULTS AND DISCUSSION

AMMI analysis

Twelve percent of the total sum of squares (TSS) is accounted for by the genotype by environment (G × E) interaction term in Data Set II (Table 3). This is slightly higher than the proportion of SS by G × E relative to the TSS in 1981~1996 Data. In both data sets, a very large portion of TSS is accounted for by genotype sum of squares (84%~89%) and small portion by environment sum of squares. The first three principal components (IPCA) accounted for at least 63% of the variation contained in the G × E interaction term in both data sets. There was no environmental variable observed in Data Set II found to be significantly correlated with IPCA 1 and IPCA 2. Cooper and DeLacy (1994) reported this possi-

Table 1. Test varieties used in G × E analysis in the Korean Rice Blast Nursery in Data Set I, II.

Varietal Type	Variety
Japonica	Caloro, Chiakbyeo, Akibare, Dobongbyeo, Dongjinbyeo Fukunishiki, Gwanakbyeo, Hangangchalbyeo, Ishigarishiroge Jinheung, Kante 51, Nagdongbyeo, Nongbaeg, Nonglimna 1 Pi No 4, Pungok, Seogwangbyeo, Seolagbyeo, Shao-Tiao-Tsao Shin 2, Doride 1, Tsuyuake, Yashiromochi, Zenith Gwanok[†], Paldal, Palgeum
Tongil	Baegunchalbyeo, Baegyongbyeo, Cheongchongbyeo, Chupungbyeo Milyang 23, Milyang 42, Nopung, Pungsanbyeo, Raegyeong Taebaegbyeo, Tongil, Yushin, Nampungbyeo, Milyang 30
Indica	Np 125, Tetep.Usen,

[†]Entries written in bold letters were not included in the 1997~1999.

Table 2. Test sites used in G × E analyses in the Korean Rice Blast Nursery in Data Set I, II.

Region	Sites
High elevation	Jinbu
Mid-mountains	Cheolwon, Unbong, Jinan[†], Jacheon , Sangju
Plains	Suweon, Hwaseong, Daejeon, Daegu , Icheon, Iksan1, Iksan2 , Milyang, Cheongju, Jinju, Naju , Youngdug, Chuncheon
Sea coastal	Gyehwa, Namyang

[†]Entries written in bold letters were not included in the 1997~1999.

Table 3. Combined ANOVA for Data Set I (1981~1996) and II (1997~1999).

Source	Data set II			Data Set I		
	Sum of Squares	%Total SS	%G × E SS	Sum of Squares	%Total SS	%G × E SS
Genotype	1797.04	84		5012.51	89	
Environment	86.96	4		162.80	3	
G × E	261.88	12		453.14	8	
IPCA1	87.89		33.6	189.51		41.8
IPCA2	44.58		17.0	66.53		14.7
IPCA3	33.57		12.8	43.89		9.7
IPCA4	25.90		9.8	35.55		7.8
Residual	69.94		26.8	117.66		26.0

bility. In this analysis, no biological element of different environments including race composition or virulence frequency was studied. But In Data Set I major environmental factors affecting G × E in blast nursery test were temperature and precipitation during the testing periods. Composition of different races and aggressiveness of blast pathogen (Ahn, 1994) in different test sites should be analyzed in the future. It is also possible that environmental factors that could influence G × E interaction like relative humidity, canopy surface temperature, and wind speed were not recorded in this study. It should be noted that environment sum of squares was only a small fraction of the total variability.

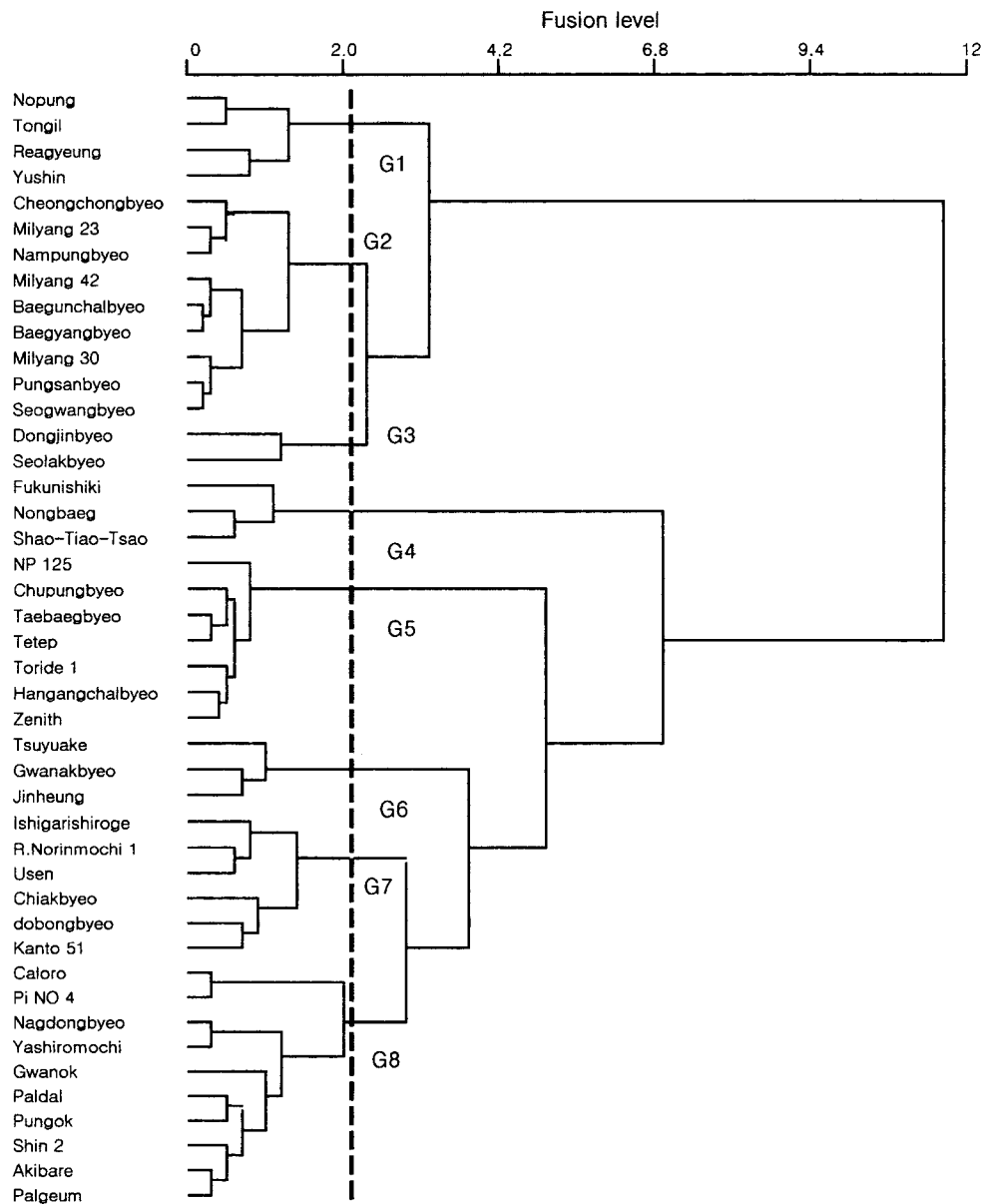


Fig. 1. Dendrogram for the classification of genotype in Data Set I (1981~1996).

Thus the role of biological environmental factor might play an important role in blast evaluation in the KRBN.

Pattern analysis

It was done to reduce the genotypes and environments to groups with similar interaction patterns. The number of clusters was made similar to the one generated in Data Set I (Fig. 1). Eight genotype groups were generated (Fig. 2). Gc group had only one variety (Nagdongbyeo) while Ga group had eight. All groups with at least two members had a mixture of indica and japonica varieties except for Gh group which was composed of japonica varieties only. The composition of genotype groups differed substantially between the two data sets. One possible reason for the changing group composition from Data Set I to II could be a change in the genetic composition of blast pathogen in test sites. For example, Yushin was known to be highly resistant to blast in

the seventies. In recent trials, its blast reaction ranged from resistant to susceptible.

Varieties within a group have similar interaction patterns. However, varieties within a group could differ greatly in their blast reaction. For example, Gg group has one member (Cheongchongbyeo) with high response scores (6.0~8.0) and therefore susceptible; and four members with low scores (0.7~4.3) and therefore resistant. One member (Caloro) of Ga group has high scores (6.0~8.7) while others have low scores (Ex, Taebaegbyeo with scores of 0.3~2.7). One possibility is that resistance or susceptibility is controlled by major genes whose expression could be modified by minor genes. This resistance is thought to be combining multiple major and minor genes conferring both complete and partial resistance in rice (Ikehashi and Khush, 1979). Although major-gene resistance to blast has been useful, resistance conditioned by a single major gene has often proved unstable (Kiyosawa, S. 1982). Varieties within a group could

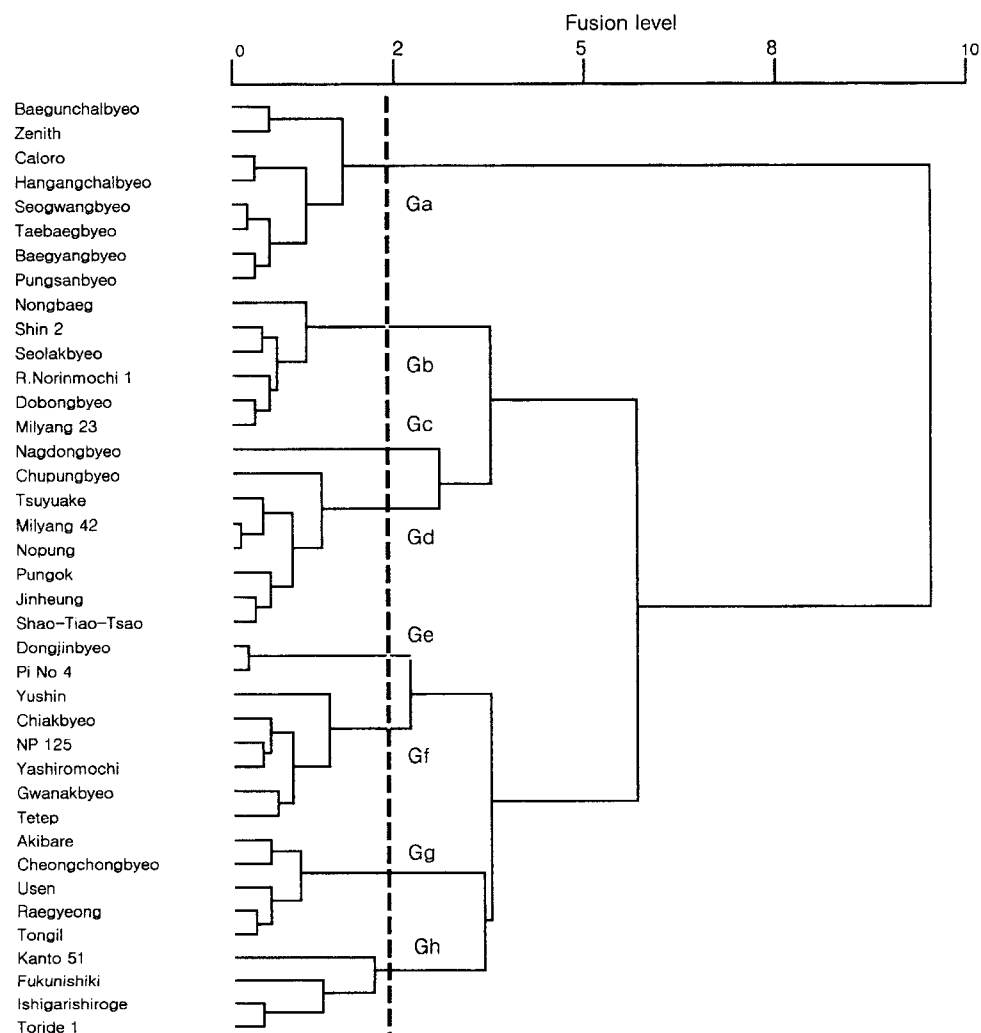


Fig. 2. Dendrogram for the classification of genotypes in Data Set II (1997~1999).

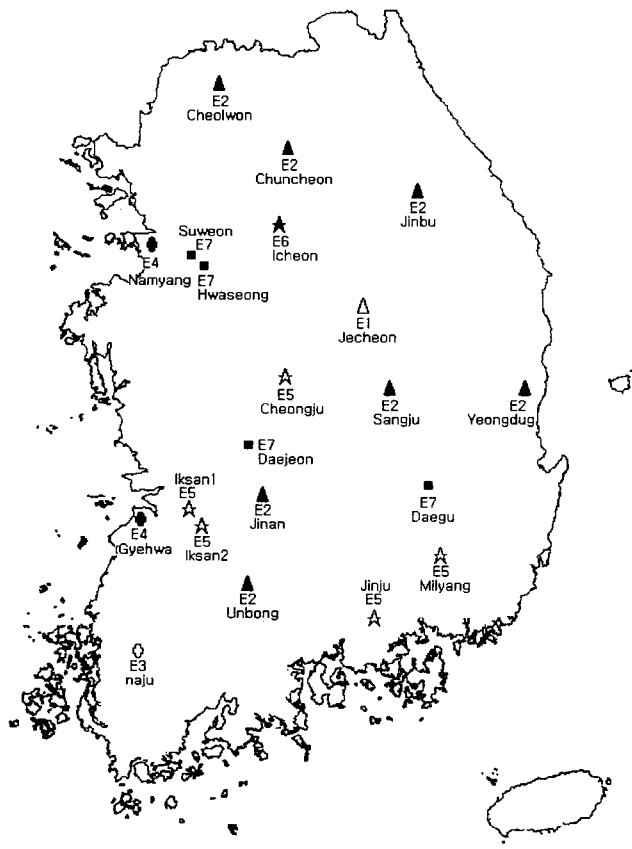


Fig. 3. Cluster Grouping of test sites base on Rice Blast Reaction Pattern in Data Set I (1981~1996).

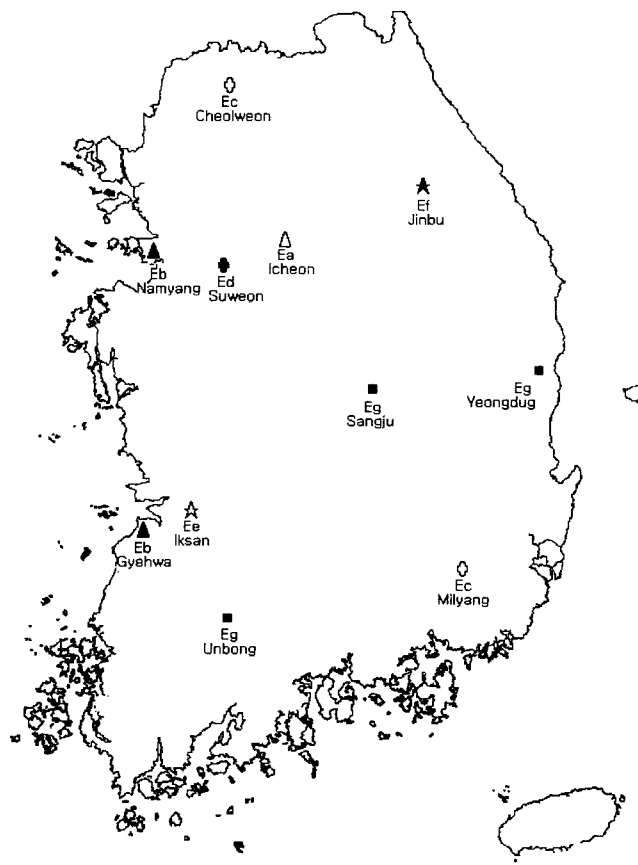


Fig. 4. Cluster Grouping of test sites base on Rice Blast Reaction Pattern in Data Set II (1997~1999).

have different alleles for a major gene loci and they share common genes responsible for the same interaction pattern.

In identifying discriminative genotypes, the following criteria were used. They should be commercial japonica or Tongil type varieties since only these types are grown in Korea. They should belong to different genotype groups and thus represent diverse interaction pattern. They should have a high degree of resistance or susceptibility to blast. The susceptible probes identified were Nagdongbyeo (4.2~8.0) and Akibare (6.0~8.7). The resistant probes identified were Hangchalbyeo (0.6~3.3) and Seogwangbyeo (0.3~2.6). Furthermore, interaction between these varieties' resistant/susceptible genes and pathogen's related genes should be investigated.

Seven location groups (E1~E7 and Ea~Eg) were generated (Fig. 3, 4). In Data Set I, E2 group has five sites (Cheolwon, Yeongdug, Jinbu, Unbong and Sangju) common to Data Set II. Yeongdug, Sangju and Unbong formed one group in Eg group while Cheolwon (Ec group) and Jinbu (Ef group) were in separate groups in Data Set II. Iksan and Milyang were in the same group (E5 group) in Data Set I but in separate groups in the other data set. Cheolwon and Mily-

ang were in separate groups in Data Set I but in the same group in Data Set II. This could also be explained by the change in the blast pathogen composition in test sites or the change in meteorological factors at the same site. In Data Set I, Jecheon and Naju having distinguished blast response patterns (Roh *et al.*, 1998) were excluded in Data Set II. This elimination of blast hot spots could have affected decline of blast response discrimination in blast nursery test. And current test sites should include these sites representing distinct location groups. On the other hand, Park (1988) reported southern coastal area (ex. Chinju) was another distinct blast reaction area in 1979-1990.

Selection of sites for future screening work could be based on location groups since each group represents a particular interaction pattern. Based on Data Set II, Suwon, Jinbu, Iksan and Icheon should be represented in future studies being single location groups. For the other groups which have 2-3 member locations, the site with the strongest $G \times E$ interaction should be selected. Discrimination through test site, therefore, was maintained after reduction of test site even though a certain extent loss of information about rice blast reaction due to remarkable variations of genotypes.

This study is still needed to prolong generating detailed comprehensions on genotypic and environment groups.

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