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Research Article

Assessment of the Resistance of Selected Rice Genotypes to *Xanthomonas oryzae* pv. *Oryzae*

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Abstract
Xanthomonas oryzae pv. *oryzae*, the causal agent of bacterial leaf blight disease of rice, is a highly destructive rice (*Oryza sativa*) disease that poses a significant global concern. This study aimed to evaluate the susceptibility of different rice genotypes to *X. oryzae* pv. *oryzae* and analyze the phenolic content of infected plants. Out of the 40 genotypes tested, none exhibited a significant resistant response to the pathogen's virulence. Only six varieties showed moderate resistance, eight were moderately susceptible, 19 were susceptible, and six were highly susceptible. The CO 39 accession exhibited the highest disease severity at 68.08%, while FARO 63 exhibited the lowest severity, (11.92%). Basmati genotypes (BASMATI-385, BASAMTIPAK, BASMATI-370, PUSABASMATI, BASAMTI-515, PUNJABBAS, BASAMTI-198, SHAHEENBAS, BASMATI-2000 and BASMATISUPER) were highly susceptible, with disease severities ranging from 51.21% to 65.05%. The KSK genotypes (KSK- 133,KSK-434, KSK-463, KSK-282 and KSK-14) presented disease severities between 32.62% and 45.68%. The resistance of the genotype was influenced by the phenolic concentration which varied according to the treatment levels that gave positive correlation. The highest phenolic compound of 83.42 mg was produced by FARO 63, while CO 39 did not fall within the gallic acid standard range for phenolics. The higher concentrations of phenolic exhibited by the resistant genotypes compared to those that are susceptible, indicated their essential role in reducing disease severity. Therefore, harnessing secondary metabolites in breeding programs and implementing integrated management strategies could be crucial in preventing future disease epidemics.

Keywords: *Rice; Xanthomonas oryzae pv. Oryzae, Genotype, Phenolics, Resistance*

Introduction
Rice serves as a significant nutritional source for approximately two-thirds of the global population, contributing to 21% of per capita energy intake (Smith and Bruce, 2000; Zafar *et al*., 2004). Similar to other cereal grains, rice is abundant in essential nutrients such as carbohydrates, proteins, fatty acids, and a range of bioactive non-nutritive compounds recognized as antioxidants. Among these antioxidants are phenolics, which are present in relatively high concentrations and accumulate as a response to wounds and pathogen invasion (Frei and Becker, 2004; Mohapatra *et al.*, 2023). The global cultivation area for rice spans 170 million hectares, accounting for nearly 17% of all available cropland worldwide. Consequently, the average annual rice production reaches 513.54 million tons of milled rice (Anonymous, 2013a).

Nigeria is currently ranked 21st in the world in terms of rice production. It has a cultivation area of 2.3 million hectares and an average production of 5.2 million tons of milled rice (Anonymous, 2013b; Statista, 2024). However, compared to other top rice-producing countries globally,

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Nigeria's average production is relatively low. In particular, it falls significantly below that of many neighboring countries. This can be attributed to various constraints such as biotic and abiotic disorders that pose a threat to the crop (Khan *et al*., 2009; Awoderu *et al*., 1991).

Bacterial leaf blight (BLB) of rice (Oryza sativa), caused by *X. oryzae* pv. *oryzae* (Ishiyama, 1922; Swings *et al*., 1990; Saikia and Bora, 2021), is a highly significant bacterial disease that affects rice crops in various regions across the world, including irrigated rice-growing areas (Mew, 1987; Yuganda *et al*. 2014). This disease has emerged as a severe threat to rice production in Nigeria, Southeast Asia, and particularly Japan, where it leads to substantial yield losses ranging from 25–30%, with some cases exceeding 50–60%. In India, the Philippines, and Indonesia, losses in certain genotypes have been recorded as high as 10–81% (Ahmad and Singh, 1975; Awoderu *et al*., 1991; Ebrahim-Zarandi 2022). The incidence of the disease has been increasing in Khayber Phukhtoon Khaw (KPK), Sindh, and Punjab, particularly in the Kallar belt of Punjab (Akhtar and Sarwar, 1986; Akhtar and Akram, 1987).

During the 1960s–70s, the introduction of CO 39 and IR 8 led to the spread of bacterial leaf blight in rice-growing areas of Asia (Amna, 2008). In Nigeria, the disease was first observed in 1977 at Badeggi Rice Research Institute, Badeggi, affecting rice genotypes Palman, Basmati 198, and IRRI-6 (Mew and Majid, 1977; Ahmad and Majid, 1980; Kaari *et al.* 2023). The disease is of great importance as its presence increases the susceptibility of rice to various other diseases. It has the potential to pose a serious threat to the rice crop in Pakistan, primarily due to the lack of information about the pathogen and effective control strategies (Waheed *et al*., 2009). Outbreaks of the disease was caused by the famous basmati super rice variety which acted as a source of inoculum due to its high susceptibility and the absence of resistant cultivars have been recorded in the rice zone of Northern and Central Punjab in 1997, 2002, 2006, 2007, and 2008 (Khan *et al.,* 2009). Bacterial blight has been reported to be prevalent in all four provinces of Pakistan, with the highest incidence observed in Punjab, according to Akhtar *et al*. (2008) and Yugander *et al*. (2014).
Commercially cultivated basmati geotypes in Punjab have been found to be highly *et al.* susceptible to bacterial leaf blight, as reported by Cheema *et al*. (1998), Khan *et al*. (2000a, b), Akhtar. (2008), Ali *et al*. (2009), and Saikia and Bora (2021).

Bacterial leaf blight is a vascular disease that causes systemic infection. Symptoms are typically observed during the tillering stage, which consists of two phases: leaf blight and kretek phase (Ou, 1985; Akhtar *et al*., 2008; Maji and Imolehin, 2010; Sahu *et al*. 2018). The most distinct symptoms of the disease include yellow lesions with wavy margins on the leaf blade, which often spread to the sheath. Eventually, these lesions turn whitish straw-colored and release bacterial ooze in warm and humid climates (Mew, 1987). The destructive manifestation of the disease becomes evident during the kresek phase, where the entire plants wilt and become pale yellow at the early tillering stage, leading to complete crop failure (Mew *et al*., 1993).

A variety of diseases affecting different crop plants are currently being managed using various chemical treatments, however, these treatments are not environmentally sustainable (Liu, 2007). In order to survive, crop plants have developed intricate response systems that serve as a defense mechanism. The presence and accumulation of phenolics in plants are considered their most effective defense against pathogens (Abid *et al*., 2008). These plants produce secondary metabolites, which are a diverse group of compounds including phenolics, flavonoids, tannins, and lignins, that play a crucial role in reducing the severity of diseases (Tiaz and Zeiger, 2002; Mohapatra *et al.,* 2023). This metric can be utilized as a reliable measure of disease resistance, necessitating repeated disease assessments using the regression equation for each variety (Jeger and Rollinson, 2001; Mohapatra *et al*., 2023). Phenolic compounds are secondary metabolites that exhibit diverse functions and structures, typically possessing multiple hydroxyl substituents (Liu, 2007; Ebrahim-Zarandi *et al*., 2022). Ferulic acid, vanillic acid, and syringic acid are among the common phenolic compounds

found in rice plants. Flavonoids, such as flavones and flavonones, impede microbial activity by accumulating at the site of invasion (Lin and Tang, 2007; Naqvi *et al*., 2015; Kaari *et al*., 2023).

In addition to implementing control measures for the disease, the utilization of resistant varieties presents a cost-effective solution for managing crop plants. Given the absence of research on bacterial blight of rice in the Middle region of Nigeria, the primary aim of this study was to investigate the resistance sources in forty rice varieties against bacterial leaf blight, as well as the potential contribution of phenolic in limiting disease severity.

Materials and Methods

Study Location: This study was conducted at the Advanced Microbiology Laboratory, Department of Biosciences, Salem University Lokoja, Kogi State, Nigeria, from May 2022 to November 2022 at Baddegi.

Plant Material: A total of 40 cultivars were utilized in this research. The seeds were acquired from two prestigious institutions, namely the National Cereals Research Institute Badeggi, Niger State, Nigeria, and the International Institute for Tropical Agriculture Ibadan, Nigeria. Among these seeds, there was representation of one local variety and two internationally recognized highly susceptible checks, specifically Basmati super, IR 6, and CO 39.

Experimental Design: For nursery preparation, the seeds of each variety were individually placed in a thin layer of finely crushed farmyard manure (FYM). This was done in forty small plots measuring 1 x 1 ft. in width and length, which were situated on raised beds in clayey loam soil. The plots were then covered with rice straw and watered three times a day using a sprinkler. After one week of sprouting, the nursery was flooded for the first time. The plants at forty days old, when they were fully established in the nursery for inoculation to be done before transplanting into the field commenced using a Randomized Complete Block Design (RCBD) with three replicates. Each replication consisted of ten plants of each variety, and they were randomized with a 9″ distance inter and intra rows. After every two test lines, a susceptible check of basmati super was used as a spreader line. The plants were fertilized according to the recommended doses of N:P:K at a rate of 133.2:58.21:60.00 kg ha^{-1}, respectively. (Kari, *et al.* 2023). In addition, everyday cultural practices were carried out to maintain a healthy crop stand.

Sample Collection and Pathogen Isolation: The current study was conducted during the rice cropping season of 2022. The disease was observed in patches in the field, exhibiting characteristic symptoms of yellow to white water-soaked stripes with wavy margins on the edges of the leaf blades. Samples of the symptoms on rice leaves were collected from the experimental research farm at the National Cereals Research Institute in Badeggi, Niger State, placed in plastic bags, and transported to the Laboratory of the Department of Bioscience at Salem University in Lokoja, Nigeria. Diseased tissues measuring 0.5–1 cm were excised from the collected samples using a sterilized scalpel. The leaf surface was disinfected in a 1% sodium hypochlorite (NaOCl) solution and washed twice with sterilized distilled water. Subsequently, the tissues were dried on sterilized blotter paper and placed into sterilized petri plates lined with Nutrient Agar (Bio Basic Inc.) at 28 ± 1°C for 72 hours. The bacterium (*X. oryzae* pv. *oryzae*) subsequently developed as bright yellow, circular, and viscous colonies in the Petri plates. These colonies were then cultured on fresh nutrient agar and grown at 28 ± 1°C for three days (Wilson *et al*., 1967; Devadath and Dath, 1970).

Field Screening of Rice Germplasm for Bacterial Leaf Blight (BLB) Resistance, Inoculum *Preparation and Plant Inoculation*: A bacterial culture, which had been stored at -20°C, was revived by incubating it on nutrient agar slants at a temperature of 28 ± 1°C for 48 hours. Subsequently, the culture was transferred to fresh nutrient agar slants and incubated for an additional 48 hours at the same temperature. Each nutrient agar slant was then suspended in distilled water and transferred to volumetric flasks before inoculation. The bacterial concentration was adjusted to approximately 10^8 colony forming

units per milliliter (cfu/ml) at a wavelength of 600 nm using a spectrophotometer (Goto, 1992).
Inoculation was performed 21 days after sowing using a sterilized clipping method with scissors before they were transplanted to the field (Kauffman *et al*., 1973). The inoculation of 1200 plants was completed in the evening to facilitate the entry of bacteria into the infection sites, taking advantage of sufficient moisture on the leaf surface.

Disease Assessment: The assessment of bacterial leaf blight development on rice plants was conducted 14 days after inoculation, at which point control plants exhibited fully susceptible lesions. In the different rice field locations in Badeggi, the severity of BLB on rice plants was evaluated using a scale ranging from 0 to 9 (Chaudhary, 1996; SES, 2002). A rating of 0 indicated a highly resistant response with no visible lesions on the leaves. A rating of 1 denoted a resistant response with a lesion area ranging from 0.1% to 10.0%. Ratings of 3 and 5 reflected a moderately resistant to moderately susceptible response, covering lesion areas of 10.0% to 25.0% and 25.1% to 40.0%, respectively. Conversely, ratings of 7 and 9 indicated a susceptible to highly susceptible response, encompassing lesion areas of 40.1% to 60.0% and 60.1% to 100% on rice plants. The disease severity index of BLB was calculated from September 2022 to November 2023 using the below-mentioned formula, and the dataset was averaged to ascertain the response of different rice cultivars (Anonymous, 1996).

Disease Severity index = Sum of all the scores of Individual plants/varieties × 100
Total No. of Plants Observed Maximum Scale

The area under the disease progress curve (AUDPC) was determined by calculating the trapezoidal integration of percent disease severity over time for each variety, while considering the total duration of the crop evaluation period (Madden *et al*., 2007).

$$AUDPC = \sum_{i=1}^{n-1} [(xi+xi+1)/2] (ti+1-ti)$$

Where n represents the number of recorded dates on which the disease was observed; Xi denotes the percentage of disease severity on the ith date; and (ti+1-ti) represents the duration between two consecutive assessments.

Estimation of Phenolic Compounds: The leaf samples of individual varieties were collected from the rice research field Badeggi, Niger State, stored in an icebox, and transported to the laboratory for the examination of total phenolic contents. The modified Folin–Ciocalteu assay, as described by Singleton et al. (1999), was utilized for this investigation. A stock solution of gallic acid (Sigma-Aldrich, USA) was prepared at a concentration of 1 mg/10 mL, and working standard concentrations of 0, 10, 25, and 50 ppm were prepared in distilled water to create the gallic acid calibration standard curve. A sample of 0.5 g was homogenized in 2.0 mL of 70% ethanol (Merck, Germany) to produce the plant extract, which was then incubated for two hours in a water bath at 65ºC. Subsequently, the samples were centrifuged at 14,000 rpm for five minutes using centrifuge tubes from Centurion (UK). Following this, 4 mL of Folin–Ciocalteu phenol reagent (Sigma–Aldrich, USA) was added to 1 mL of supernatant obtained from the sample. The mixture was allowed to rest for seven minutes at room temperature, after which sodium carbonate was added to the treated sample. Test tubes were vigorously shaken and incubated in darkness for two hours. The optical density of the test sample for each variety was determined at 765 nm using a spectrophotometer (UV 300, ORI, Germany). The total phenolic concentration (w/v) was determined based on the standard concentration of gallic acid, as outlined by Kelsey and Harmon (1989).

Statistical Analysis: All the collected data sets were subjected to statistical analysis using the statistical software package SAS (2002). The treatment means of all datasets were compared using the least significant difference (LSD) and multiple mean comparisons was carried out using Duncan's Multiple Range (DMR) tests at a significance level of ($P \leq 0.05$). The varieties were classified into different levels of resistance by constructing a dendrogram using cluster analysis, specifically using Minitab 1.5.

Results and Discussion

Infected leaf samples displaying symptoms of bacterial blight were procured, and the causative bacterium was isolated on nutrient agar medium from fresh lesions on the leaves, as it provided

superior isolation material. The bacterium exhibited light yellow, raised, and circular colonies on the medium.

Disease Severity Assessment: Analysis of variance revealed significant variation among all the varieties at different rice field located in Badeggi, Niger State for bacterial blight resistance in the natural environment ($P < 0.05$). Out of the forty genotypes, eight of them exhibited a moderately susceptible response, 19 genotypes were categorized as susceptible, six genotypes demonstrated moderate susceptibility to the pathogen's virulence, and six genotypes displayed a highly susceptible response. The highest disease severity (68.08%) was recorded in the international susceptible check CO 39, which exhibited a highly susceptible response. In contrast, the lowest disease severity (11.92%) was observed in FARO 63, which proved to be moderately resistant. All KSK genotypes (Table 1) exhibited disease severity ranging from 32.61% to 45.68% and displayed a susceptible response, while basmati genotypes showed the maximum disease severity against the pathogen's virulence. The area under the disease progress curve (AUDPC) was calculated to demonstrate disease progression throughout the entire season in the field (Table 1). Five distinct groups were identified among the forty genotypes: groups one and two included twenty genotypes that displayed a susceptible to highly susceptible response, while clusters three, four, and five comprised twenty genotypes that demonstrated a moderately susceptible to moderately resistant response to the disease (Table 2; Fig. 1).

Bacterial leaf blight of rice, which is the focus of this study, is increasingly prevalent in rice-growing regions of Nigeria and poses a significant threat to crop yields. The pathogen was isolated from field samples and cultured on artificial media. Each genotype exhibited distinct behavior in response to the pathogen, with the virulence reaction potentially being influenced by specific genotypes. In field experiments, IRRI-type varieties displayed poor resistance to the pathogen, while FARO group demonstrated relatively better resistance compared to other varieties. Basmati genotypes exhibited lower natural resistance to bacterial leaf blight of rice (Ali *et al.*, 2004; Shah *et al.* , 2009; Kaari *et al.*, 2023). The present study observed that all basmati genotypes were highly susceptible to the disease, as evidenced by a significantly higher disease severity index. Among the twelve evaluated basmati varieties, three (namely basmati super, basmati 2000, and basmati 198) were classified as highly susceptible, six as susceptible, FARO 67 and 15, as moderately resistant and the remaining four as moderately resistant. This is in line with the findings by (Cheema *et al.* 1998)

Determination of Phenolic Contents: The total phenolic concentration exhibited significant variation in response to the inoculation treatment and demonstrated a negative correlation with the severity of the bacterial leaf blight disease. The findings of the study revealed a significant increase in the phenolic concentration in the leaves of cultivars that exhibited a lower degree of infestation to bacterial blight. Notably, FARO 63 recorded the highest phenolic content (183.42 mg/100 g), followed by FARO 60 (157.66 mg/100 g) and FARO 52 (150.80 mg/100 g). Furthermore, resistant genotypes exhibited a higher concentration of phenolic compared to the susceptible genotypes.

The Pearson correlation coefficient was used to determine the relationship between disease severity and the phenolic compounds produced in response to the inoculation of *X. oryzae* pv. *oryzae* in various rice varieties. Out of the forty susceptible genotypes tested, a significant correlation at the $P=0.05$ level was observed in nineteen genotypes, while four genotypes showed a highly significant correlation at the $P=0.01$ level with the disease severity index. Additionally, eighteen genotypes exhibited a non-significant correlation (refer to Table 3). The overall correlation between disease severity and phenolic contents yielded a coefficient of $r = -0.933$, indicating a negative correlation (Fig. 2).

Amna (2008) reported that basmati super is a susceptible genotype against all strains of *X. oryzae* pv. *oryzae*, while basmati 385 showed moderate resistance to the disease. Previous studies have demonstrated that basmati genotypes imported from Asia exhibited a range of susceptibility, from moderate to highly susceptible

(Cheema *et al*., 1998; Khan *et al*., 2000a, b; Akhtar *et al*., 2008, 2011; Khan *et al*., 2009; Ebrahim-Zarander *et al*., 2022). Zhang and Mew (1985) and Saikia and Bora (2021) conducted controlled experiments to test the resistance of thirteen genotypes against four isolates at different plant growth stages. They found that the disease infestation was highest during the early stages of plant growth. Ou *et al*. (1971), Awoderu *et al*. (1991), and Sahu *et al*. (2018) demonstrated that preliminary evaluation of rice cultivars can be performed at the seedling and flag leaf stages, with the interaction between pathogen diversity and genotype playing a significant role in the host's reaction.

The lack of resistance in genotypes with basmati backgrounds has emerged as a pressing issue that requires attention; otherwise, the severity of the disease will escalate in the future. The area under the disease progress curve was calculated to gauge the disease progression throughout the crop season, a complex phenomenon influenced by both host and pathogen genes. In our research, it has been observed that diseases tend to be less severe in plant varieties that produce higher concentrations of phenolic compounds. Conversely, varieties with lower phenolic contents exhibit more severe disease symptoms. These findings have led to speculation that phenolic compounds may play a role in inhibiting pathogen infection and colonization of the host (Blodgett and Stanosz, 1997; Sahu *et al*., 2018).

Varieties with higher phenolic contents have proven to be more resistant to severe infections caused by pathogens, thanks to their potent antimicrobial activity. Plants are capable of producing secondary metabolites, such as flavonoids, tannins, and lignins, which include phenolics. These compounds play a crucial role in reducing the severity of diseases (Tiaz and Zeiger, 2002; Wahid and Ghazanfar, 2006; Mohapatra *et al*., 2023). Furthermore, phenolics possess strong antimicrobial activity and exhibit a wide range of physiological properties (Zhou *et al*., 2004).

Our findings that diseases tend to be less severe in plant varieties that produce higher concentrations of phenolic compounds are in line with the studies conducted by Muntana and Prasong (2010), Naqvi *et al*. (2015), and Ebrahim-Zaranda *et al*. (2022). These studies assessed various Thai rice cultivars for their total phenolic content and antioxidant activity using the Folin-Ciocalteaue assay, and demonstrated a high level of antioxidant efficacy across all tested genotypes.

In our experiment, some genotypes that exhibited high disease severity did not show a significant impact on phenolic compound concentrations. However, this lack of significant effect on phenolic compound concentration aligns with previous research conducted by Gershezon (1984) and Naqvi *et al*. (2015). These findings hold potential for the evaluation of blast-resistant varieties, where these resilient genotypes can be directly or indirectly utilized for future breeding programs, genetic engineering, and biotechnology aimed at the development of genetically modified crops.

Conclusion

The evaluation of available rice genotypes revealed that none of them exhibited resistance to the pathogen's virulent reaction. All basmati cultivars proved to be susceptible to diseases prevalent in rice the rice research fields in Badeggi, Niger State Nigeria, particularly in the southwest. However, the FARO group exhibited relatively better performance compared to other genotypes. The findings of this study indicate that phenolic compounds play a crucial role in mitigating disease severity through their antioxidant activity. Varieties displayed varied responses in terms of phenolic production, which determined their level of resistance or susceptibility. Those genotypes exhibiting minimal disease severity were observed to have the highest concentration of phenolic accumulation. Conversely, the phenolic content demonstrated a negative correlation with the resistance of the varieties. Therefore, further investigation into their role in plant defense mechanisms is imperative for future plant breeding programs.

Declaration of Competing Interest

The authors hereby declare that there are no conflicts of interest associated with the manuscript.

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Table1: Rice genotypes used in bacterial leaf blight evaluation, diseases verity with AUDPC and their response

Genotypes	Percent disease		Scale for infection rate	Response resistance/[d]	Clip inoculation 30 plants/variety
	Severity[a]	AUDPC[b]		Susceptible	(Percent plant infection)
KSK133	45.24a-g	444.47fgh	7	S	73.33c-e
KSK-434	42.68a-i	425.51fgh	7	S	73.33c-e
KSK-463	45.26a-g	454.72fg	7	S	73.33c-e
KSK-282	47.16a-f	472.13efg	7	S	73.33c-e
KSK-14	32.61c-j	316.38ij	5	MS	50.00gh
IR-6	62.26ab	632.81abc	9	HS	93.33ab
IR-9	60.93abc	617.96abc	9	HS	90.00a-c
FARO 52	15.83hij	155.91k	3	MR	33.33hi
FARO 60	15.12ij	148.12k	3	MR	30.00i
JAJAI-77	26.26e-j	261.82j	5	MS	50.00gh
PS-2	44.63a-h	444.17fgh	7	S	76.67b-d
SATHRA	29.58e-j	280.39ij	5	MS	50.00gh
FARO 51	18.77f-j	177.45k	3	MR	33.33hi
JP-5	41.13a-i	413.12gh	7	S	73.33c-e
PK-386	45.46a-g	456.96fg	7	S	70.00d-f
SARSHAR	29.82e-j	296.33ij	5	MS	50.00gh
DILROSH-97	30.17d-j	290.74ij	5	MS	53.33gf
MALHAR-346	42.37a-i	419.91fgh	7	S	76.67b-d
PAKHAL	43.64a-i	435.34fgh	7	S	73.33c-e
SHANDAR-2006	31.91d-j	303.71ij	5	MS	50.00gh
FARO 63	11.92j	117.68k	3	MR	33.33hi
SWAT-1	42.23a-i	417.85gh	7	S	56.67e-g
SWAT-2	44.34a-h	440.76fgh	7	S	70.00d-f
DR-82	32.22c-j	319.67ij	5	MS	50.00gh

DR-83	47.03a-f	470.65efg	7	S	70.00d-f
DR-92	48.86a-e	487.97efg	7	S	70.00d-f
BASMATI-385	51.21a-e	509.95efg	7	S	70.00d-f
FARO 67	17.73g-j	170.15k	3	MR	30.00i
FARO 15	16.05hij	157.82k	3	MR	30.00i
BASAMTIPAK	54.73a-e	552.03cde	7	S	73.33c-e
BASMATI-370	49.84a-e	496.88efg	7	S	73.33c-e
PUSABASMATI	36.72b-j	356.71hi	5	MS	50.00gh
BASAMTI515	58.76a-d	598.56cd	7	S	76.67b-d
PUNJABBAS	47.03a-f	470.65efg	7	S	70.00d-f
BASAMTI198	63.55ab	652.27ab	9	HS	96.67a
SHAHEENBAS	52.22a-e	515.73def	7	S	76.67b-d
BASMATI2000	64.73ab	660.52ab	9	HS	96.67a
BASMATISUPER	65.05ab	661.96ab	9	HS	100.00a
IR-24	66.71a	681.33ab	9	HS	100.00a
CO 39	68.08a	697.56a	9	HS	100.00a

a Mean with the same letter are not statistically different at P=0.05, DF=798, S.E for comparison =7.45

b Area under disease progress curve (Mean with the same letter are statistically similar at P=0.05, DF=39

c Randomized complete block with standard error

d Response, R=resistant, S=susceptible, MR= moderately resistant, MS = moderately susceptible, HS = highly susceptible, e = Basmati

Table 2: Cluster analysis of various rice genotypes on the basis of genetic resistance

Clusters	Observations	SS*	AD*	MD*
1	14	81.1639	2.12026	4.17224
2	8	76.4100	2.45783	6.05442
3	8	65.7282	2.41904	4.99498
4	6	359377	1.96093	4.28732
5	4	13.7384	1.54277	2.79594

*SS: Sum of square within cluster; *AD: Average distance from centroid;

*MD: Maximum distance from centroid

Table 3: Concentration and correlation of total phenolic compounds with disease severity in Xanthomonas oryzae pv. oryzae inoculated rice varieties

Genotype	Phenolic compounds mg/g (dry weight±S.E.)[a]	Correlation coefficients[b]
KSK133	23.85±0.43i-n	[c]-0.999*(0.016)[d]
KSK-434	26.95±4.54i-m	[d]-0.971(0.152)
KSK-463	30.66±4.53ij	-0.976(0.138)
KSK-282	18.95±0.87lmn	-0.999*(0.017)
KSK-14	63.33±1.24h	-0.999*(0.014)
IR-6	00.95±3.12p	-0.192(0.876)
IR-9	06.23±1.16op	-0.973(0.146)
FARO 52	150.80±2.39c	-0.997**(0.004)
FARO 60	157.66±7.58bc	-0.999**(0.001)
JAJAI-77	106.57±0.33e	-0.999*(0.005)
PS-2	23.80±2.95i-n	-0.984(0.112)
SATHRA	90.47±4.13f	-0.998*(0.037)
FARO 51	136.90±1.71d	-0.999*(0.016)
JP-5	29.57±1.64ijk	-0.996(0.053)
PK-386	28.09±3.32i-m	-0.985(0.107)
SARSHAR	93.00±0.08f	-0.998*(0.030)
DILROSH-97	72.47±3.24gh	-0.998*(0.037)
MALHAR-346	33.04±5.85i	-0.970(0.154)
PAKHAL	22.76±1.28i-n	-0.993 (0.071)
SHANDAR-2006	78.80±1.53g	-0.998*(0.040)
FARO 63	183.42±0.44a	-0.999**(0.001)
SWAT-1	23.66±1.24i-n	-0.997*(0.044)
SWAT-2	13.71±0.72on	-0.999*(0.016)
DR-82	63.42±0.94h	-0.997*(0.046)
DR-83	28.52±4.35i-l	-0.971 (0.152)
DR-92	17.66±5.14mn	-0.913(0.267)
BASMATI-385	19.61±1.33k-n	-0.997*(0.041)
FARO 67	163.28±0.91b	-0.998*(0.036)

FARO 15	148.52±0.98c	-0.999*(0.014)
BASAMTIPAK	20.23±1.49j-n	-0.996(0.056)
BASMATI-370	15.09±0.63on	-0.998*(0.036)
PUSABASMATI	65.76±0.13h	-0.999**(0.002)
BASAMTI515	18.57±0.79lmn	-0.998*(0.035)
PUNJABBAS	14.19±0.76on	-0.994(0.068)
BASAMTI198	4.85±0.74r	-0.999(0.065)
SHAHEENBAS	15.38±0.62on	-0.998*(0.038)
BASMATI2000	36.81±7.84q	-0.954(0.191)
BASMATISUPER	3.23±5.06s	-0.991(0.082)
IR-24	4.66±6.62sr	-0.098(0.112)
CO 39	1.61±3.78t	-0.997(0.069)

[a]Total phenolic concentration (mg/g, dry weight) calculated on the basis of standard concentrations of gallic acid

[b]Correlation (*r*) are for genotypes inoculated with *X. oryzae* pv. o*ryzae*,

*Significant at $P \leq 0.05$ and ** Highly Significant at $P \leq 0.01$

[c]Figures without parenthesis are the pearson correlation coefficient

[d]Figures in the parenthesis are the probability levels (P)

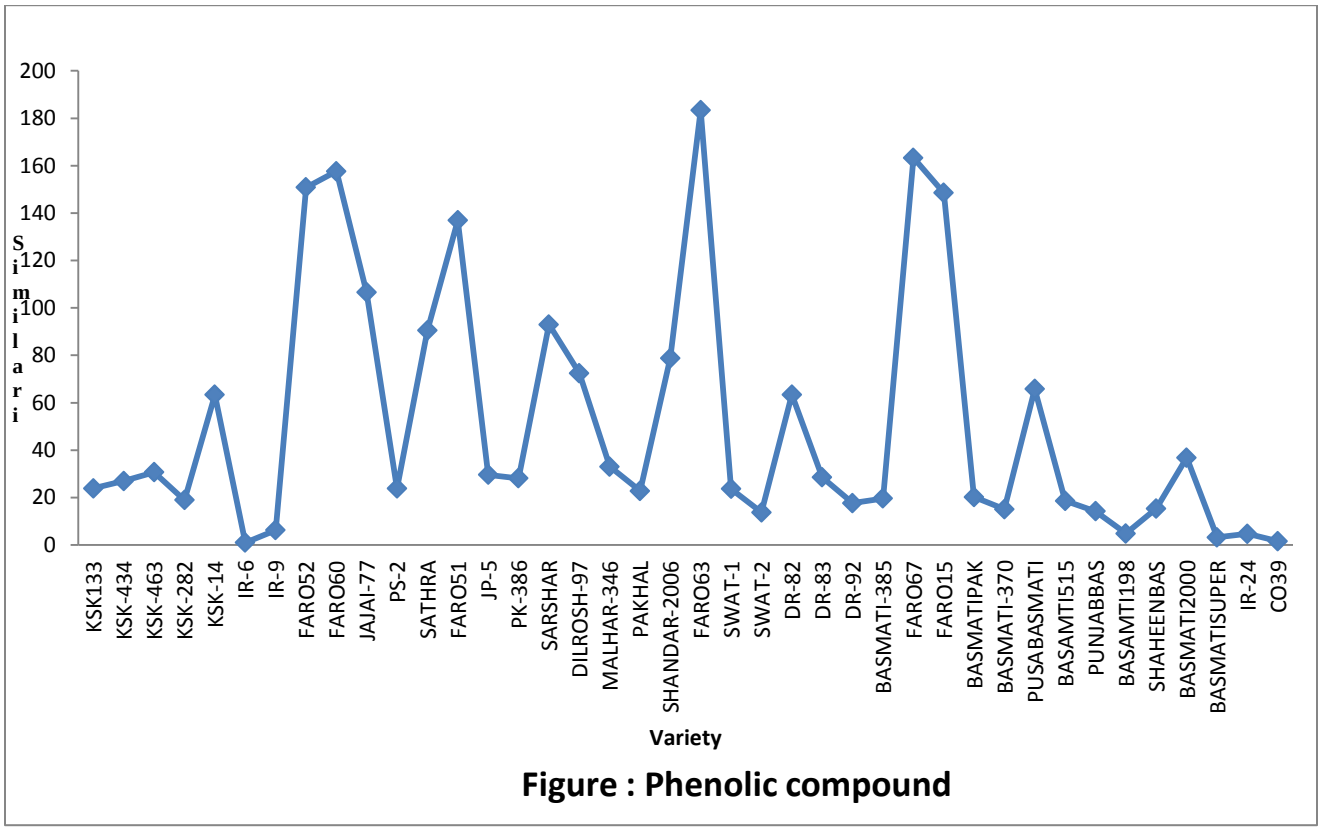

Fig. 1: Dendrogram showing genetic similarity among 40genotypes of rice

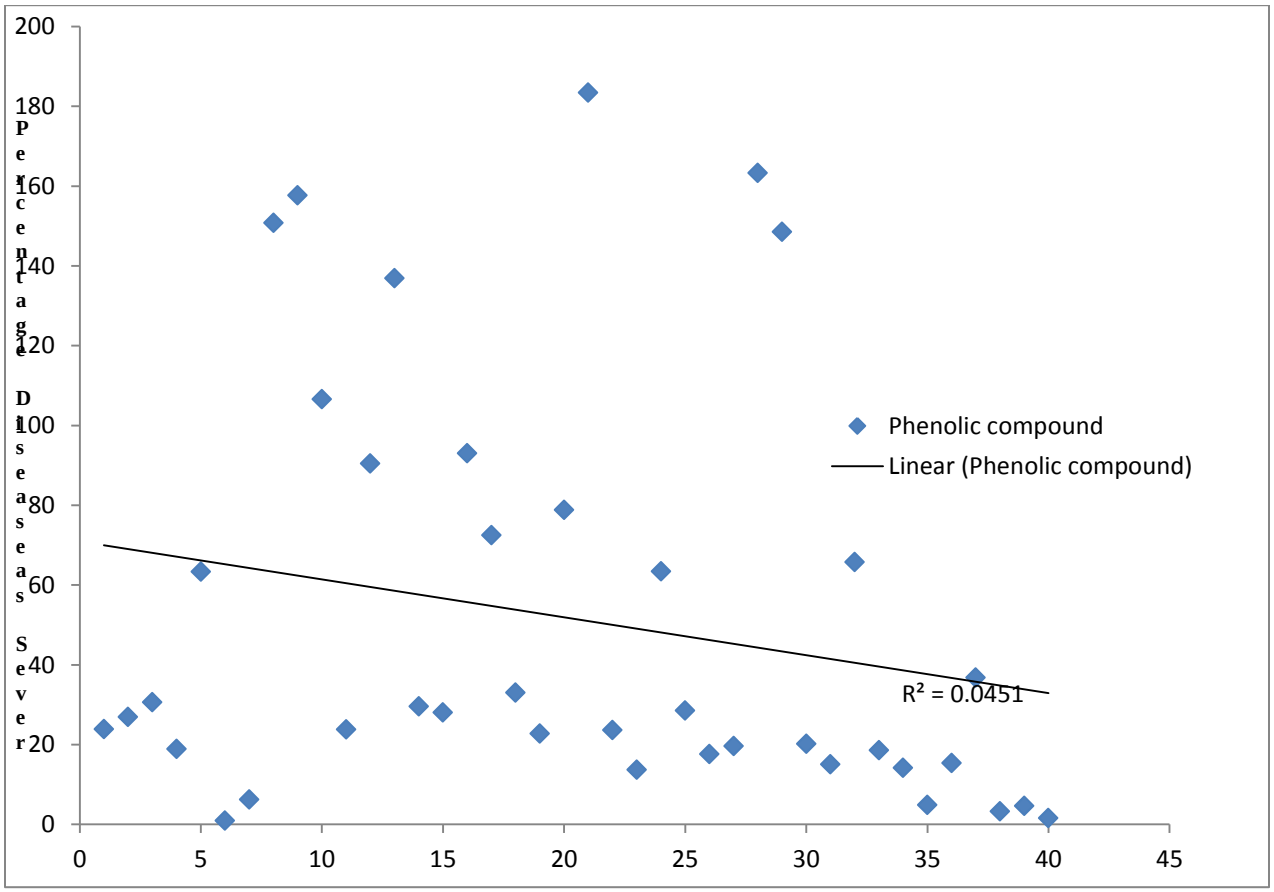

Fig. 2: Correlation of Phenolic compound concentration with disease severity of bacterial leaf blight of rice in various genotypes