Exploring the multi-seasonal relationships between yield traits with natural screening of rice blast disease under hot spot conditions

Abstract:

The experiment was conducted to study the comparative performance and blast disease screening 80 diverse rice cultivars including land races, obsolete varieties, modern cultivars and released varieties, local prevailing cultivars and advanced breeding/varietal lines as AICRIP testing trials for two successive seasons during *Kharif*-2021 and *Kharif*-2022 at AHRS Ponnampet, Karnataka- India, The results from ANOVA revealed that, MSS due to genotypes, were significant ($p<0.01$ and $p<0.05$) for all the yield traits studied. GYKH was varied from 270.65-6039.89, while 940.17-6039.88 with mean grain yield Kg/ha of 3596.01 and 3483.92 kg/ha during Kh-21 and Kh-22. High GCV and PCV with high heritability coupled with high GAM were observed for GYKH, while the remaining traits revealed low to medium GCV and PCV, heritability coupled with low to medium GAM. Correlation analysis revealed that significant and positive association was observed for PH, DFF, PL and GYKH. PCAs revealed that PC1, PC2 and PC3 showed 32.45%, 29.66% and 14.83% of contribution with 76.94% of total variation during *Kharif-21* and 33.20%, 29.67% and 14.33% of contribution with 77.20% of variation for the studied traits during *Kharif*-22 respectively. Field screening of leaf and neck blast under natural hot spot area among 80 diverse genotypes resulted in identification of resistant sources as KPR-1, KPR-2, KHP-5, Mud-1014, IET-28515 and Kajajayawith promising yield performances.

Key words: Rice (*Oryza sativa* L.), Natural hot spot, Blast screening, Principal component analysis, Correlation matrix

Introduction:

Rice (*Oryza sativa* L.) is the oldest but most valuable primary food crop of the world and nation in addition to wheat, which contributing to the food security interns still it is the prime source for providing energy, fibre, minerals and protein in the dietary food. Its cultivation in the word occupied by 1/3rd of its land and the Asian continent is the biggest in rice production accounting nearly 90% of the total production in the world Fsysal et al. 2022 [8]. Globally India is now world's 2nd largest rice producing country after China, followed by Indonesia and Bangladesh Fsysal et al. 2022 [8]. For any crop improvement effort to begin, existence and magnitude of genetic variation in the base populations, germplasm, cultivars and wild relatives of cultivated species is crucial to integrating the favorable alleles and to bring desired modification in the plants as to breed good idiotype of the crop cultivars.

The green revolution in India and world during 1960 century witnessed by releasing high yielding varieties (HYVs) to increase the production-productivity of the cultivated crops, however now a days the modern cultivars are declining for its per unit yield *per se* performance due to narrowing of genetic base. So the breeding by selection and agricultural development needs a thorough understanding of current available genetic diversity to increase genetic gain of the yield Wouw et al., 2010 [41]; Govindaraj et al., 2015 [12]. The global rice demand is predicted to be rise from 439 MT (milled rice) in 2010 to 555 MT during 2035, while the current production rate is not sufficient to meet better living standard to feed the world and to the ever increasing population of nearly 9 billion people in the word by 2050 where we are surpassing to the China, the world highest populated country Verma et al. 2021 [39]. The ever growing demand for rice requires the development of outstanding cultivars, so the use of variability in genotypic and phenotypic level is important for elevating the rice production potential in the era of changing climatic conditions.

Rice is widely distributed and cultivated under diverse agro-climatic conditions ranging from lowland rainfall situation to upland irrigated situations, so the basically cultivated rice belongs to four ecosystem, *viz*., irrigated rice also known as Boro rice, rainfed cultivation known as Aus and Aman rice, rainfed upland (direct seeded Aus rice cultivation) and deep water cultivation of broadcasted Aman rice, so cultivation of rice is considered as a part of socio-cultural life of rural India. Due to the wider distribution of rice cultivation under diverse agro-ecological zones and climatic conditions, it is highly prone to the attack by both biotic and abiotic stress, among the biotic stress, rice blast (leaf blast and neck blast) is most harmful threat to the economic productivity of rice,Miah et al., 2013 [27]. The blast fungus (*Magnaportheoryzae*), is able to develop resistant to both chemical treatments and genetic resistance which is a continuous threat to the effectiveness of blast- resistant rice varieties. The new races of the fungal pathogens are evolving as the changing climatic conditions are unpredictable, so it is a need of hours to find out strategies for developing durable resistant by screening under natural hotspot area where the most prevailing races are surviving, so the loss of rice yield should be minimized in order to help the marginal and poor farmers of developing countries Scheuermann et al., 2012 [30].

Magnaportheoryzae can infect rice plant right from seedling to late vegetative/reproductive stages affecting leaves, nodes, collar, panicles, panicle neck, and roots Zhu et al., 2005 [46]. Repeated epidemics and frequent break down of rice blast resistance causing yield losses of 20–100% have been reported over the last decades in India Khush and Jena, 2009 [22]. The fungal pathogen, *M. oryzae* has been placed among the top 10 fungal plant pathogens in the world based on its scientific and economic importance Dean et al., 2012 [5]. Use of resistant cultivars, fungicides, optimum fertilizer applications and appropriate planting dates are some of the strategies to manage the disease Bonman, 1992 [2]. Resistance is generally conferred by either major R genes that provide complete protection against few races of the pathogen or minor genes, which conferred partial protection Wang et al., 1994 [40]. To date, more than 100 R genes, and more than 350 QTLs for resistance to rice blast have been identified, and 27 have been molecularly cloned and characterized viz., Pib, Pb1, Pita, Pi9, Pi2, Pizt, Pid2, Pi33, Pii, Pi36, Pi37, Pikm, Pit, Pi5, Pid3, Pid3–A4, Pikh, Pish, Pik, Pikp, Pia, PiCO39, Pi25, Pi1, Pi21, Pi50 and Pi65(t) Zheng et al., 2016 [44]; Zhu et al., 2016 [45]; Yadav et al., 2019 [42]. The rapid changes in virulence characteristics that take place in pathogen populations remains a constant challenge to the success of existing blast– resistant varieties of rice. However, the major blast resistance gene has been useful and should play a vital role in rice production if they are cautiously selected and deployed Chen et al., 2006 [4]. Hence, there is an imperative need for mining the new R genes/alleles and minor resistance genes.

Cultivation of resistant genotypes as host plant resistance is the effective and eco-friendly method to combat the disease; hence several genotypes should be screened to identify the desirable cultivar showing durable resistant under prevailing races of pathogens in natural hotspot ecosystem and to explore the relationship between yield and yield attributing traits, in this view the present study was undertaken to screen the rice genotypes under natural hot spot condition, to study the genetic variability, correlation-path and principle component analysis to determine the relative contribution of each character towards yield and its related traits.

Material and Methods:

Experimental locations: The hot spot for Blast and genotype sources

The experiment was conducted for two successive seasons during *Kharif*-2021 and *Kharif*-2022 at Agricultural Horticultural Research Station (AHRS) Ponnampet, Karnataka- India, the Ponnampet which is situated at 12.1515° N, 75.9430° E as a lattitude and longitude respectively, with mean elevation of 856 m MSL in Karnataka and it is known as one of the hotspots for natural screening of blast disease of rice where the most of the prevailing races of pathogens are survived due to its agro-climatic zones as its comes under southern hilly region along with suitable weather climatic condition including heavy rainfall, high relative humidity, low temperature with low sun shine hours. The weather data such as maximum and minimum temperature (^{o}C), relative humidity (%) during morning and afternoon hours, wind speed in Km/hrs and rainfall (mm) with number of rainy days were recorded for each month of the two successive years during 2021 and 2022, the southern hill zones comes under (Zone-9) of agro climatic zones, where it is specialized by receiving the annual rainfall up to 3220 mm, during 2021 we recorded total annual rainfall of 2936.30 mm with 141 number of rainy days, while in 2022 we recorded 3118.70 mm annual rainfall with 116 days.

The maximum rainfall was observed during active crop growth period from July, August, September and October, where we have recorded 220 mm to 980 mm in kh-21 and 560-813 mm during *Kharif*-22, along with high RH which will coincide with the most favorable condition for blast disease development. The maximum temperature was ranged from 20-34^{O}c, while the minimum temperature was 15 to 30^{O}C, the relative humidity was consistent during early morning hours and it was varied from 85-95% as compared with afternoon hours, the wind seed was ranged from 3-15 Km/hrs (Figure 1) which make the pathogen as a congenial conditions to survive and propagate by asexual means causing heavy infection throughout the crop growing seasons.

The material under study consisting of 80 rice diverse groups of cultivars including land races, obsolete varieties, modern cultivars and released varieties, local prevailing cultivars and advanced breeding/varietal lines as AICRIP testing trials which are provided from (ICAR-IIRR - Hyderabad), the details of the cultivars along with parental cross combination and salient features were presented in (Table 1).

Experimental layout and statistical analysis

The experiment was conducted by using A Randomized Complete Block Design (RCBD) with two replications, 25 days old seedlings from nursery bed were transferred to the main field and a single genotype was planted in 4.05 m × 4.05 m plot with providing 15 ×15 cm spacing between rows and plants. During the growing seasons all the important intercultural operations, gap filling, weeding along with fertilizer application as RDF were fallowed. The data were collected as days to 50% flowering (DFF), days to maturity, Plant height (cm), number of productive tillers/plant and per m^2 panicle length/ plant (cm) and grain yield were recorded as per plot basis and converted into per kg/ha. The multi seasonal analysis including Annova, genetic variability, character association along with path and principle component analysis (PCA) was carried out by using standard protocol package called R software (*version 4.3.2*). The blast disease was scored as (0-9) scale for two conjugative seasons at maximum tillering stage according to the IRRI, SES, 1996 [19] standards, after observing disease symptoms on most susceptible checks, the germplasm lines exhibiting reactions of score as given in (Table 2)

Results and discussion:

ANOVA and Genetic variability:

Selection for grain yield may not be successful unless other factors interconnected to yield are taken into account because grain yield is a complex trait related by numerous quantitative parameters. The plant breeders need to have blueprint for selection of specific trait since the enhancement of one yield-related feature has a knock-on effect on multiple other yield-related characters Hasan et al., 2020 [13]. The results of present study exhibited substantial deviation in the studied material for all the traits (Table3). The extent of variation in grain yield and its contributing agronomic traits including growth and yield parameters such as days to 50% flowering (DFF), days to maturity (DM), plant height (PH) (cm), number of tillers per plant (NTPP), number of tillers per square meter (NTPSM), panicle length (PL) (cm) and grain yield Kg per hector (GYKH) were examined, the mean value ($\sum x$), range, genetic variance components such as genotypic and phenotypic coefficient of variation (GCV and PCV) ($\sigma^2 g$ and $\sigma^2 p$), broad sense heritability (h^2) and genetic advance percent mean (GAM) were shown in Table 4 along with box plot showing multi seasonal graphical representation of frequency distribution for each traits during *Kharif*-21 and *Kharif*-22, here the box indicating the existence of the 50% of our data within the box, the lower end of the box is 1st quartile (Q_1), the upper end of the box is 3rd quartile (Q_3) which shows the existence of the 25% of our data above the Q_3 and below the Q_1 we find remaining 25% of the data distribution, the range between Q_1 and Q_3 are called inter-quartile range with solid line indicating the median value of the data distribution, the points above the outlier are the maximum value for the traits as shown in Figure 2. Mean sum of square due to genotypes reported existence of significant difference for grain yield Kg per hectors revealing extensive genetic variance in GYKH (Table 3) similar reports were cited in Ketema et al 2022 [21]; Sarker and Mian 2003 [29]; Ganapati et al., 2014 [11], GYKH was varied from 270.65-6039.89, while 940.17-6039.88 with mean grain yield Kg/ha of 3596.01 and 3483.92 kg/ha during *Kharif*-21 and *Kharif*-22 as shown by graphical representation of frequency distribution box plot respectively . The $\sigma^2 g$ and $\sigma^2 p$ were high (24.04-28.71; 24.76-28.90) for multi-seasonal environmental conditions during *Kharif*-21 and *Kharif*-22 with high h^2 in broad sense (70.09 and 73.39) plus high GAM of 41.46 and 43.69 respectively (Table 4), here the broad sense heritability (h^2) was classified as high (>60%), moderate (40-60%) and low (40%), the results indicated that all the genotypes for grain yield per ha displayed significant deviations across the traits of other morphological traits, so the trait expressivity was significantly impacted by genetic rather than the environmental variation as narrow difference between $\sigma^2 g$ and $\sigma^2 p$ along with ample amount heritability suggesting that scope for selection of desirable genotype for genetic grain with high trait value by improving the yield *perse* performance. This observation is in consistence with the previous results Dhurai et al., 2014 [6]; Shilpashree et al., 2021 [32]; Fongfon et al., 2021 [10].

ANOVA for plant height (PH) showed the presence of significant difference due to genotypes for mean sum of squares (Table 3), these differences exposed a high variability for PH across the two seasons as shown in the frequency distribution in box plot with more number of outlier on the data pints (Figure 2). The PH ranged from 65.25-155.00 cm with mean of 93.69-92.44 cm (Figure 2), exhibiting significant difference between the genotypes for mean sum of squares (Table 3) during kh-21 and 22, moderate $\sigma^2 g$ and $\sigma^2 p$ (16.63-17.99; 15.09-17.20) with high h^2 in broad sense (85.40 and 77.02) connected to high GAM of 31.66 and 27.28 for two successive environments boosting trait improvement respectively, indicating apparent variation for the trait improvement. Similarly the remaining traits such as days to 50% flowering (7.43-7.49; 7.85-

7.97), days to maturity (49-5.51:7.17-7.33) reported presence of very low GCV and PCV coupled with high broad sense heritability indicating peak inheritance of the traits linked to moderate genetic advance percent mean, however even though the trait has exhibited high broad sense h^2, selection may not effective based on this traits , due to existence of very low genotypic and phenotypic variance contributing lesser diversity for improving days to 50% flowering. These results are in comparable with the previous report Li et al., 2019 [25]; Fentie et al., 2021 [9]. The panicle length per plant (PL) recorded low GCV and PCV (4.84-9.50 & 4.87-9.53) with moderate heritability (25.97 & 26.08) influencing the character for low genetic advance percent mean under multi-seasonal environment revealing existence of environmental interaction for the traits leading to less genetic gain for improvement. The main characters such as number of productive tillers per plant and per square meters, which significantly contributing to the progress in the economic grain yield output showed low to moderate GCV and PCV of (7.81-16.73; 8.05-16.60 NTPP) and (7.16-14.25; 8.16-14.12 NTPSM) with fair heritability of 21.78-23.50 for NTPP and 25.28-33.45 for NTPSM connecting to the very low GAM (Table 4), the level of GAM were ranked as low, moderate and high with corresponding ranges of 10%, 10-20% and >20% respectively. So the results revealed selection has to be undertaken for the trait improvement to achieve highest yield potential. Among seven yield and yield component traits studies DFF,DM, PH and GYKH along with moderate heritability indicating high possibility of selection for improvement of rice. In literature the similar work were reported from Fageria et al., 2011 [7]; Huang et al., 2011 [18]; Zahid et al., 2006 [43]. Hosagoudar and Kovi, 2018 [17] evaluated the advanced varietal line and reported as genotype IET-1912 produced maximum grain yield (5172.60 kg/ha) and found to be 20.77% superior in grain yield than local check Tunga (3096.09 kg/ha) followed by IET-1914 (5059.61 kg/ha) which found 19.64% superior, whereas IET-1908 was found to be 3.74% inferior in grain yield (2722.42 kg/ha) than local check.

Correlation matrix

The multi-seasonal correlation coefficient for seven phonological characters were studied which contributing to both growth and yield attributing traits (Figure 3), S1 that is during *Kharif*-2021 days to maturity has shown positive significant association (r=0.86) with days to maturity in S2 (*Kh*-2022). Days to 50% flowering during *Kharif*-21 (S1) has reported positive significant association with days to maturity in S1 and S2 with r values of 0.90 and 0.80 respectively. In the same way days to 50% flowering during S2 has revealed highest significant positive correlation with days to 50% flowering (r=0.93) in S1 fallowed by days to maturity (r=0.88 and r=0.85) in S2 and S1 respectively. Panicle length in S2 has shown significant positive correlation with panicle length in S1 (r=0.96). Plant height in S1 has revealed highest significant positive correlation with panicle length in S2 (r=0.56) and S1 (r=0.55) respectively, followed by days to maturity in S1 (r=0.34) and S2 (r=0.31), days to 50% flowering in S1 (r=0.30) and S2 (r=0.28). Plant height in S2 has exhibited highest positive significant correlation with plant height in S1 (r=0.85), followed by panicle length in S2 (r=0.50) and S1 (r=0.48), days to maturity in S2 (r=0.36) and S1 (r=0.30) and days to 50% flowering in S2 (r=0.28) and S1 (r=0.26) respectively. Number of tillers per plant in S2 has shown significant positive association with number of tillers per plant in S1 (r=0.98), while number of tillers per square meters has exhibited highest positive association with number of tillers per plant in S1 (r=0.81) and S2 (r=0.78) respectively. Number of tillers per squares meters has exhibited highest positive significant association with number of tillers per plant in S2 (r=0.87) and S1 (r=0.84) fallowed by number of tillers per square meter in S1 (r=0.84). Grain yield Kg per hector in S2 has revealed significant positive correlation with grain yield Kg per hector in S1 (r=0.68) fallowed by number of tillers per square meter in S2 (r=0.21), however the number of panicles per plant has positive non-significant association with grain yield Kg per ha. Chandra et al., 2009 [3] reported correlation studies in rice as genotypic correlation coefficients were higher than phenotypic correlation coefficients for most of the characters under study. Character association analysis revealed significantly positive association of grain yield per plant with number of productive tillers per plant, 1000-grain weight, panicle length and number of grains per panicle. Correlations among yield components were positive, encouraging rapid improvement of yield. Premkumar et al., 2015, [28] investigated 43 rice genotypes including 30 hybrids and 13 parents for grain yield and kernel characters to understand the association among yield components and their direct and indirect influence on the grain yield. The correlation analysis indicated that grain yield was significantly associated with number of productive tillers per plant, kernel breadth, hundred grain weight and number of filled grains per panicle.

Principal component analysis (PCA):

For selecting the desired plant types, estimation of existing diversity among the genotypes through genetic diversity analysis plays crucial role. The compiled information on the kind and extent of genetic variability is important for selecting the best breeding lines. Multi seasonal PCA analysis was carried out for yield and yield related traits of rice genotypes in order to describe and to gain the better understand the source of genetic variation among the studied genotypes during *Kharif-21* and *Kharif-22*. The three component *viz*., PC_1, PC_2 and PC_3 showed 32.45%, 29.66% and 14.83% of variations during *Kharif-21* and 33.20%, 29.67% and 14.33% of variations among the studied traits during *Kharif*-22 respectively with the help of scree plot (Table 5 and Fig. 4). The first three main PCAs are extracted from the complicated seven PCA components, the total cumulative variance of these first three principal components (PC_1, PC_2 and PC_3) account for 76.94% of the total variation during *Kharif*-21 and 77.20% of the total variation during *Kharif*-22 respectively. In literature similar results were reported for PCA analysis of rice germplasm lines under high temperature stress by Mahendran *et al*., 2015,[26] Anandan et al., during 2012 [1] studied and reported similar kind of results by using multivariate analysis for salt tolerance rice genotypes. Sinha et al., 2001 [34] studies genetic divergence of upland rice cultivars by PCA techiniques.

The eigenvectors decreased significantly from PC_1 (2.27:2.32) to PC_3 (1.03:1.00) during *Kharif-21* and *Kharif-22* respectively, it indicates that decrease in the eigenvalues after PC_3, the remaining principal components did not described much variation, thus only the first three PCs were considered which explaining much of the variation for the studied population. Elbow type with semi curve line is obtained after PC_3 tended to straight with minute difference observed in each PC and from the graph, it is clear that maximum variation was observed in PC_1 in comparison to the other four PCs, therefore the selection of lines for characters under PC_1 may be desirable, further principal components having more than one eigenvalue that showed more variation which act as key factor for selection of diverse breeding lines. The principle component with <1 Eigenvalue should be eliminated due to their minimum contribution towards variability. In literature similar results obtained from the Verma et al., 2019,[38] revealed PCA analysis with maximum diversity in a population of 114 rice germplasm was governed by fresh shoot weight, root volume, dry shoot weight, fresh root weight, they confirmed that the sufficient diversity and genotypes identified to be superior for one or more traits from different clusters might be useful in the hybridization programme to identify desirable segregants for the traits under study.Korada et al., 2021,[23] reported multivariate analysis study for 46 rice genotypes with yield and drought stress conditions.Results from rotated component matrix showed that the PC_1 is highly loaded with characters such as GYKH (1.00: 1.00), NTPSM (0.13: 0.21), NTPP (0.06: 0.09), while, PC_2 is loaded with characters such as NTPSM (0.98:0.97), NTPP (0.81:0.87), DM (0.09:0.10), DFF (0.03:0.09), PC_3 is loaded with the characters such as PH (0.89:0.82), DM (0.60: 0.77), DFF (0.54: 0.69) and PL (0.48: 0.38) during *Kharif-21* and *Kharif-22* respectively, contributed in positive direction as shown in Table 5 and Fig. 5A &B in variable PCA plot explaining most contribution of each traits towards both dimensions of PCs.

Further PC_1 and PC_2 confirmed the maximum variability in association with the following 34 genotypes in the positive direction (IET-27620, CTH-3, CR-Dhan-506, IET-26938, IET-7191, IET-25029, PUMB-8, IET-26726, KHP-11, KHP-9, IET-26719, KHP-2, Uma, IET-28515, IET-25228, IET-27106, IET-26934, IET-28890, IET-26566, Dhanarasi, IET-25826, Mud-1010, Mud-1014, Pooja, KHP-5, Tanu, IR-64, RNR-15048, Hemavathi, IET-25281, Tunga, Mud-1015, IET-24195, IET-28285 and IET-27610) with high degree of variability to the yield and yield attributing traitsduring *Kharif*-21 as shown in Fig.5C with PCA biplot explaining individual genotypes contribution in the both dimensions. Similarly during *Kharif*-22, PC_1 and PC_2 confirmed the maximum variability in association with the following 36 genotypes in the positive direction such as KHP-11, IET-25029, IET-26938, IET-26726, Kajajaya, KHP-9, Sayadhrikaveri, IET-26713, CTH-3, IET-7191, IET-27620, IET-27466, Krishnaleela, Uma, IET-26939, KHP-2, Dhanarasi, IET-26566, RNR-15048, IET-25826, CR-Dhan-505, IET-28884, Hemavathi, IET-25281, IR-64, Mud-1010, Pooja, Mud-1014, KHP-5, Tanu, IET-25826, IET-28519, IET-27610, IET-28285, Mud-1015 and Athira. It clearly indicated that the genotypes belongs to the PC_1 and PC_2 with positive association related to the major traits like PL, NTPP, NTPSM, GYKH and DFF as explained in PCA variable plot towards both dimensions of PCs inFig. 5A &B. Thus, these attributes could effectively be used as selection criteria for the genetic improvement of rice cultivars. Similar results were reported from Sharma et al., 2014,[31]Shrestha et al., 2021,[33] Tejaswini et al., 2018 [36] used application of principal component analysis for 114 rice F_5 families derived from the six crosses (MTU 7029/MTU1081 ;MTU7029/JGL 11118 ; MTU7029/NLR 34449 ; MTU7029/ PAU 3116-25-5-1 ; MTU7029/ MTU 1121 and MTU7029/ PAU 3140-126-1) characterization and evaluation for yield attributing traits. Upadhyay et al., 2022 [37] reported PCAs analysis in rice RILs populations derived from the cross between PUSA 44 and CSR 43 for yield and yield attributing traits with eigenvalue more than one controlling 91.68% of variance

Natural screening of blast disease in hot spot area

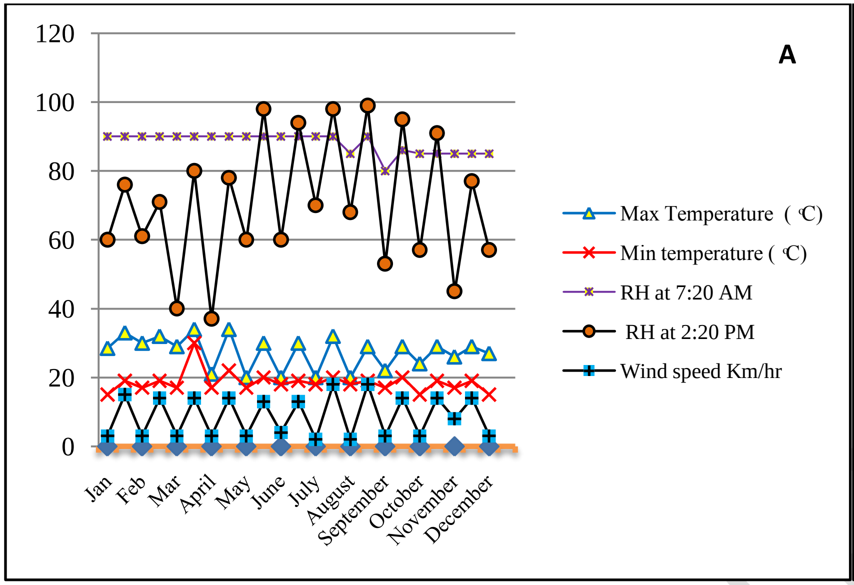
The multi seasonal response of 80 rice cultivars to leaf and neck blast under natural hot spot epiphytic condition with (0 to 9 scale as shown in Table 2, SES, IRRI,1996) during *Kharif*-21 and *Kharif*-22 was presented in Table 6, to know the source of resistance against leaf and neck blast disease. Results on field screening of genotypes for leaf blast reaction revealed that out of eighty entries, none of the genotypes was found to be highly resistant with no lesion, 26 genotypes were observed as tolerance or resistance as the genotypes revealed small necrotic grey spot on the upper leaf surface such as Mo-4, Sahyadri Kaveri (IET-24451), KPR-1, KPR-2, KHP-2, KHP-5, Bili Mukhti (CTH-3), IET-7191, PUMB-8, IET-25029, IET-23422, IET-26934, IET-26712, IET-26713, IET-25228, IET-24195, Mud-1013, Mud-1014, IET-27637, IET-27641, IET-28018, IET-28515, Kajajaya, CR-Dhan-506, IET-29351 andKMP-220).Similarly 47 genotypes were shown with moderately tolerant reaction with 5 to 10% panicle infections (Sayadhri Megha, SayadhriKempumukthi, KHP-10, Uma (Mo-16), Jyothi, Aathira, Tunga, IR-64, KHP-9, KHP-11, KHP-13 (Bharath) (IET 21479), Intan, MTU-1001, Jaya, Hemavathi, BR-2655, Thanu, IET-24491, IR-10A-155, IET-25281, IET28285, Dhanarasi, IET-24395, IET-26938, IET-26940, IET-25959, IET-26694, IET-25856, IET-26726, IET-26566, IET-26573, Mud-1010, IET-27610, IET-27620, IET-27466, IET-25826, IET-28017, IET-28509, Krishnaleela, CR-Dhan-505, Pooja, CR-1017, IET-28895, IET-28884, PA6444 (HC), RNR-15048, Gamanasanna). The five genotypes such as Sharavathi, KHP-12, IET-26690, Jeerigesanna and IET-27537 were identified with moderately susceptible with typical blast symptoms having more than 3 mm lesion and 4 % of leaf infections under natural conditions as shown in the Fig. 2. In the present study only two genotypes namely IET-27547 and IET-28890 were identified as susceptible one with more than 3 mm typical blast symptoms with 26to 50% leaf infections (Table 6). Hosagoudar et al., 2018, [15] studied and reported genetic variability for short duration fine grain paddy varieties with blast resistance. Hosagoudar et al., 2018, [15] reported field screening of genotypes for leaf blast reaction revealed that out of thirteen entries, none of the genotypes was found to be highly resistant. 3 genotypes found resistant (IET-24471, Tunga (local check), Savitri (zonal check), 8 genotypes were found to be moderately resistant

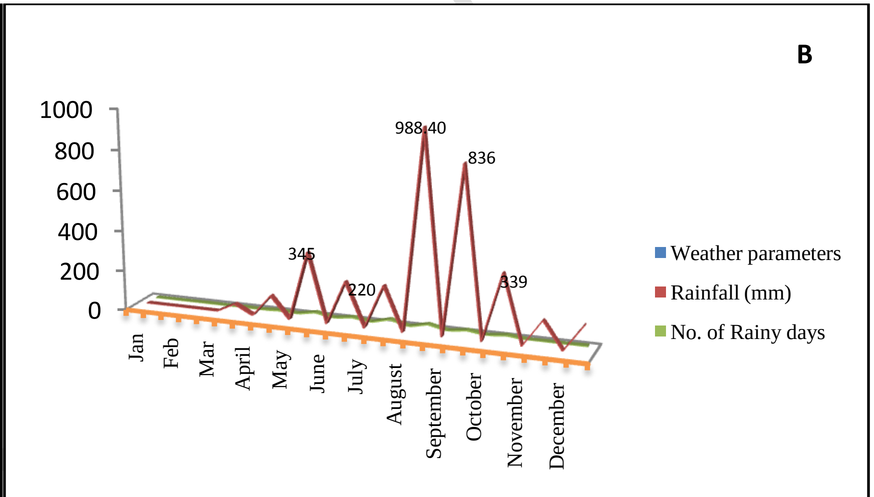
(IET-24443, Dhanrasi (NC), 24480, 24474, 23565, 23930, 24450, 24367), 2 genotypes were found to be moderately susceptible (IET-24451, 23561), none of the genotype was found to be susceptible and highly susceptible.

The results from the neck blast scored according to the SES, IRRI 1996 and study revealed that 21 genotypes recorded moderate resistant reactions with 5 to 10% infected panicles namely SayadhriKempumukthi, Aathira, KPR-1, KPR-2, KHP-5, KHP-9, KHP-11, KHP-12, KHP-13 (Bharath) (IET 21479), Dhanarasi, IET-24395, Mud-1014, IET-27610, IET-27620, IET-25826, IET-28509, IET-28515, CR-1017, Kajajaya, Gamanasanna and IET-27466. Similarly 21 genotypes recorded moderately susceptible with 11-25% of panicle infection namely Sayadhri Megha, Sharavathi, Uma (Mo-16), Mo-4, Tunga, IR-64, KHP-2, Intan, Bili Mukhti (CTH-3), IET-7191, Hemavathi, PUMB-8, IET28285, IET-26934, IET-25228, CR-Dhan-505, Pooja, CR-Dhan-506, IET-29351, RNR-15048 and KMP-220. Thirty-three genotypes such as Jyothi, Sahyadri Kaveri (IET-24451), MTU-1001, Jaya, BR-2655, Thanu, IET-25029, IET-24491, IET-23422, IR-10A-155, IET-25281, IET-26938, IET-26940, IET-25959, IET-26690, IET-26694, IET-25856, IET-26712, IET-26713, IET-26726, IET-26566, IET-26573, IET-24195, Mud-1010, Mud-1013, IET-27637, IET-28017, IET-28018, Jeerigesanna, Krishnaleela, IET-28895, IET-28884 and PA6444 (HC) recorded 25-50% of panicle infection. Among the 80 genotypes studied for neck blast disease only five genotypes namely KHP-10, IET-27641, IET-27537, IET-27547 and IET-28890 recorded with more than 50% of panicle infection showing high susceptibility reactions (Table 6).Kumar et al., 2018, [24] assessed the rice germplasm lines for blast resistance and reported that the resistant checks (Tadukan and Tetep), shown highly resistant response, KPR-1, KPR-2, Kiruwana and IR-64 recorded resistant response and whereas Jaya, Intan, Ambemori, Bheemasaali, Chittiga and FR-13A were recorded highly susceptible to the leaf blast along with susceptible checks (CO-39 and HR-12).Hosagoudar, and Babu., 2018, [16]Hosagoudar, 2019 [14] studied for host plant resistance with 102 rice cultivars and reported that field of screening for neck blast shown 13 entries i.e., IET-24205, 24188, 24227, 24231, 23542, 23543, 23541, 22979, 22957, 23528, Benibhog, RP-Bio-226, CO-39 were found resistant reaction to neck blast disease and remaining entries were found moderately resistant to susceptible reaction to neck blast disease.

Conclusions

The present investigation was carried out in order to study the nature and amount of variability, heritability and genetic advance and association between traits under study leaf and neck blast screening. Analysis of variance revealed highly significant sum of squares due to genotypes for all the characters indicated the existence of ample variability among the genotypes. The estimates of PCV were higher than the GCV which indicated high influence of environment on the expression of the traits. GYKH was varied from 270.65-6039.89, while 940.17-6039.88 with mean grain yield Kg/ha of 3596.01 and 3483.92 kg/ha during *Kharif*-21 and *Kharif*-22. High GCV and PCV with high heritability coupled with high GAM were observed for GYKH, while the remaining traits revealed low to medium GCV and PCV, heritability coupled with low to medium GAM. Correlation analysis revealed that significant and positive association was observed for PH, DFF, PL and GYKH. PCAs revealed contribution with 76.94% of total variation during Kh-21 and 77.20% of variation among the studied traits during Kh-22 respectively. Field screening of leaf and neck blast under natural hot spot area among 80 diverse genotypes resulted in identification of resistant sources as KPR-1, KPR-2, KHP-5, Mud-1014, IET-28515 and Kajajaya with promising yield performances.





Annual rainfall dataa recorded in mm during Kh-2021 @ crop growth period

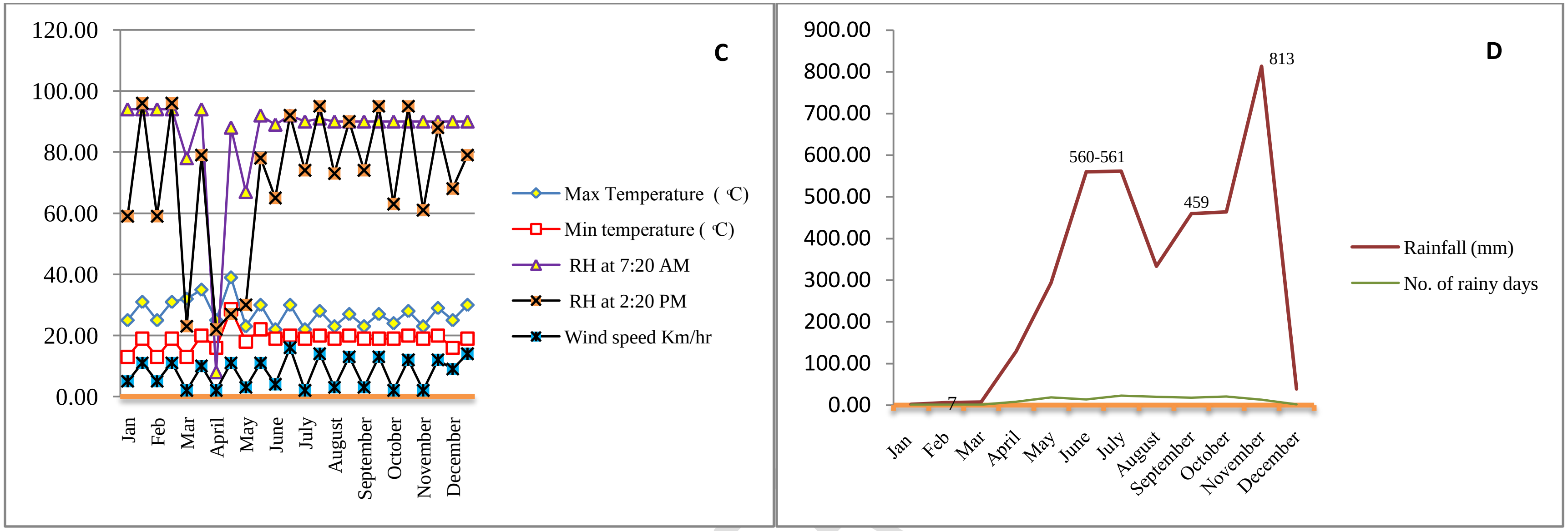


Figure 1: Annual weather data report recorded for two successive crop growth period during Kharif-2021 and Kharif-2022; A & B are weather report of 2021; C & D are weather report of 2022 : **(Source: Digital weather data meter from college of forestry college & Manual rain gauge from AHRS Ponnampete)**

Table 1: The details of study material used along with their parentage details and salient features

Sl. No.	Entries	Parentage details	Salient features
1	Sayadhri Megha	Jyothi × Akkalu	Red rice cultivar with protien rich (12.48%) in addition resitant to blast
2	SayadhriKempumukthi	-	Red rice cultivar released 2020, suitable for hill regions of karnataka
3	KHP-10	(M-63-83 × RP-79-5) × Rikuto Norin 21	Non-lodging red rice cultivar with leaf & neck blast tolerant
4	Sharavathi	(FRR843-3/IR38784-137-2-5-5) × (FRR843-3/IR38787-26-2-2-3)	Red rice cultivar tolerant to blast suitable for hill zones of Karnataka
5	Uma (Mo-16)	MO6 x Pokkali	Cultivar from Kerala released in 1999 which is suitable for cultivation of irrigated rice ecology
6	Mo-4	-	Mo4 is also known as Bhadra one of the most popular cultivar suitable for coastal zones of Karnataka
7	Jyothi	-	Cultivar with long bold grain which is suitable for rainfed upland (Northern trasition zone)
8	Aathira	BR51-46-1 × Cul23332-2	Cultivar with short bold grain with moderatly resistant to leaf & neck blast
9	Sahyadri Kaveri (IET-24451)	-	Cultivar with long bold grain with moderatly resistant to leaf & neck blast, suitable for hill zones of Karnataka
10	Tunga	(Pankaj × Mahsuri) × TKM-6	Cultivar good for puffed rice with wide accetability having tolerance to blast which is suitable for hill zones of karnataka
11	KPR-1	UPLRI5 × IR12979-24-1	Blast resistant cultivar with IET No. IET-21214
12	KPR-2	-	Blast resistant cultivar with Basmati type
13	IR-64	IR-5857-33-2-1 x IR-2061-465-1-5-5	A mega HYV released from CGIAR-IIRR; Semi-dwarf cultivar with resistant to blast
14	KHP-2	-	Known as Karnataka Hill paddy-2 with medium slender grain having wider adaptability due to its higher grain and straw yield
15	KHP-5	Intan x IET-7191	A medium bold dwarf variety known as Karnataka Hill paddy-5 suitable for upland direct sowing
16	KHP-9	Intan x IET-7191	A long duration cultivar with medium bold grain known as Karnataka Hill paddy-9, suitable for hill zones of karnataka with tolerant to blast
17	KHP-11	Intan x IET-7191	A long slender grain with good quality traits known as Karnataka Hill paddy-11, suitable for hill zones of karnataka with blast tolerance
18	KHP-12	Mutant of BKB local variety	Known as Karnataka Hill Paddy-12 with medium slender grain suitable for hill zones of Karnataka having blast tolerance
19	KHP-13 (Bharath) (IET 21479)	--	A medium slender grain with non-lodging blast tolerant cultivar known as Karnataka Hill paddy-13 which is

Sl. No.	Entries	Parentage details	Salient features
			suitable for Hill Zone of Karnataka
20	Intan	Introduction from Indonesia	Semi-dwarf cultivar highly suitable for hill zones of karnataka with blast resiatant
21	MTU-1001	MTU5249 x Vajram x MTU7014	Semi-dwarf cultivar having wider acceptability due medium slender grain with blast resistant also known as Vijetha which is released from ANGRAU
22	Jaya	T(N)1 x T-141	A dwarf cultivar with long bold grain resistant to blast
23	Bili Mukhti (CTH-3)	TR2053-521-1-1 x K116 x KN-1B-361-1-8-6-9-1	A medium bold grain with cold & blast tolerant cultivar selection from International Rice Cold Tolerant Nursery with IR No. IR9202-25-1-3
24	IET-7191	--	Long bold grain suitable for drill sowing
25	Hemavathi	Introduced from Bangladesh	Semi dwarf variety with medium slender grain having tolerance to leaf & neck blast suitable for hill zones of karntaka
26	PUMB-8	--	Cultivar with medium slender grain released in 2009 all India
27	BR-2655	(BR-10 x BR-4) x (BR-7 x Palghar 84-3); Pideegree breeding	Blast tolerant medium bold cultivar with non-lodging suitable for irrigated areas of southern Karnataka
28	Thanu	Mandya Vijaya x CTH-3	A cultivar with earliness plus medium slender grain having good cooking & milling recovery known by the name KMP-101
29	IET-25029	Selection from Quing Livan o.1	Also called as CIARI Dhan-1 having medium slender grain
30	IET-24491	Ciherang 2 x IR 64 Sub-1	Also known as Ciherang sub-1 having long bold grain
31	IET-23422	IR 5657-33-2-1 x IR 2061-465-1-5-3	Also known as JRB-1which is suitable for irrigated early condition with short bold grains
32	IR-10A-155	--	--
33	IET-25281	MTU-1010 x NLR 34449	A cultivar with long slender grains
34	IET28285	IR 73907-753-2-3 x Pratikshya	A cultivar with long slender grains
35	Dhanarasi	B32 Sel.4 x O.rufipogon x B127	Semi-dwarf short bold grain tolerant to water logged condition resitant to blast suitable for rainfed shallow low land conditions of Karnataka
36	IET-24395	MTU 1075 x MTU 1010	A cultivar with medium slender grains
37	IET-26934	MEPH-142	A hybrid having medium slender grain
38	IET-26938	CN1233-33-9 x IR85260-148//IR72176-307-4-2-2-3	A cultivar with short bold grains
39	IET-26940	IR-1659-54-35//IR81896-B-B-195/2 x IR05F102	A cultivar with long slender grains
40	IET-25959	Indravathi x IR6529-22-1	A cultivar with short bold grains
41	IET-26690	Pyzum x Sambha mahsuri	A cultivar with long slender grains
42	IET-26694	Indravati x CR780-1937	A cultivar with short bold grains
43	IET-25856	MTU-1081 x MTU-1064	--
44	IET-26712	IR91659-54-35//IR81896-B-B-19512 x IR05F102	A cultivar with medium slender grains
45	IET-26713	NPG-210 x Dhanrasi	A cultivar with short bold grains
46	IET-26726	Reeta x Swarna sub-1	A cultivar with short bold grains
47	IET-25228	OR 1334-8 x Swarna	A cultivar with short slender grains
48	IET-26566	Pant Dhan10 x NPR2065	--
49	IET-26573	Bhalum3 x Naveen	A cultivar with long slender grains
50	IET-24195	TRC2013-11-IR84898-B-171-CRA-43-1 x IR78877-208-B-1-	

Sl. No.	Entries	Parentage details	Salient features
		2//IR-78878-53-2-2-2	
51	Mud-1010	--	Mudigeri selection1010
52	Mud-1013	--	Mudigeri selection1013
53	Mud-1014	--	Mudigeri selection1014
54	IET-27610	Swarna x IR84895-B-127-22-1-3-1	A cultivar with medium slender grains
55	IET-27620	Indrabati x Vijetha	--
56	IET-27637	IR142-99 x MTU1065	A cultivar with short bold grains
57	IET-27641	KMR-3 x O. rufipogon	A cultivar with short bold grains
58	IET-27466	Kataktara x Swarna	A cultivar with long slender grains
59	IET-25826	Fulbadam x Naveen	A cultivar with long slender grains
60	IET-28017	Pussa-44 x IR81896-B-B-142//Pusa-4 x 3	A cultivar with long slender grains
61	IET-28018	Pussa-44 x IR81896-B-B-142//Pusa-4 x 3	A cultivar with long slender grains
62	Jeerigesanna	Landraces	Traditional rice variety of karnataka having short grain
63	IET-27537	TRCF-41 x TRC2008-1	A cultivar with long slender grains
64	IET-27547	Upahar x CN1231-11-7	A cultivar with long slender grains
65	IET-28890	Gomatidhan x Tripura nirog	A cultivar with long slender grains
66	IET-28509	MTU-1064 x MTU-1075	A cultivar with long bold grains
67	IET-28515	IR73963-86-1-5-2-2 x CR-2324-1-1	A cultivar with long bold grains
68	Krishnaleela	Landraces	Traditional rice variety of karnataka having long grain
69	CR-Dhan-505	CRLC 899 x Ac. 38606	Medium slender grain moderatly tolerant to leaf & neck blast with submergence tolernance
70	Pooja	Vijaya x T.141	Blast rsistant cultivar released in 1999 with IET No.(IET-12241)suitable for Rainfed shallow low land with medium slender grain
71	CR-1017	Pankaj x Jagannath	Also known as Dharitri short bold semi-dwarf cultivar with moderatly tolerant to blast suitable for lowland ecosystem
72	Kajajaya	Landraces	Local variety of coastal zone suitable for very long floudedsuitivation
73	CR-dhan-506	CRLC 899 x Warda 2	A cultivar with IET no. (IET-23053) released in 2017 having moderately resistant to leaf blast, neck blast, brown spot, sheath blight,
74	IET-28895	VL 31339 x BL 122	--
75	IET-28884	Bhalum 3 x Naveen	--
76	IET-29351	MTU1081 x BM71	--
77	PA6444 (HC)	Arize Bayer Bio-Science hybrid	Hybrid with medium slender grain with high milling (74%) & HRR (64%) suitable to direct seeded rice system
78	RNR-15048	MTU1010 x JGL2855; Pidigree method	Known as Telangana sona having low Glycemic index of 51% helps for diabitic patents short duration blast resiatant rice variety released from PJTSAU Telangana hyderabad
79	KMP-220		Red rice paddy variety under drum seeder technology
80	LRNR-5 (F5)	LR-6 x RNR-15048	--

Table 2 Scoring of leaf blast and neck blast under main filed was done by using Standard Evaluation Scale (SES) as given by IRRI (1996)

Leaf blast disease scale to score the genotypes			Neck blast disease scale to score the genotypes		
Scale	Disease severity	Host response	Scale	Disease severity	Host response
0	No lesions observed	HR	0	No incidence/No symptoms	HR
1	Small brown specks of pin point size	R	1	<5% infected panicles T	R
2	Small necrotic grey spots with brown margin of 1-2 mm diameter found on lower leaves	MR T			
3	Significant number of lesion with necrotic grey spots on the upper leaves	MR	3	5-10% infected panicles	MR
4	Typical blast symptoms with >3mm lesions plus 4% leaf area infection	MS			
5	Typical blast symptoms with >3mm lesions plus 4-10% leaf area infection	MS	5	11-25% infected panicles	MS
6	Typical blast symptoms with >3mm lesions plus 11-25% leaf area infection	MS			
7	Typical blast symptoms with >3mm lesions plus 26-50% leaf area infection	S	7	26-50% infected panicles	S
8	Typical blast symptoms with >3mm lesions plus 51-75 % leaf area infection along with many dead leaves	HS			
9	Typical blast symptoms with >3mm lesions plus > 75 % leaf area infection along with many dead leaves	HS	9	>50% infected panicles	HS

Note1: HR: Highly resistant; R: Resistant; MR: Moderately resistant; MS: Moderately susceptible; S: Susceptible; HS: Highly susceptible;

Note 2: The genotypes scoring with 2 to 6 for leaf blast are considered as tolerant genotypes with yield compensation.

Note 3: In the present study the host response of HY, R, MR and MS reactions are considered as tolerant genotypes for the disease.

Table 3. ANOVA for yield and its component traits of rice genotypes under multi seasonal conditions

Mean sum of squares									
Source of variation	**Seasons**	***df***	**DFF**	**DM**	**PH**	**NTPP**	**NTPSM**	**PL**	**GYKH**
Replication	*Kh-21*	1	7.65*	4.23*	25.20	0.16	133.22	3.31	2469469.14*
	Kh-22		19.60*	79.81*	14.40	0.00	130.51	3.28	2352142.56*
Genotypes	*Kh-21*	79	130.68*	127.60*	526.92*	1.96*	2796.19*	5.94*	1813615.05*
	Kh-22		144.75*	216.51*	447.36*	1.96*	2832.57*	5.75*	1758380.96*
Error	*Kh-21*	79	1.09	0.44	41.48	1.26	1571.44	3.49	318890.45
	Kh-22		2.22	4.83	58.08	1.21	1412.47	3.51	269857.75
CV (5%)	*Kh-21*		0.97	0.46	6.87	14.79	12.23	8.18	15.70
	Kh-22		1.38	1.53	8.24	14.52	11.52	8.20	14.91
CD (5%)	*Kh-21*		2.08	1.32	12.82	2.23	78.90	3.71	1124.01
	Kh-22		2.96	4.37	15.16	2.19	74.80	3.73	1033.99
Sem±	*Kh-21*		0.74	0.46	4.55	0.79	28.03	1.32	399.31
	Kh-22		1.05	1.55	5.38	0.77	26.57	1.34	367.32

Table 4. Estimation of Genetic variability parameters for yield and yield attributing characters of rice genotypes under multi-seasonal condition

		Range			Coefficient of variation (%)			
Traits	Seasons	Min	Max	Mean	GCV	PCV	h^2	GAM
DFF	*Kh-21*	94.00	126.00	108.41	7.43	7.49	98.33	15.17
	Kh-22	86.00	126.00	107.60	7.85	7.97	96.98	15.92
DM	*Kh-21*	128.00	165.00	145.16	5.49	5.51	99.31	11.28
	Kh-22	115.00	175.00	143.51	7.17	7.33	95.63	14.44
PH	*Kh-21*	65.25	155.00	93.69	16.63	17.99	85.40	31.66
	Kh-22	65.25	155.00	92.44	15.09	17.20	77.02	27.28
NTPP	*Kh-21*	5.00	14.00	7.58	7.81	16.73	21.78	7.51
	Kh-22	5.00	14.00	7.59	8.05	16.60	23.50	8.03
NTPSM	*Kh-21*	220.00	429.00	324.91	7.16	14.25	25.28	7.42
	Kh-22	220.00	429.00	326.20	8.16	14.12	33.45	9.73
PL	*Kh-21*	15.75	31.75	22.84	4.84	9.50	25.97	5.08
	Kh-22	15.75	31.75	22.89	4.87	9.53	26.08	5.12
GYKH	*Kh-21*	270.65	6039.89	3596.01	24.04	28.71	70.09	41.46
	Kh-22	940.17	6039.88	3483.92	24.76	28.90	73.39	43.69

Note 3: GCV, PCV and GAM was classified as High (> 20%); Moderate (10-20%); Low (<10%) as proposed by Sivasubramanian and Madhavamenon (1973) [35]; (h^2) estimates were categorized as: High (> 60%); Moderate (30-60%); Low (0-30%); GAM estimates were categorized as: High (> 20%); Moderate (10-20%); Low (<10%) suggested by Johnson et al. (1955) [20].

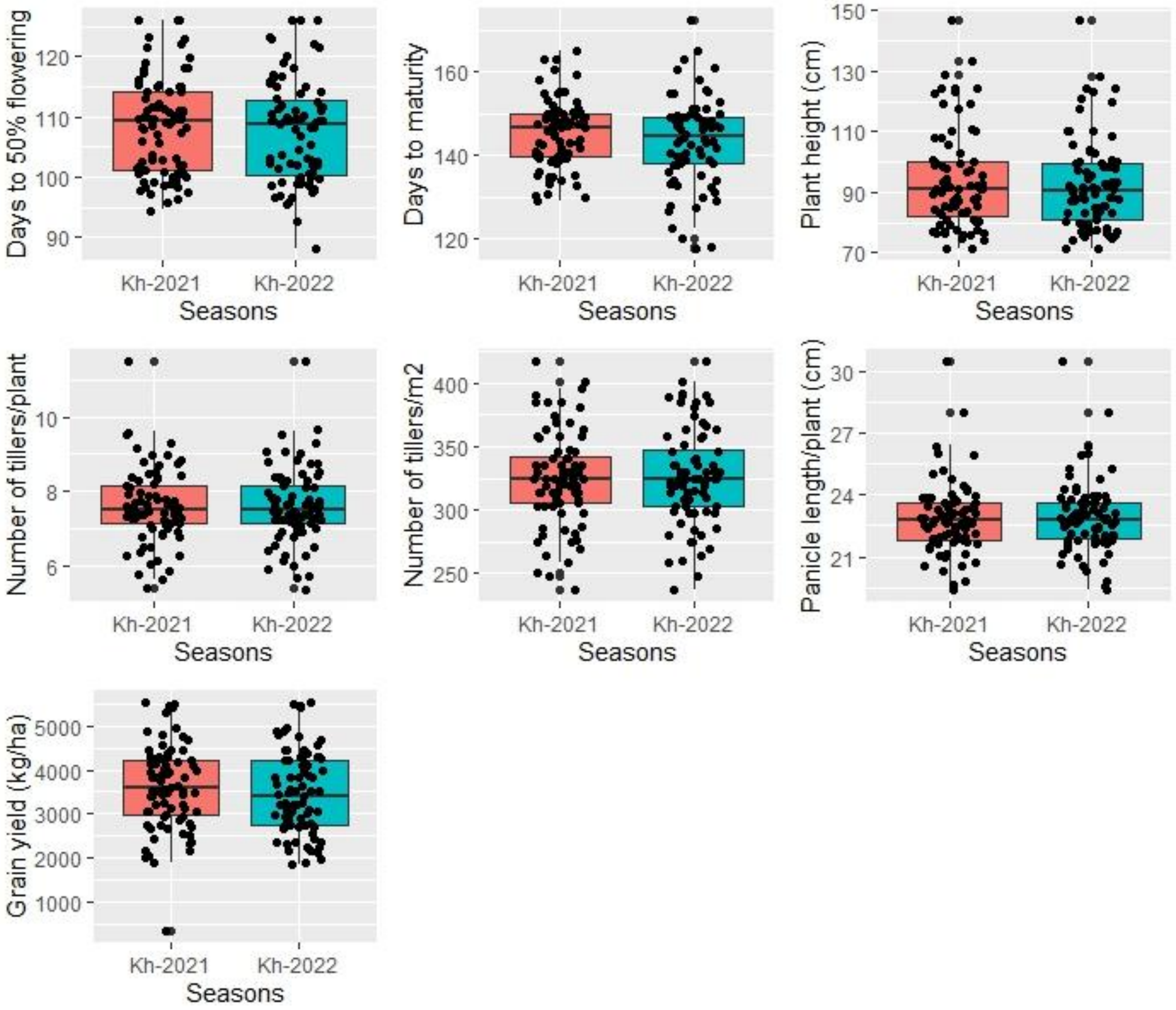
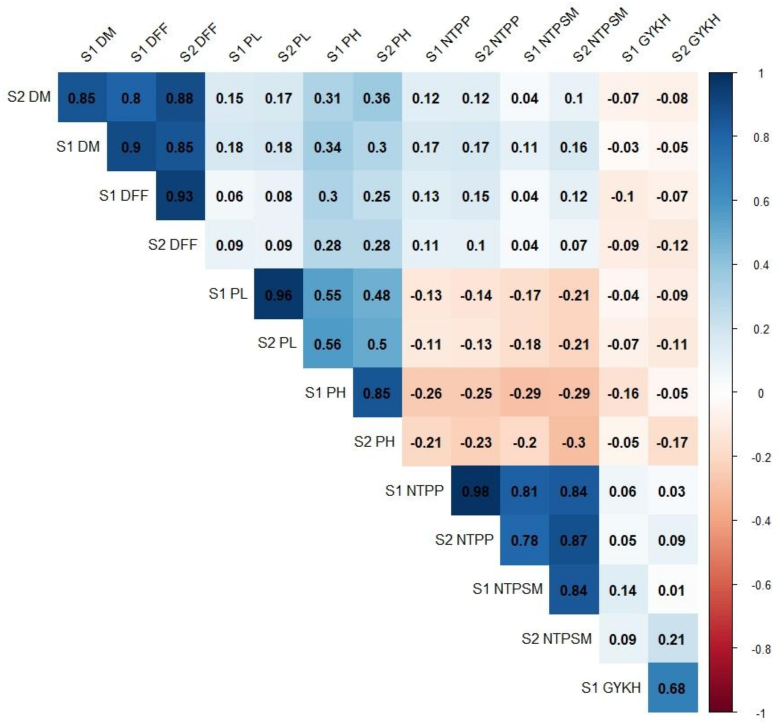


Fig 2 Box plots showing multi-seasonal frequency distribution of yield and yield attributing traits of rice genotypes

Red colour box showing the frequency distribution of genotypes in Kh-2021

Blue colour box showing the frequency distribution of genotypes in Kh-2022



	S1 DM	S1 DFF	S2 DFF	S1 PL	S2 PL	S1 PH	S2 PH	S1 NTPP	S2 NTPP	S1 NTPSM	S2 NTPSM	S1 GYKH	S2 GYKH
S2 DM	0.85	0.8	0.88	0.15	0.17	0.31	0.36	0.12	0.12	0.04	0.1	-0.07	-0.08
S1 DM		0.9	0.85	0.18	0.18	0.34	0.3	0.17	0.17	0.11	0.16	-0.03	-0.05
S1 DFF			0.93	0.06	0.08	0.3	0.25	0.13	0.15	0.04	0.12	-0.1	-0.07
S2 DFF				0.09	0.09	0.28	0.28	0.11	0.1	0.04	0.07	-0.09	-0.12
S1 PL					0.96	0.55	0.48	-0.13	-0.14	-0.17	-0.21	-0.04	-0.09
S2 PL						0.56	0.5	-0.11	-0.13	-0.18	-0.21	-0.07	-0.11
S1 PH							0.85	-0.26	-0.25	-0.29	-0.29	-0.16	-0.05
S2 PH								-0.21	-0.23	-0.2	-0.3	-0.05	-0.17
S1 NTPP									0.98	0.81	0.84	0.06	0.03
S2 NTPP										0.78	0.87	0.05	0.09
S1 NTPSM											0.84	0.14	0.01
S2 NTPSM												0.09	0.21
S1 GYKH													0.68

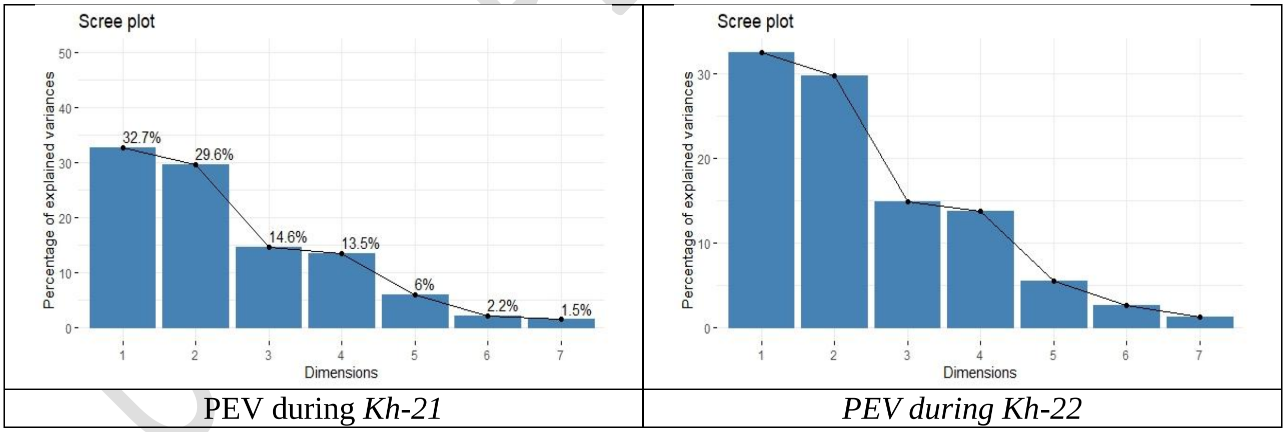
Figure 3: Multi-seasonal phenotypic correlation coefficient matrix among the 80 rice genotypes for yield and its related traits

Note: DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NTPP: number of tillers per plant; NTPSM: Number of tillers per squares meter; PL: Panicle length (cm); GYKH: Grain yield Kg/ha; S1: Kh-2021 Season; S2: Kh-2022 Season; Significance level: 0.05*= 0.217; 0.01= 0.282**

Table 5: Eigen values, Percent variance, cumulative proportion and component loading for yield and its related traits in rice under multi-seasonal conditions

Parameters	Seasons	PC1	PC2	PC3
DFF	*Kh-21*	-0.10	0.03	0.54
	Kh-22	-0.11	0.09	0.69
DM	*Kh-21*	-0.02	**0.09**	**0.60**
	Kh-22	-0.07	**0.10**	**0.77**
PH	*Kh-21*	-0.15	-0.33	**0.89**
	Kh-22	-0.17	-0.31	**0.82**
NTPP	*Kh-21*	**0.06**	**0.81**	0.04
	Kh-22	**0.09**	**0.87**	0.05
NTPSM	*Kh-21*	**0.13**	**0.98**	0.05
	Kh-22	**0.21**	**0.97**	0.03
PL	*Kh-21*	-0.04	-0.19	**0.48**
	Kh-22	-0.11	-0.21	**0.38**
GYKH	*Kh-21*	**1.00**	-0.00	-0.00
	Kh-22	**1.00**	-0.00	-0.00
Eigen value	***Kh-21***	**2.27**	**2.07**	**1.03**
	Kh-22	**2.32**	**2.07**	**1.00**
Proportion of variance	***Kh-21***	**32.45**	**29.66**	**14.83**
	Kh-22	**33.20**	**29.67**	**14.33**
Cumulative proportion	***Kh-21***	**32.45**	**62.11**	**76.95**
	Kh-22	**33.20**	**62.87**	**77.20**

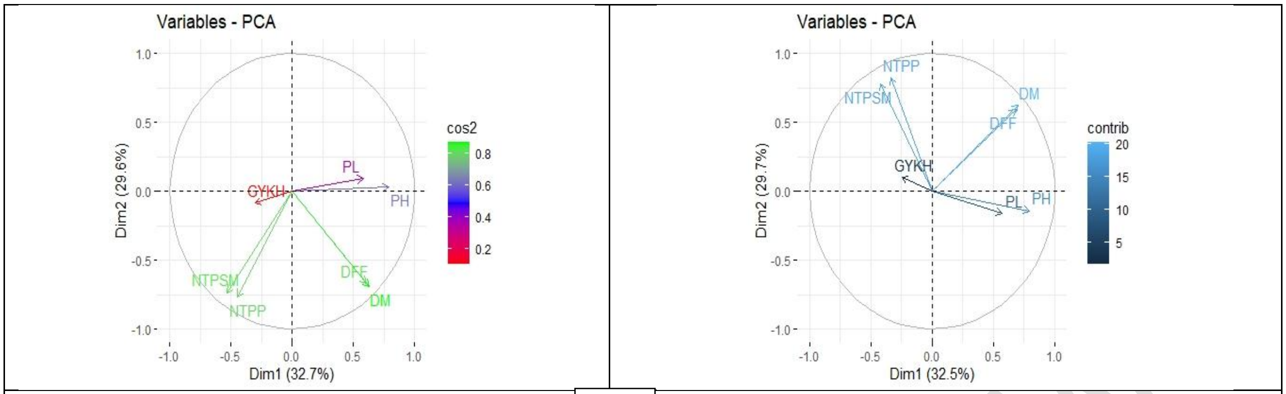
Note: DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NTPP: number of tillers per plant; NTPSM: Number of tillers per squares meter; PL: Panicle length (cm); GYKH: Grain yield Kg/ha;



PEV during *Kh-21* | *PEV during Kh-22*

Fig. 4: Scree plot showing percentage of explained variance in response to number of components for the estimated variables of yield and its component traits in rice genotypes under multi seasonal conditions

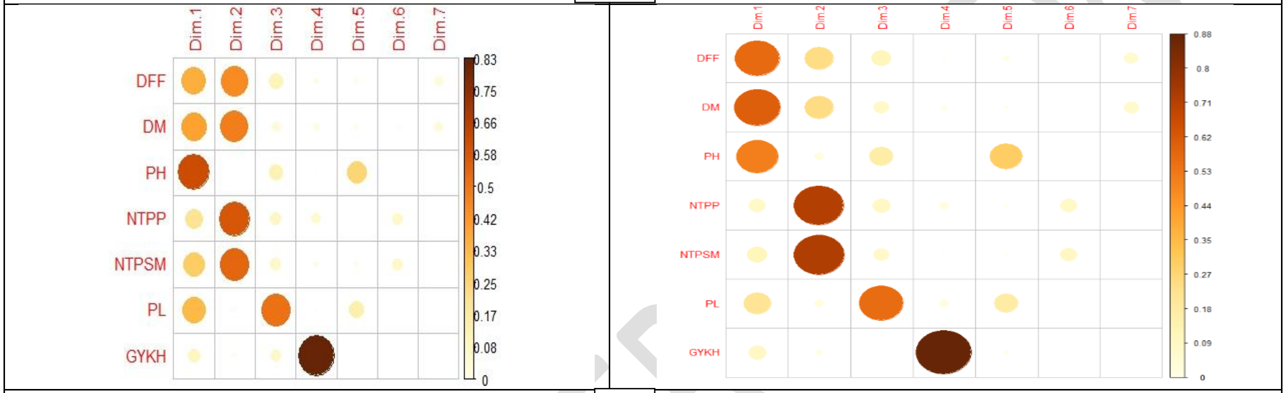
Note: 1 to 7 numbers = component numbers; PEV during *Kh-21* and *Kh-22*: Scree plot graph showing the percent explained variance during *Kharif-2021* and *Kharif-2022* seasons



Variable PCA contribution during *Kh-21*

A

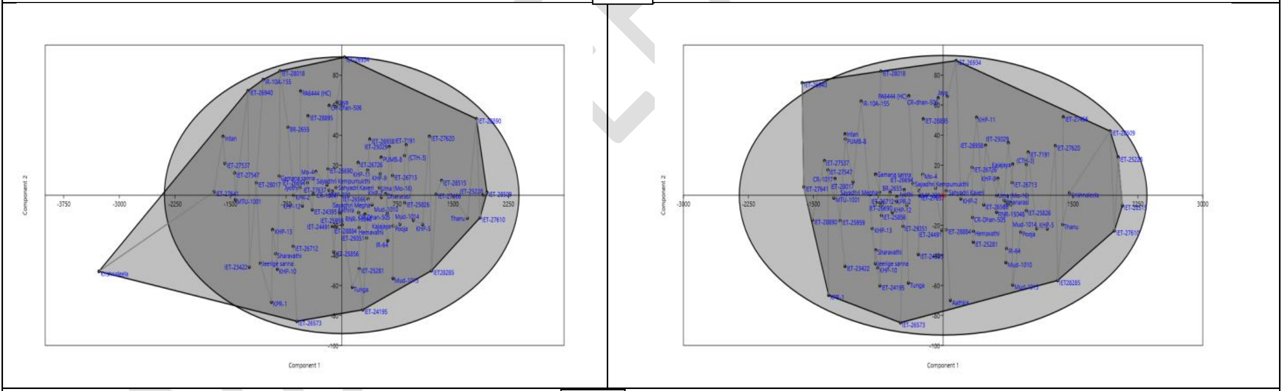
Variable PCA contibution during Kh-22



Trait wise correlation of the PCA during *Kh-21*

B

Trait wise correlation of the PCA during *Kh-22*



Genotypic contribution to the PCA variables during *Kh-21*

C

Genotypic contribution to the PCA variables during *Kh-22*

Fig. 5: A) 2D PCA- Variable plot; B) traits wise correlation for each PCA components C) PCA plots showing the contribution of the rice genotypes to the variability under multi seasonal conditions (*Kharif-2021* and *Kharif-2022*).

Table 6. Multi-seasonal response of studied genotypes for leaf and neck blast disease of rice during kh-2021 &22

		Leaf Blast			Neck Blast		
Sl. No.	**Entries**	**Kh-2021**	**Kh-2022**	**Host response**	**Kh-2021**	**Kh-2022**	**Host response**
1	Sayadhri Megha	4	3	MT	5	5	MS
2	SayadhriKempumukthi	4	5	MT	3	3	MR
3	KHP-10	5	3	MT	9	7	HS
4	Sharavathi	6	5	MS	3	5	MS
5	Uma (Mo-16)	3	5	MT	5	3	MS
6	Mo-4	3	3	T	5	5	MS
7	Jyothi	4	3	MT	7	5	S
8	Aathira	3	5	MT	3	3	MR
9	Sahyadri Kaveri (IET-24451)	3	3	T	5	7	S
10	Tunga	3	4	MT	5	3	MS
11	KPR-1	3	3	T	3	3	MR
12	KPR-2	3	3	T	3	3	MR
13	IR-64	4	3	MT	5	5	MS
14	KHP-2	2	3	T	3	5	MS
15	KHP-5	2	3	T	3	3	MR
16	KHP-9	4	4	MT	3	3	MR
17	KHP-11	5	3	MT	1	3	MR
18	KHP-12	6	5	MS	3	1	MR
19	KHP-13 (Bharath) (IET 21479)	3	5	MT	3	3	MR
20	Intan	6	4	MT	5	3	MS
21	MTU-1001	4	5	MT	7	5	S
22	Jaya	4	3	MT	5	7	S
23	Bili Mukhti (CTH-3)	3	3	T	5	3	MS
24	IET-7191	3	3	T	1	5	MS
25	Hemavathi	3	4	MT	5	1	MS
26	PUMB-8	3	3	T	3	5	MS
27	BR-2655	5	3	MT	7	7	S
28	Thanu	3	4	MT	7	7	S
29	IET-25029	3	3	T	3	7	S
30	IET-24491	3	5	MT	7	5	S
31	IET-23422	3	3	T	7	7	S
32	IR-10A-155	4	3	MT	7	7	S
33	IET-25281	3	5	MT	5	7	S
34	IET28285	4	5	MT	3	5	MS
35	Dhanarasi	4	4	MT	3	3	MR
36	IET-24395	4	5	MT	3	3	MR
37	IET-26934	3	3	T	5	3	MS
38	IET-26938	4	3	MT	7	5	S
39	IET-26940	3	5	MT	7	7	S
40	IET-25959	4	3	MT	5	7	S
41	IET-26690	5	6	MS	7	3	S
42	IET-26694	2	5	MT	3	7	S
43	IET-25856	3	4	MT	7	3	S
44	IET-26712	3	3	T	7	7	S
45	IET-26713	2	3	T	7	7	S
46	IET-26726	3	5	MT	5	7	S
47	IET-25228	3	3	T	5	5	MS
48	IET-26566	4	3	MT	7	5	S
49	IET-26573	3	5	MT	5	7	S
50	IET-24195	3	3	T	7	5	S
51	Mud-1010	3	4	MT	7	7	S
52	Mud-1013	3	3	T	5	7	S
53	Mud-1014	3	3	T	3	3	MR
54	IET-27610	4	3	MT	3	3	MR

		Leaf Blast			Neck Blast		
Sl. No.	**Entries**	**Kh-2021**	**Kh-2022**	**Host response**	**Kh-2021**	**Kh-2022**	**Host response**
55	IET-27620	3	5	MT	1	3	MR
56	IET-27637	3	3	T	7	5	S
57	IET-27641	2	3	T	9	7	HS
58	IET-27466	3	5	MT	1	1	R
59	IET-25826	4	3	MT	3	1	MR
60	IET-28017	4	3	MT	7	3	S
61	IET-28018	3	3	T	7	7	S
62	Jeerigesanna	6	5	MS	7	7	S
63	IET-27537	6	5	MS	9	7	HS
64	IET-27547	7	5	S	7	9	HS
65	IET-28890	7	7	S	9	7	HS
66	IET-28509	5	3	MT	3	3	MR
67	IET-28515	3	3	T	3	3	MR
68	Krishnaleela	3	5	MT	7	3	S
69	CR-Dhan-505	4	3	MT	5	3	MS
70	Pooja	4	3	MT	3	5	MS
71	CR-1017	4	5	MT	3	3	MR
72	Kajajaya	3	3	T	3	3	MR
73	CR-Dhan-506	3	3	T	5	3	MS
74	IET-28895	5	3	MT	7	5	S
75	IET-28884	3	5	MT	3	7	S
76	IET-29351	3	3	T	5	3	MS
77	PA6444 (HC)	4	3	MT	7	5	S
78	RNR-15048	3	5	MT	5	3	MS
79	KMP-220	3	3	T	5	5	MS
80	Gamanasanna	4	5	MT	3	3	MR

Note1: HR: Highly resistant; R: Resistant; MR: Moderately resistant; MS: Moderately susceptible; S: Susceptible; HS: Highly susceptible;

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