

An insight into variability and association among yield and its components under alkalinity and inland salinity stress in rice (*Oryza sativa* L.)

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ABSTRACT

An experiment was conducted to study the variability, correlation, and direct and indirect effects of yield and its attributing traits in 36 genotypes and to identify suitable parents for breeding of alkalinity and inland salinity stress tolerant lines at ARS, Kammasagar, Nalgonda during rabi, 2021-22. Analysis of variance revealed a plentiful quantum of variation among the tested genotypes. Wide variation, high PCV, GCV, heritability, and genetic advance were observed for seedling mortality, sterility percentage, and number of filled grains per panicle. The number of productive tillers/hill and number of filled grains per panicle had a positive and significant correlation with yield whereas seedling mortality and sterility percentage had a negative and significant association with yield. Path analysis inferred that traits such as the number of productive tillers/hill, number of grains per panicle, and 1000 grain weight had a positive direct effect on yield. Hence, priority should be given to the above-mentioned traits to develop alkalinity and inland saline-tolerant rice cultivars. Lines CT118911, Sahel177, M202, and KPS10654 were found promising to be utilized as tolerant parents in the breeding programs.

Keywords- Alkalinity, inland salinity, correlation, path analysis, rice.

Introduction

Salinity is the major abiotic stress after drought in rice-growing areas of the world and nearly 6.73 million hectares of land in India are saline-affected soils [10]. The area under salinization is increasing due to low precipitation, high surface evaporation, weathering of native rocks, irrigation with saline water, and poor cultural practices [17]. Though irrigated lands are further expected to suffer from secondary inland salinization, the situation is likely to be aggravated by an increase in sea level due to climate change [23]. It has been estimated that more than 50% of the arable land will be affected by salinity by the end of 2050 [8]. Effects of salinity and alkalinity vary on plants and even though, both the soils produce ionic and osmotic stress, alkalinity leads to a high pH environment. High pH affects both plants and soil hence, alkaline stress has a more detrimental effect on plants than salt stress. In general, salt affects the growth of crop plants by limiting the absorption of water through the roots affecting the metabolic processes of the plant. It has an immediate effect on cell growth and enlargement, as a high concentration of salt results in toxicity. Ion toxicity is the primary cause while osmotic stress and oxidative damage are secondary causes of salt damage. The saline stress has adverse effects on rice crop during the entire crop duration resulting in low seed germination rate, retarding the seedling growth, seedling mortality, low biomass accumulation, reduction in the main root length and several lateral roots, reduction in tillering ability, a lesser number of spikelets per panicle, greater spikelet sterility percentage, reduced panicle weight thereby causing a significant reduction in grain yield.

The presence of sufficient genetic variability, knowledge of the nature of association among different characters, and the relative contribution of different characters to yield are

prerequisites for a successful breeding program. Heritability and genetic advance are important selection parameters and are more helpful in predicting genetic gain under effective selection [2]. Therefore, the present investigation was undertaken to estimate the genetic parameters, character association, and path coefficients in a set of 36 genotypes to be used as genetic stock for developing high-yielding alkalinity and inland salinity-tolerant paddy varieties.

MATERIALS AND METHODS

Experimental material

In the present study, 36 genotypes (Table 1) were evaluated in randomized block design with three replications at Agricultural Research Station, Kammasagar, Nalgonda during rabi, 2021-22. The field is an in-situ alkaline stress block with a pH of 9.30, E.C of 4.68 dSm⁻¹ and ESP value of 88.0. Seeds were sown in the nursery and 30 days old seedlings were transplanted in the main field *i.e.*, the stress block. For saline resistance FL478, for alkaline resistance, CSR23 and CSR36, and for susceptibility Pusa44 were used as checks. All the recommended package of practices and need-based plant protection measures were followed to ensure a normal crop. Data on 10 traits *viz.* seedling mortality (SM), days to 50% flowering (DFF), plant height (PH), panicle length (PL), number of productive tillers/hill (NPT), number of grains per panicle (NGP), number of filled grains per panicle (NFG), sterility percentage (SP), 1000 grain weight (TW), grain yield (kg/ha) were taken on five randomly selected plants in each genotype in each replication. Data on the days to 50 % flowering and yield (kg/ha) were recorded on a whole plot basis.

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The analysis of variance and its significance for all the traits were worked out [12] and the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation were also calculated [3]. Heritability in the broad sense (h^2 (b.s.)) and genetic advance as a percent of the mean was estimated [6 and 9]. Path and correlation coefficient analysis was done to find the association between yield and its components [4].

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the tested genotypes for the majority of the traits indicating the existence of variability (Table 2). The genetic variability depicted in the form of box plots (Fig 1) showed the frequency distribution for ten traits among the genotypes. The traits, namely, DFF, PH, PL, NPT, NGP, NFG, SP, TW, and GY exhibited greater genetic variability under alkali and inland saline situations. Concerning the normal probability plot, under saline conditions, treatments depicted normal distribution for seedling mortality while the remaining traits, viz., DFF, PH, PL, NPT, NGP, NFG, SP, TW, and GY had few accessions slightly deviating from the normal distribution indicating variability among the genotypes.

Thirty-six genotypes along with checks were evaluated for grain yield and yield attributing traits and the means of the entries in three replications were also analyzed for the estimation of components of genetic variance. Seedling mortality had a general mean (Table 3) of 27.4% ranging from 10.3% (FL478) to 60.3% (Pusa44). The genotypic and phenotypic coefficients of variation estimates (Table 4) for SM were high i.e., 33.6% and 35.5%, respectively. The observed heritability estimate for seedling mortality was high (89.9%) with high genetic advance (65.7%) indicating the preponderance of additive gene action in governing the trait so, this trait can be further improved by simple selection.

Days to 50 percent flowering had a general mean value of 100.9 days with a range of 93.3 (IRRI154) to 108 days (KPS10651). The genotypic and phenotypic coefficients of variation estimates were found to be low i.e., 2.2% and 4.9%, respectively suggesting a narrow range of genetic variability. Further, a low heritability estimate (20.3%) coupled with a low genetic advance (2.0%) indicated the preponderance of non-additive gene action and selection is highly ineffective in improving this trait. These results conform with the findings of [7] and [13].

In the present study, the plant height exhibited a range of 78.33 cm (Sahel177) to 111.33 cm (IR13F167) with an average of 94.2 cm. Low GCV (8.0 %) and PCV (9.0 %) estimates were observed for this trait suggesting a narrow range of genetic variability. High heritability (78.1%) with moderate genetic advance (14.5), revealed the predominance of additive gene effects and simple selection would be rewarding for improvement of this trait. These results are similar to the findings of [15] and [18].

The panicle length ranged from 18.2 (KPS10651) to 24.3 cm (Sahel177) with an average value of 21.3 cm. The genotype Sahel177 had the highest panicle length compared to other genotypes and checks and therefore can be used as a donor parent in hybridization programs. The GCV and PCV for this trait were low i.e., 3.0% and 7.9%, respectively indicating the narrow range of genetic variability. Low heritability (17.3%) and genetic advance (3.0%) were observed for this trait indicating selection is ineffective in improving the trait and [5] and [19] mentioned similar findings.

The average value for productive tillers was 5.4 with a range from 3.9 (KPS10661 and KPS10667) to 6.9 (Sahel177). The genotype Sahel177 had the highest number of productive tillers

suggesting its utilization in yield improvement programs. Moderate values of GCV and PCV were found (12.9% and 17.0%, respectively) revealing moderate genetic variability. Heritability was moderate (56.5%), and low genetic advance (1.1%) limits further improvement through direct selection due to the favorable influence of the environment on the trait. These results were following that of [13] and [20].

The number of grains ranged from 33.3 to 80.0 with an average value of 61.6. The genotypes IR69726 and KPS10321 had the lowest and the highest number of grains per panicle, respectively. Moderate GCV and high PCV were observed for this trait (17.8 and 22.3, respectively) indicating the existence of an adequate amount of genetic variation. The heritability estimates for this trait were high (63.8%) coupled with high genetic advance (29.3%). Hence, direct selection could be effective for desired genetic improvement for this trait. Similar kind of results was reported by [15] and [18].

The number of filled grains per panicle had shown a very wide distinctness (21.3-29.3 g) among the genotypes as very low in three genotypes i.e., Pusa44, IR69726 and IRR154, and highest in KPS2874. High GCV (20.7%) and PCV (26.6%) were observed with a high heritability estimate of 60.2% coupled with high genetic advance (33.1%) inferring the preponderance of additive gene action in governing the trait.

The sterility percentage was in the range of 12.2% (M202) to 56.1% (Pusa44) with a mean value of 29.9%. The magnitude of GCV (40.8%) and PCV (47.1%) was high suggesting the existence of an ample genetic variation. High heritability (74.9%) coupled with high genetic advance (72.7%) were found indicating the presence of additive gene action and [7] obtained similar results.

Low 1000 grain weight was observed in eight genotypes viz. KPS10316, KPS10319, KPS10628, KPS10654, KPS10656, KPS10658, KPS10672, and KPS10683 ranging from 15.6-17.0 g, and grain weight was medium (17.1-24.5g) in the majority of the genotypes and only two genotypes NSICRC240 and FL478 had highest grain weight (25.7g and 25.9g, respectively). Moderate GCV (17.2%) and PCV (17.6%) were recorded with a high heritability of 96.0% coupled with high genetic advance (34.8%) showing the presence of additive gene action in the inheritance of the trait. These findings were following that of [14] and [19].

In the present study, grain yield ranged from 1825 kg/ha (Pusa44) to 4096 kg/ha (KPS10654) with an average value of 3075 kg/ha. The genotypes showed much lesser yield as compared to the checks due to high seedling mortality and sterility percentage. The genotypes KPS10633, KPS10642, KPS10651, KPS10654, M202, Sahel177, and CT11891 had comparable yields with the checks and can be used as donor parents in hybridization programs. Moderate GCV (14.5%) and PCV (16.0%) were observed for this trait suggesting a moderate range of genetic variability. A high heritability estimate (82.4%) coupled with high genetic advance (27.2%) indicated the control of additive genetic effects and selection was very effective through direct selection for the improvement of this trait and [1] and [21] mentioned similar findings.

Character association is driven by the correlation coefficient which aids in the evaluation of the relative influence of various yield-attributing traits on grain yield. In the present study, the correlation between yield and its attributing traits (Table 5) revealed that grain yield was positively significant with the number of productive tillers (0.5171**) and the number of filled grains per panicle (0.5413**). Traits i.e., number of productive

tillers and number of filled grains per panicle could be considered as a selection criteria for higher grain yield as these traits were mutually and directly associated with grain yield [11]. However, seedling mortality (-0.6391^{**}) and sterility percentage (-0.506^{**}) had a significant and negative association with grain yield and would hinder the expression of the grain yield [22]. Hence, the selection of the genotypes with a low percentage of seedling mortality results in a low sterility percentage.

An estimate of simple correlation would not provide the true contribution of the characters towards the yield and path analysis allows separating into the direct effect and indirect effects through other attributes by apportioning the correlations for better interpretation of cause and effect (Table 6, Figure 2). Path coefficient analysis revealed a positive direct effect of several productive tillers/hill (0.2749), number of grains per panicle (0.5647), and 1000 grain weight (0.0032) on yield (kg/ha). These findings are in line with the findings of [11] and [16]. The number of filled grains per panicle had positive indirect effects on yield through the number of productive tillers/hill (0.0643) and the number of grains per panicle (0.3396). Seedling mortality and sterility percentage had a negative direct effect (-0.3715 and -0.4821, respectively) as well as a significant negative correlation with yield (kg/ha) (-0.6391^{**} and -0.506^{**}, respectively). Therefore, it is logical to select genotypes with low seedling mortality and sterility percentage for improvement of yield in paddy.

In the present study, an adequate amount of genetic variation, high heritability coupled with high genetic advance was observed for seedling mortality, number of filled grains per panicle, and sterility percentage. Hence, a simple and early-generation selection of promising lines by involving present genotypes in future hybridization programs would be very effective. The yield had a positive and significant association with the number of productive tillers/hill and the number of filled grains per panicle, and the latter exhibited high positive indirect effects on yield *via* the number of productive tillers/hill and the number of grains per panicle. Therefore, these traits would be most suitable for direct and indirect selection of yield in rice improvement programs. Lines CT118911, Sahel177, M202, and KPS10654 were found promising with early flowering and tolerant to salinity stress with low yield reduction and can be utilized as donor parents in future breeding programs.

Table 1: Experimental material used in the study.

S. No	Genotype	S. No	Genotype	S. No	Genotype	S. No	Genotype
1	FL478	10	IRRI154	19	KPS10633	28	KPS10667
2	Pusa44	11	GSRIR2	20	KPS10640	29	KPS10669
3	CSR23	12	CT11891	21	KPS10642	30	KPS10672
4	CSR36	13	IR13F167	22	KPS10651	31	KPS10676
5	RNR11718	14	Sahel177	23	KPS10654	32	KPS10683
6	KPS2874	15	Jasmine85	24	KPS10656	33	KPS10316
7	IR69726	16	M202	25	KPS10657	34	KPS10319
8	IR77186	17	KPS10628	26	KPS10658	35	KPS10321
9	NSICRC240	18	KPS10631	27	KPS10661	36	KPS10329

Table 2: Analysis of variance for yield and its components under alkalinity and inland salinity stress in rice.

Source of variation	d.f	Mean sum of squares									
		SM	DFF	PH	PL	NPT	NGP	NFG	SP	TW	GY
Replications	2	13.481	54.065	42.954	7.148	0.944	95.071	60.731	1.410	1.366	5958.371
Genotypes	35	264.07 ^{**}	33.978 [*]	185.597 ^{**}	3.806 [*]	1.838 ^{***}	427.606 ^{**}	283.53 ^{**}	495.550 ^{**}	35.145 ^{**}	642548.400 ^{**}
Error	70	9.548	19.246	15.849	2.336	0.364	68.048	51.131	49.715	0.476	42684.700
Total	107	92.877	24.715	71.880	2.907	0.857	186.166	127.332	194.646	11.833	238215.300

^{**}, ^{*} - significant at 1% and 5% level, respectively, d.f - degrees of freedom

Table 3: Mean performance of 36 rice genotypes for yield and its components under alkalinity and inland salinity stress.

Genotypes	SM	DFF	PH	PL	NPT	NGP	NFG	SP	TW	GY
FL478	10.3	101.7	92.3	21.8	5.5	43.7	37.3	14.9	25.9	3047
Pusa44	60.3	103.7	88.0	22.3	4.1	50.3	21.3	56.1	22.1	1825
CSR23	12.0	97.7	104.3	22.2	6.0	48.3	41.3	14.7	22.8	3195
CSR36	17.7	98.3	101.0	21.8	5.8	55.0	43.7	20.6	23.8	3538
RNR11718	16.7	95.0	92.3	21.2	5.5	62.0	52.7	15.3	17.9	3572
KPS2874	19.7	99.0	99.7	22.8	5.7	75.0	61.3	19.3	16.9	3429
IR69726	31.0	100.0	91.7	22.3	5.5	33.3	26.0	21.8	21.7	2698
IR77186	28.7	100.0	87.0	23.0	5.1	44.0	32.7	26.1	22.4	2814

NSICRC240	33.3	97.3	83.7	20.7	4.3	51.3	35.7	30.7	25.7	2427
IRRI154	21.3	93.3	84.0	20.5	6.3	41.7	29.3	29.1	24.1	3290
GSRIR2	20.0	102.3	106.7	20.7	5.5	49.7	40.3	19.0	22.7	2868
CT11891	15.0	99.0	84.3	21.0	6.1	60.9	49.0	19.6	23.4	3712
IR13F167	20.3	104.3	111.3	21.0	5.5	60.3	46.3	23.0	24.2	3206
Sahel177	18.7	101.7	78.3	24.3	6.9	57.8	41.3	26.5	23.9	3755
Jasmine85	28.7	103.0	93.0	20.6	6.5	59.3	44.3	25.5	23.3	3334
M202	21.3	103.0	83.0	22.3	6.7	67.5	59.7	12.2	24.5	3889
KPS10628	25.0	99.7	91.0	22.3	4.3	77.3	58.7	23.9	15.6	3351
KPS10631	31.0	97.0	90.7	20.2	4.6	72.7	48.7	32.7	16.3	3024
KPS10633	27.0	102.7	91.3	20.6	5.2	60.3	46.3	23.2	16.6	3241
KPS10640	31.3	100.7	86.7	19.7	5.6	50.7	36.3	27.6	17.8	3375
KPS10642 (contd.) (contdCon	26.7	102.0	100.3	20.8	5.7	59.0	46.0	22.0	16.9	3194
KPS10651	31.3	108.0	95.0	18.2	6.1	64.3	48.7	24.1	17.1	3324
KPS10654	26.0	98.7	103.7	20.1	6.1	76.3	56.0	26.6	16.3	4097
KPS10656	22.0	99.0	108.0	20.0	6.5	64.0	55.3	13.2	16.4	3327
KPS10657	35.3	104.3	91.3	22.0	5.7	72.3	57.7	21.6	17.0	2632
KPS10658	31.7	106.3	90.3	21.1	5.1	60.3	39.7	34.8	16.2	2490
KPS10661	41.3	103.7	101.0	21.0	3.9	65.2	43.7	33.5	22.2	2517
KPS10667	30.0	103.3	96.3	20.3	3.9	75.0	39.0	47.4	17.1	3038
KPS10669	34.7	98.0	102.3	21.8	4.9	75.3	43.0	42.6	16.6	2974
KPS10672	42.3	104.7	103.0	22.5	5.4	71.3	32.0	54.8	17.0	2615
KPS10676	30.3	103.0	102.0	21.2	5.1	50.7	29.7	40.7	20.7	2523
KPS10683	29.3	105.0	93.3	20.6	5.9	70.0	42.3	39.5	16.9	2877
KPS10316	36.3	105.0	94.0	20.9	4.3	76.3	34.7	54.2	16.4	2790
KPS10319	25.7	100.0	91.3	20.7	5.7	77.3	39.7	49.0	16.7	3020
KPS10321	25.7	97.7	92.7	22.3	5.3	80.0	35.7	55.4	17.0	2763
KPS10329	28.3	95.7	87.3	21.2	4.8	58.0	37.0	35.8	18.2	2939
Mean	27.4	100.9	94.2	21.3	5.4	61.6	42.6	29.9	19.7	3075
C.V (%)	11.28	4.35	4.22	7.18	11.10	13.40	16.80	23.57	3.50	6.72
C.D (0.05)	5.03	7.14	6.48	2.49	0.98	13.43	11.64	11.48	1.12	336.44
S. E \pm	1.78	2.53	2.30	0.88	0.35	4.76	4.13	4.07	0.40	119.28

SM-Seedling mortality DFF-Days to 50 % flowering, PH-Plant height (cm), PL-Panicle length (cm), NPT-Number of productive tillers/hill, NGP-Number of grains per panicle, NFP-Number of filled grains per panicle, SP-Sterility percentage, TW-1000 grain weight (g), GY-grain weight(kg/ha)

Table 4: Genetic variability parameters for yield and its components in rice.

S.no	Trait	PCV (%)	GCV (%)	h^2 (b.s.)	GAM
1	SM	35.5	33.6	89.9	65.7
2	DFF	4.9	2.2	20.3	2.0
3	PH	9.0	8.0	78.1	14.5
4	PL	7.9	3.0	17.3	3.0
5	NPT	17.0	12.9	57.5	20.2

6	NGP	22.3	17.8	63.8	29.3
7	NFG	26.6	20.7	60.2	33.1
8	SP	47.1	40.8	74.9	72.7
9	TW	17.6	17.2	96.0	34.8
10	Yield (kg/ha)	16.0	14.5	82.4	27.2

PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, h^2 (b.s.) = heritability in a broad sense, GAM= Genetic advance as a percent of the mean (at 5%)

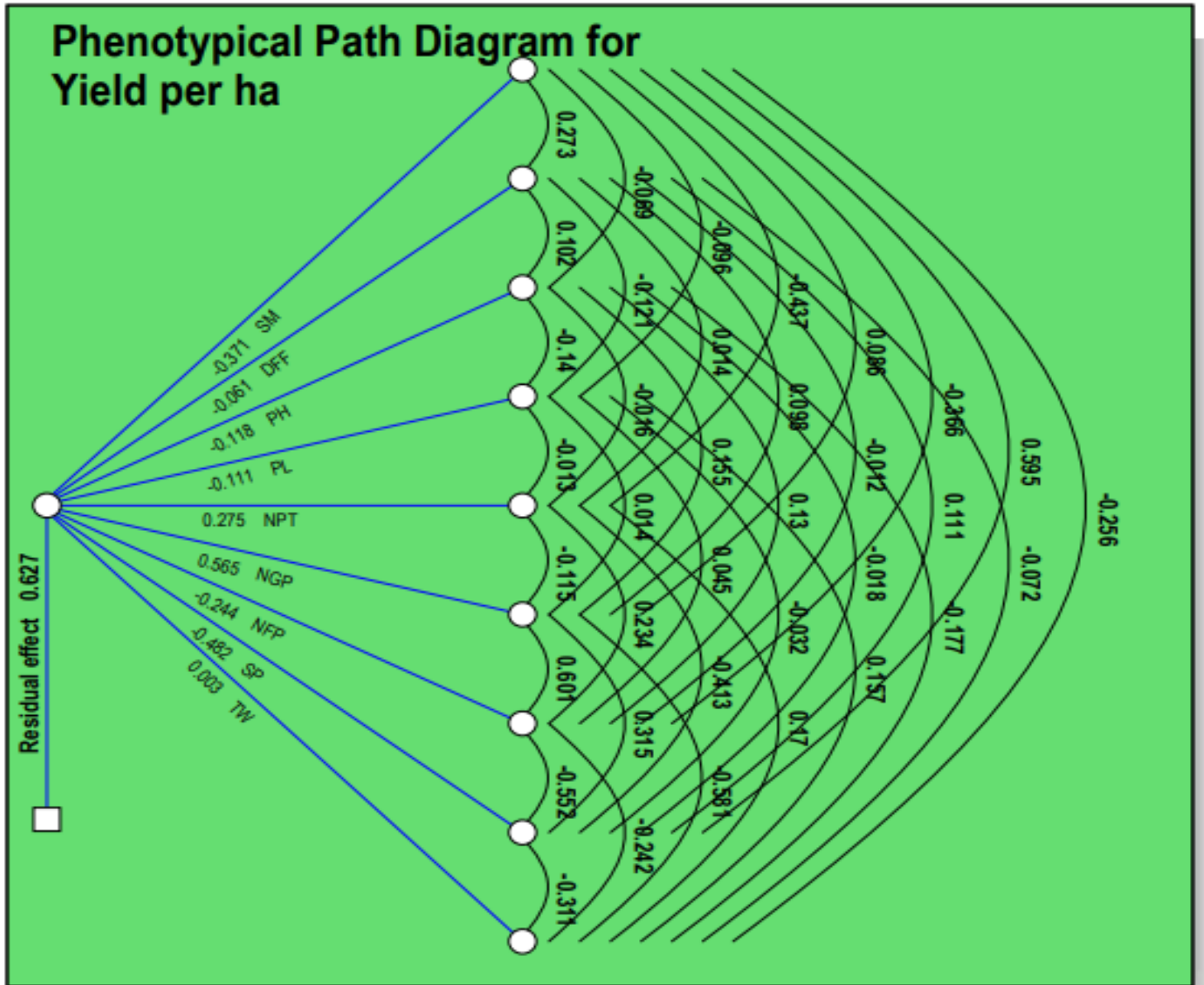


Figure 2: Phenotypical path diagram for yield (kg/ha)

Table 5: Phenotypic correlations for yield and its components in 36 genotypes of rice.

TRAIT	SM	DFF	PH	PL	NPT	NGP	NFG	SP	TW	GY
SM	1.0000	0.272	-	-	-	0.0860	-	0.5946	-	-
DFF		1.000	0.1022	-	0.0141	0.0984	-	0.1110	-	-
PH			1.000	-	-	0.1548	0.1302	-	-	-
PL				1.000	-	0.0141	0.0453	-	0.1574	-
NPT					1.000	-	0.2341	-	0.1700	0.517
NGP						1.000	0.6014	0.3150	-	0.174

NFP							1.000	-	-	0.541
SP								1.000	-	-
TW									1.000	0.034

** , * - significant at 1% and 5% levels, respectively

Table 6: Phenotypic path coefficient analysis for yield and its components in 36 rice genotypes. Phenotypic Residual Effect=0.6270

Trait	SM	DFF	PH	PL	NPT	NGP	NFG	SP	TW	GY
SM	-	-	0.0256	0.0356	0.1622	-	0.1358	-	0.0951	-
DFF	-	-	-	0.0073	-	-	0.0007	-	0.0044	-0.1522
PH	0.0081	-	-	0.0165	0.0019	-	-	0.0021	0.0209	-0.0237
PL	0.0106	0.0133	0.0155	-	0.0015	-	-	0.0035	-0.0174	-0.0420
NPT	-	0.0039	-	-	0.2749	-	0.0643	-	0.0467	0.5171**
NGP	0.0486	0.0556	0.0874	0.0079	-	0.5647	0.3396	0.1779	-0.3278	0.1748
NFP	0.0893	0.0030	-	-	-	-	-	0.1348	0.0591	0.5413**
SP	-	-	0.0086	0.0155	0.1990	-	0.2661	-	0.1499	-
TW	-	-	-	0.0007	0.0009	-	-	-	0.0032	0.0341

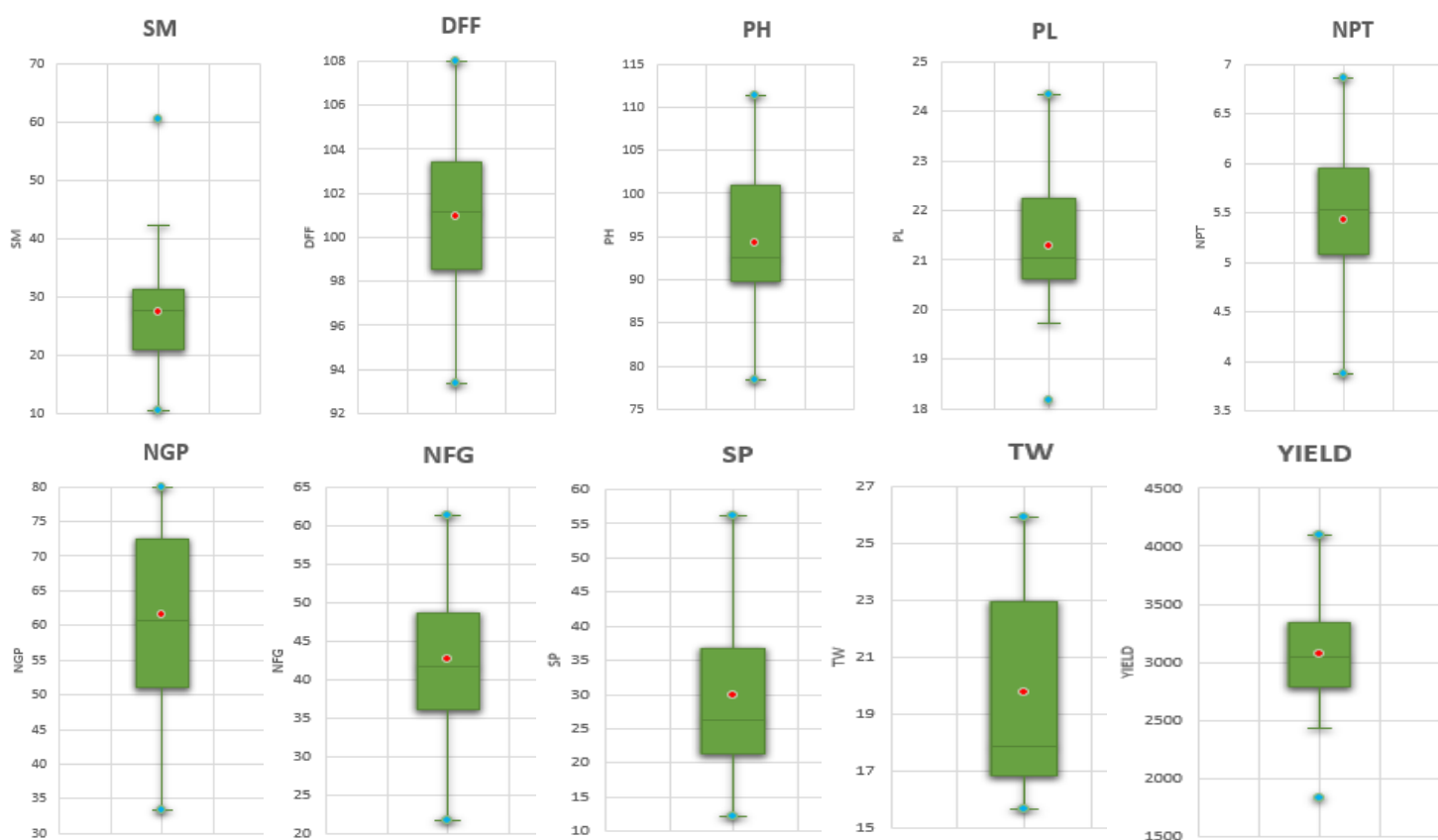


Fig 1: Box plots depicting the variation in data for eight traits studied in rice genotypes. The 75th, 50th, and 25th percentiles of the genotypes are represented by the upper, median, and lower quartiles, respectively. The vertical lines depict the population's variation. The outliers are represented by dots.

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