

Studies on Aluminium Tolerance and Morphological Traits in Rice Lines from North Eastern India

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Abstract Genetic variation is prerequisite for any crop improvement program as it helps in development of superior recombinants. Forty eight genotypes were evaluated for agronomic traits, yield and characters related to Al tolerance. The components of variability revealed high magnitude and highly heritable nature of the variations. High heritability with high to moderate value of genetic advance over mean was exhibited by majority of morphological traits used in the study. Significant correlations were observed for aluminum tolerance related traits, agronomic and yield traits. Principal components analysis revealed that the first three most informative components accounted for 70 % of the variance. The clustering pattern as revealed by dendrogram, based on average distance, classified the accessions into five clusters. Several high performing genotypes namely, N-861, Khougjai Phou, Posimot, Aaha and Epyo were found in the study which can be used for future breeding purposes.

Keywords Aluminium tolerance · Rice · Soil acidity · Variability · Grain yield

Introduction

Soil acidity is the single largest constraint to crop productivity in north east India, with nearly 65 % of the soil

being affected by strong acidity ($\text{pH} < 5.5$). Aluminum (Al) toxicity is often the most limiting factor for crop grown in these soils. Under highly acidic soil conditions, Al^{3+} is solubilized into the soil solution and is highly phytotoxic. Al^{3+} causes a rapid inhibition of root growth that leads to a stunted root system, thus having a direct effect on the ability of the plant to acquire both water and nutrients [1]. Thus poor crop growth in acid soils can be directly correlated with the degree of Al saturation in the soil solution [2]. The root apex is the primary target which plays a central role in Al tolerance [3]. In particular, inhibition of root growth as the result of Al-induced impairment of cell division and elongation is a well known early and dramatic symptom of Al phytotoxicity in acid soils [2, 4–6]. Although crop production on acid soils can be sustained by the application of lime, runoff pollution is an undesirable effect. Liming is often not economical or practical because of the slow movement of lime especially in the deeper layers of sub-soil [7, 8]. Furthermore, heavy application of lime may have adverse effects on some crops in the rotation or may cause deficiencies of certain nutrients [9]. Thus, developing cultivars with improved tolerance to acid soil stress is a more pragmatic solution to solve this problem [10]. In this regard present study has been conducted to identify Al tolerant genotypes with a higher yield potential. Considerable genetic variability exists for Al tolerance within rice genotypes which can be exploited to develop a tolerant genotype.

Material and Methods

A set of forty eight genotypes were screened for agronomic traits, yield and characters related to Al tolerance. These genotypes were either locally collected/procured germplasm

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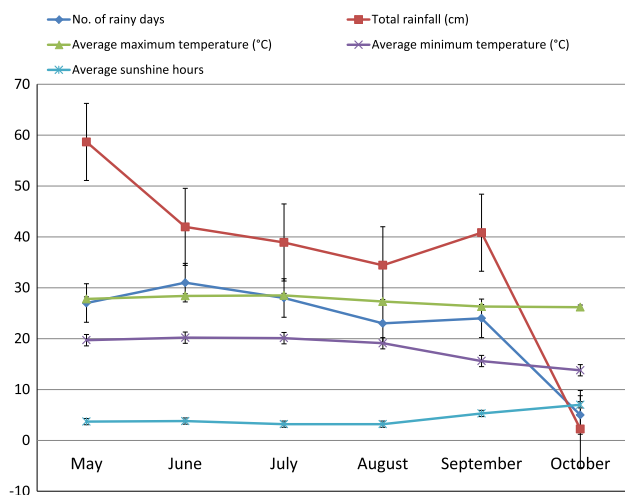


Fig. 1 Weather conditions of experimental site during the crop growth period

or selected lines of AICRIP trials (Hyderabad) and IIRI nursery (Phillipines).

Climate and Weather

The experiment was carried out at upland experimental farm of Division of Plant Breeding, Indian Council of Agricultural Research ICAR Research Complex for NEH Region, Barapani, Meghalaya, India (latitude 25°39' north, longitude 91°54' east and elevation 1,010 m asl). Weather conditions during the crop growth period are presented in Fig. 1. A rainy day is recorded when there has been a daily rainfall total of at least 2.5 mm. Average sunshine in hours per day allows for comparison of sunshine in various seasons on the same location.

Experimental Layout

A field experiment was set up in a Randomized Block design with three replications and three checks viz., IR-64, N-861 and N-902. The checks were chosen based on their ability to perform well across different locations in India.

to 50 % flowering, days to maturity, plant height, panicle weight/plant, straw weight, panicle length, ear bearing tillers, number of healthy grains, number of chaffy grains, spikelet fertility, test weight, relative difference for root length, relative difference for root dry weight and single plant grain weight. Measurements for days to 50 % flowering and days to maturity were recorded on per plot basis; days to 50 % flowering were calculated as number of days required for 50 % of the plants to flower. For other agromorphological traits a set of 10 plants were used to constitute one replication and likewise three replications were used for screening purposes.

The lab experiment was conducted in completely randomized design with three replications each for control and Al solution. Ten plants were selected from each replication of each variety/germplasm for recording observations. The amount of Al in solution (100 μ M) was determined based on the level of injury observed in the roots of plants in earlier experiments [11]. These genotypes were grown in hydroponics in laboratory conditions with and without Al for 7 days to screen the root and shoot characters. Concentration of Al in hydroponic solution was maintained by $AlCl_3$. Seeds were germinated on filter paper moistened with double distilled water in a petridish overnight in dark for 4 days. The germinated seeds of each genotypes of an age of 4 days with an emerging root were shifted to hydroponic solution with and without Al.

Measurements were recorded on root length and root dry weight in both control and Al solutions. Initial measurement for root length was taken at the time of shifting genotypes to hydroponic nutrient solution. After 7 days, plants were taken out and final measurements for root length were taken for both control and Al solution. The relative root length was computed using both the initial and final values. The plants were kept in oven at 60 °C for drying and measurement was taken for root dry weight of genotypes grown in both control and Al solutions. Relative difference was calculated by taking the relative root length of control (without Al) and 100 μ M Al solutions together by the formula given below.

$$\text{Relative difference} = \frac{(\text{Final reading with Al} - \text{initial reading with Al})}{(\text{Final reading without Al} - \text{initial reading without Al})} \times 100$$

Experimental plots consisted of five rows each 4 m long. Plants were spaced 20 × 15 cm apart. The recommended agronomic practices and plant protection measures were followed to ensure normal crop growth. At field level measurements were recorded on the following traits: days

Statistical Analysis

Analysis of variance (ANOVA) was carried out on the data to assess the genotypic effects and their interaction using general linear model (GLM) procedure for

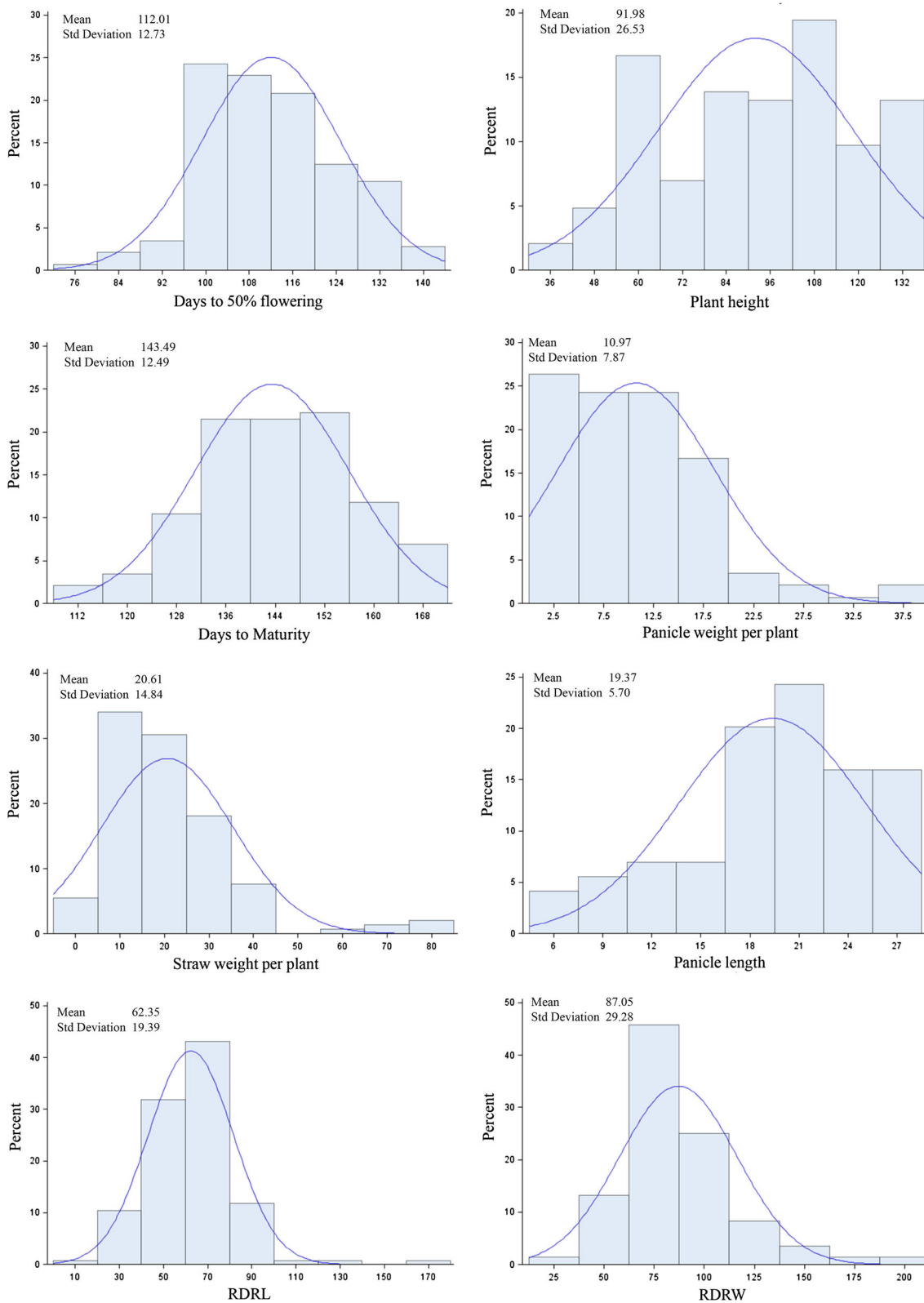


Fig. 2 Distribution of agro morphological and Al related traits in rice

randomized complete blocks design in SAS (version 9.2). Genotypic and phenotypic coefficient of variability was computed according to Burton and Devane [12].

Broad sense heritability was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage [13]. Genetic advance (GA)

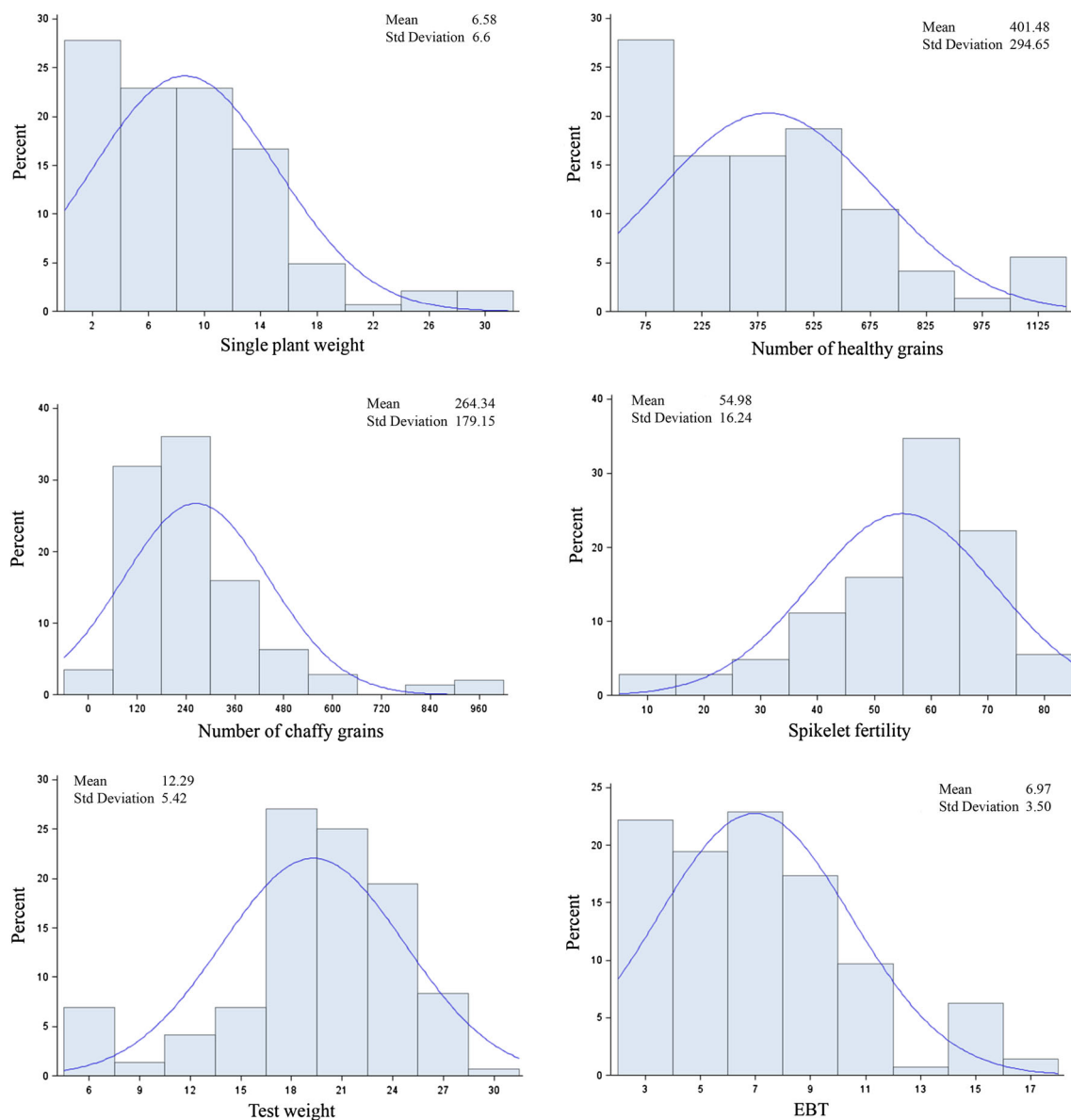


Fig. 2 continued

was computed according to the formula given by Johnson et al. [14]. Higher estimates of heritability coupled with better GA confirm the scope of selection in developing new genotypes with desirable characteristics. The correlation coefficients were calculated to determine the degree of association of characters with yield [15]. The estimates of direct and indirect effects of quantitative traits on seed yield were calculated through path coefficient analysis as suggested by Wright [16] and elaborated by Dewey and Lu [17]. The cluster analysis, correlation and principal component analysis was done using SAS 9.2 software (SAS Institute Inc., Cary, NC, USA).

Results and Discussion

Mean Performance

The detailed evaluation of forty eight genotypes was performed in solution culture for variation in AI related and morphological traits in field respectively (Fig. 2). Anjali (126), N-861 (127) and Shaku (127) were early maturing genotypes whereas Ching Moiramsbhi (168), Vai Pheitai (168) and Silky Rice (160) were late maturing. For agromorphological and yield related traits, N-861, Khougjai Phou, Posimot and Epyo were found promising. As far as AI related traits were concerned, Posimot, Epyo, Aaha and

Table 1 Components of variation in rice genotypes for agronomic and Al related traits

	Mean	CV	Max	Min	GCV	PCV	h^2_b	GAM 5 %
DFE	112.01	5.80	137.00	81.00	9.84	10.40	0.90	19.19
DM	143.49	4.73	168.00	116.00	7.35	7.84	0.88	14.18
PH	91.98	12.35	135.00	46.33	26.05	27.01	0.93	51.76
PWPP	10.97	40.72	40.00	1.67	60.52	64.93	0.87	86.21
SW	20.61	37.13	81.00	3.33	61.64	65.27	0.89	79.94
PL	19.37	18.69	27.33	10.00	21.15	23.75	0.79	38.82
EBT	6.97	33.84	15.00	2.33	37.18	42.00	0.78	67.79
NHG	401.48	38.39	1,190.00	36.00	61.79	65.65	0.89	79.82
NCG	264.34	34.41	962.00	35.33	58.93	62.19	0.90	85.03
SF	54.98	16.80	76.33	12.00	23.52	25.44	0.86	44.78
TW	19.29	16.88	27.00	10.00	21.06	23.20	0.82	39.37
RDRW	62.35	29.89	96.00	33.67	9.03	19.48	0.22	8.62
RDRL	87.05	31.33	129.00	44.33	12.38	21.92	0.32	14.40
SPGW	8.58	41.93	32.00	1.00	64.09	68.51	0.88	83.51

CV coefficient of variation, *Max* maximum value, *Min* minimum value, *GCV* genotypic coefficient of variation, *PCV* phenotypic coefficient of variation, h^2_b broad sense heritability, *GAM 5 %* genetic advance over mean under 5 % selection intensity, *DFE* days to fifty percent flowering, *DM* days to maturity, *PH* plant height, *PWPP* panicle Weight/plant, *SW* straw weight, *PL* panicle length, *EBT* ear bearing tillers, *NHG* no of healthy grain, *NCG* no of chaffy grain, *SF* spikelet fertility, *TW* test wt, *RDRL* relative difference for root length, *RDRW* relative difference for root dry weight, *SPGW* single plant grain weight

VR-14 were found responsive for relative difference for root length. This response is due to more root length in the presence of Al in hydroponic solution (100 μ M).

Genetic Variability, Heritability and Genetic Advance

Analysis of variance (Table not shown) revealed that potential genotypic differences were significant for all the characters, with high genetic variability and diversity in the material under consideration [11]. These results indicated better scope for genetic improvement through conventional breeding. The nature and magnitude of variation as assessed by the components of variation viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (H) and GA over mean for the Al related and morphological traits are presented in Table 1. GCV measures the variability of any trait. Extent of the environmental influence on any trait is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation. Large differences are due to high environmental influence, while small differences reveal high genetic influence. The PCV for traits viz., plant height, panicle weight/plant, straw weight, panicle length, ear bearing tillers, number of healthy grain, number of chaffy grain, spikelet fertility, test weight and relative difference for root length was high (>20 %) but medium for relative difference for root dry weight (19.48) and days to 50 % flowering (10.40). For days to maturity, the value was found low (<9 %). High PCV for plant height, ear bearing tillers, panicle length, test weight and number of panicles per

plant were also observed by Dutta et al. [18] which are in agreement to these findings. Phenotypic coefficients of variation were slightly higher than the genotypic coefficients of variation for all the traits studied. This indicated the presence of environmental influence to some degree in the phenotypic expression of the characters as observed by Akinwale et al. [19]. The broad sense heritability is the relative magnitude of genotypic and phenotypic variances for the traits and it plays a great role in selection procedures. This gives an idea of the total exploitable portion of variation. Higher heritability estimates in broad sense (h^2_b) (>60 %) were exhibited by all the traits except for relative difference in root length and root dry weight. Since these traits were derived from actual measurements so, the value was found to be low. Similar results for agro-morphological traits had been reported by Sarawgi et al. [20]. This can also be reflected in low value of GA over mean. Since high heritability does not always indicate high genetic gain, heritability with GA considered together should be used in predicting the ultimate effect for selecting superior varieties as high heritability values followed by high GA showed the presence of additive gene action [14, 21, 22]. High to moderate value of GA over mean was found for agro-morphological traits except for days to 50 % flowering (19.19) and days to maturity (14.18).

Character Association and Path Coefficient Analysis

Determination of correlation coefficients between various characters helps to obtain the best combinations of

Table 2 Correlations for agronomic and AI related traits in rice genotypes

	DM	PH	PWPP	SW	PL	EBT	NHG	NCG	SF	TW	RDRW	RDRL	SFGW
DFE	PC	0.993***	0.058	-0.069	-0.043	0.231**	-0.067	0.007	0.041	-0.198*	-0.091	0.09	-0.043
	GC	0.997***	0.082	-0.079	-0.040	0.268	-0.064	0.012	0.037	-0.260**	-0.214*	0.140	-0.056
DM	PC	0.057	0.057	-0.083	-0.063	0.232**	-0.07	-0.009	0.018	-0.200**	-0.108	0.071	-0.061
	GC	0.085	0.085	-0.091	-0.055	0.278***	-0.047	0.000	0.004	-0.262**	-0.255**	0.087	-0.070
PH	PC	0.633***	0.494***	0.494***	0.709***	-0.181*	0.688***	0.421***	0.571***	0.248**	0.165*	0.254**	0.686***
	GC	0.636***	0.497***	0.497***	0.730***	-0.231**	0.697***	0.435***	0.588***	0.241**	0.378***	0.584***	0.692***
PWPP	PC	0.872***	0.872***	0.872***	0.565***	0.456***	0.929***	0.600***	0.561***	0.426***	0.02	0.155	0.971***
	GC	0.886***	0.886***	0.886***	0.553***	0.433***	0.926***	0.609***	0.578***	0.443***	0.112	0.414***	0.973***
SW	PC	0.419***	0.419***	0.419***	0.590***	0.590***	0.793***	0.518***	0.375***	0.303***	-0.108	0.105	0.859***
	GC	0.413***	0.413***	0.413***	0.558***	0.558***	0.796***	0.514***	0.388***	0.331***	-0.186	0.307***	0.872***
PL	PC	0.053	0.053	0.053	0.053	0.053	0.658***	0.389***	0.593***	0.370***	0.212*	0.286***	0.631***
	GC	-0.017	-0.017	-0.017	-0.017	-0.017	0.664***	0.439***	0.597***	0.334***	0.565***	0.691***	0.625***
EBT	PC	0.402***	0.402***	0.402***	0.337***	0.337***	0.402***	0.337***	0.068	0.062	-0.134	-0.156	0.402***
	GC	0.370***	0.370***	0.370***	0.290***	0.290***	0.370***	0.290***	0.054	0.062	-0.251**	-0.269**	0.376***
NHG	PC	0.653***	0.653***	0.653***	0.653***	0.653***	0.653***	0.653***	0.622***	0.255**	0.094	0.276***	0.949***
	GC	0.672***	0.672***	0.672***	0.672***	0.672***	0.672***	0.672***	0.645***	0.254**	0.242**	0.677***	0.949***
NCG	PC	-0.027	-0.027	-0.027	-0.027	-0.027	0.658***	0.389***	-0.027	-0.085	0.200*	0.364***	0.551***
	GC	0.003	0.003	0.003	0.003	0.003	0.664***	0.439***	0.003	-0.088	0.356***	0.904***	0.564***
SF	PC	0.458***	0.458***	0.458***	0.458***	0.458***	0.458***	0.458***	0.458***	0.458***	0.101	0.167*	0.622***
	GC	0.427	0.427	0.427	0.427	0.427	0.427	0.427	0.427	0.427	0.319***	0.461***	0.644***
TW	PC	-0.095	-0.095	-0.095	-0.095	-0.095	0.658***	0.389***	-0.095	-0.095	-0.095	-0.068	0.405***
	GC	-0.070	-0.070	-0.070	-0.070	-0.070	0.664***	0.439***	-0.070	-0.070	-0.070	-0.107	0.417***
RDRW	PC	0.409***	0.409***	0.409***	0.409***	0.409***	0.409***	0.409***	0.409***	0.409***	0.409***	0.409***	0.047
	GC	0.163	0.163	0.163	0.163	0.163	0.409***	0.163	0.163	0.163	0.163	0.163	0.163
RDRL	PC	0.174*	0.174*	0.174*	0.174*	0.174*	0.174*	0.174*	0.174*	0.174*	0.174*	0.174*	0.174*
	GC	0.439***	0.439***	0.439***	0.439***	0.439***	0.439***	0.439***	0.439***	0.439***	0.439***	0.439***	0.439***
Significance levels		0.05	0.01	0.001									
If correlation r =>		0.164	0.214	0.271									

PC phenotypic correlation, GC genotypic correlation, DFF days to fifty percent flowering, DM days to maturity, PH plant height, PWPP panicle weight/plant, SW straw weight, PL panicle length, EBT ear bearing tillers, NHG no of healthy grain, NCG no of chaffy grain, NCG no of chaffy grain, SF spikelet fertility, TW test wt, RDRL relative difference for root length, RDRW relative difference for root dry weight, SFGW single plant grain weight

*** and ** means Significance level at 0.05%, 0.01% and 0.001% respectively

Table 3 Path Matrix of yield per plant in rice genotypes for agronomic and Al related traits

PATH matrix of SPGW													
DFE	DM	PH	PWPP	SW	PL	EBT	NHG	NCG	SF	TW	RDRW	RDLR	SPGW
DFE	0.1449	0.1438	0.0084	-0.0100	-0.0062	0.0335	-0.0097	0.0009	0.0059	-0.0287	-0.0131	0.0130	-0.0433
DM	-0.1587	-0.1599	-0.0092	0.0132	0.0101	-0.0371	0.0111	0.0014	-0.0028	0.0320	0.0173	-0.0113	-0.0606
PH	0.0015	0.0015	0.0255	0.0161	0.0126	0.0181	-0.0046	0.0175	0.0146	0.0063	0.0042	0.0065	0.6864
PWPP	-0.0359	-0.0430	0.3296	0.5211	0.4543	0.2942	0.2373	0.4839	0.2921	0.2219	0.0104	0.0806	0.9706
SW	-0.0054	-0.0080	0.0623	0.1101	0.1262	0.0529	0.0745	0.1000	0.0473	0.0382	-0.0137	0.0133	0.8589
PL	0.0134	0.0134	0.0411	0.0327	0.0243	0.0579	0.0031	0.0381	0.0343	0.0214	0.0123	0.0166	0.6311
EBT	0.0027	0.0028	0.0074	-0.0185	-0.0240	-0.0022	-0.0407	-0.0164	-0.0028	-0.0025	0.0054	0.0063	0.4023
NHG	0.0028	-0.0038	0.2976	0.4020	0.3431	0.2848	0.1741	0.4329	0.2692	0.1104	0.0408	0.1196	0.9490
NCG	0.0012	0.0011	-0.0522	-0.0744	-0.0642	-0.0482	-0.0418	-0.0809	0.0034	0.0105	-0.0248	-0.0451	0.5513
SF	-0.0018	-0.0008	-0.0254	-0.0249	-0.0167	-0.0263	-0.0030	-0.0276	-0.0444	-0.0203	-0.0045	-0.0074	0.6222
TW	-0.0032	-0.0033	0.0040	0.0069	0.0049	0.0060	0.0010	0.0042	0.0075	0.0163	-0.0016	-0.0011	0.4051
RDRW	-0.0022	-0.0027	0.0041	0.0005	-0.0027	0.0052	-0.0033	0.0023	0.0025	-0.0023	0.0247	0.0101	0.0465
RDLR	-0.0024	-0.0019	-0.0069	-0.0042	-0.0028	-0.0077	0.0042	-0.0075	-0.0045	0.0018	-0.0111	-0.0270	0.1740
SPGW	-0.0063	0.0097	0.0175	0.5058	0.1084	0.0366	-0.0164	0.4108	-0.0277	0.0066	0.0011	-0.0047	

R square = 0.9732 residual effect = 0.1638

DFE days to fifty percent flowering, DM days to maturity, PH plant height, PWPP panicle weight/plant, SW straw weight, PL panicle length, EBT ear bearing tillers, NHG no of healthy grain, NCG no. of chaffy grain, SF spikelet fertility, TW test wt, RDLR relative difference for root length, RDRW relative difference for root dry weight, SPGW single plant grain weigh

Table 4 Principal component analysis for agro morphological and AI related traits in rice genotypes

Eigenvectors	Prin1	Prin2	Prin3	Prin4	Prin5
DFE	-0.001	0.605	0.299	-0.037	0.11
DM	-0.007	0.605	0.305	-0.039	0.084
PH	0.312	0.159	-0.237	-0.133	-0.469
PWPP	0.395	-0.097	0.101	0.019	-0.027
SW	0.348	-0.13	0.248	0.095	-0.016
PL	0.307	0.243	-0.142	-0.155	0.037
EBT	0.157	-0.234	0.467	0.253	0.509
NHG	0.399	0.004	0.033	0.085	-0.039
NCG	0.256	0.025	0.005	0.523	-0.256
SF	0.273	0.064	-0.141	-0.413	0.281
TW	0.172	-0.184	-0.053	-0.51	0.239
RDRW	0.048	0.097	-0.516	0.272	0.508
RDRL	0.118	0.225	-0.396	0.311	0.194
SPGW	0.402	-0.06	0.063	-0.02	-0.032
Loadings					
Eigenvalue	5.821	2.233	1.739	1.568	0.751
Difference	3.588	0.495	0.171	0.817	0.161
Proportion	0.416	0.16	0.124	0.112	0.054
Cumulative	0.416	0.575	0.7	0.812	0.865

DFE days to fifty percent flowering, DM days to maturity, PH plant height, PWPP panicle weight/plant, SW straw weight, PL panicle length, EBT ear bearing tillers, NHG no of healthy grain, NCG no of chaffy grain, F spikelet fertility, TW test wt, RDRL relative difference for root length, RDRW relative difference for root dry weight, SPGW single plant grain weight

attributes in crop for obtaining higher return per unit area. Correlations between traits viz., AI related root and biomass traits and morphological traits were calculated and are presented in Table 2. Among field traits, days to 50 % flowering and days to maturity have shown negative correlation with single plant grain weight. Except these two, all other traits have shown significant association with single plant grain weight. In AI related variables, relative difference for root dry weight was not significantly correlated with single plant grain weight. Significant correlation was also found between different yield contributing traits showing that all these traits collectively contribute to grain yield. Significant association of grain yield with plant height, panicle length, panicle weight and test weight were also observed by other researchers [23]. Same trend of correlations were also found in Bangladesh and Sudanese upland rice genotypes for agronomic traits [24, 25].

Path-coefficient analysis is used to partition the correlation coefficients to find out the direct and indirect effects of yield contributing traits towards grain yield and hence effectively used in identifying useful traits as

selection criteria to improve per plant yield in rice [23]. In the present study, thirteen predictor variables were used to describe the response variable single plant grain yield (Table 3). Among the predictor variables, two were AI related variables viz., relative difference for root length and root dry weight and eleven were agronomic variables viz., days to 50 % flowering, days to maturity, plant height, panicle weight/plant, straw weight, panicle length, ear bearing tillers, number of healthy grain, number of chaffy grain, spikelet fertility and test weight. Panicle weight/plant exhibited maximum direct effect (0.521) followed by number of healthy grain (0.433). Days to maturity (-0.160), ear bearing tillers (-0.041), number of chaffy grain (-0.124), spikelet fertility (-0.045) and relative difference for root length (-0.027) have shown negative direct effect. Number of healthy grain has shown highest indirect effect (0.484) through panicle weight/plant followed by straw weight through panicle weight/plant (0.454). Panicle weight/plant has also the highest correlation with single plant grain yield (0.971) which proves its importance [1]. The residual effect was 0.1638 indicating that contribution of component traits on grain yield per plant was 83.62 % by the thirteen traits studied in path analysis; the rest 16.38 % was contribution of other factors such as traits not studied. In agreement to the present findings the highest direct positive effect of panicle weight to grain yield was also observed by Cyprien and Kumar [26]. On the other hand, negative direct effect on grain yield was also recorded by number of chaffy grains per panicle, spikelet fertility, days to maturity and plant height in other studies [27].

Genetic Divergence Studies

A large number of variables are often measured by plant breeders, some of which may not be of sufficient discriminatory power for germplasm evaluation, characterization, and management. Two methods, namely the unweighted pair group method of average linkage (UP-GMA) and principal component (PCA) were advocated to classify the accessions into groups (clusters) [28]. PCA was considered as powerful technique for data reduction which removes interrelationships among components [29]. PCA of the morphological characters yielded three principal components with eigenvalues >1 accounting for 70 % of the total variance observed (Table 4). Breakdown of this cumulative variance value revealed contributions of 41.6, 16.0 and 12.4 % for PC 1, PC 2 and PC 3, respectively. The first principal component was correlated with single plant grain weight, number of healthy grain, panicle weight/plant, straw weight and panicle length, while days to 50 %

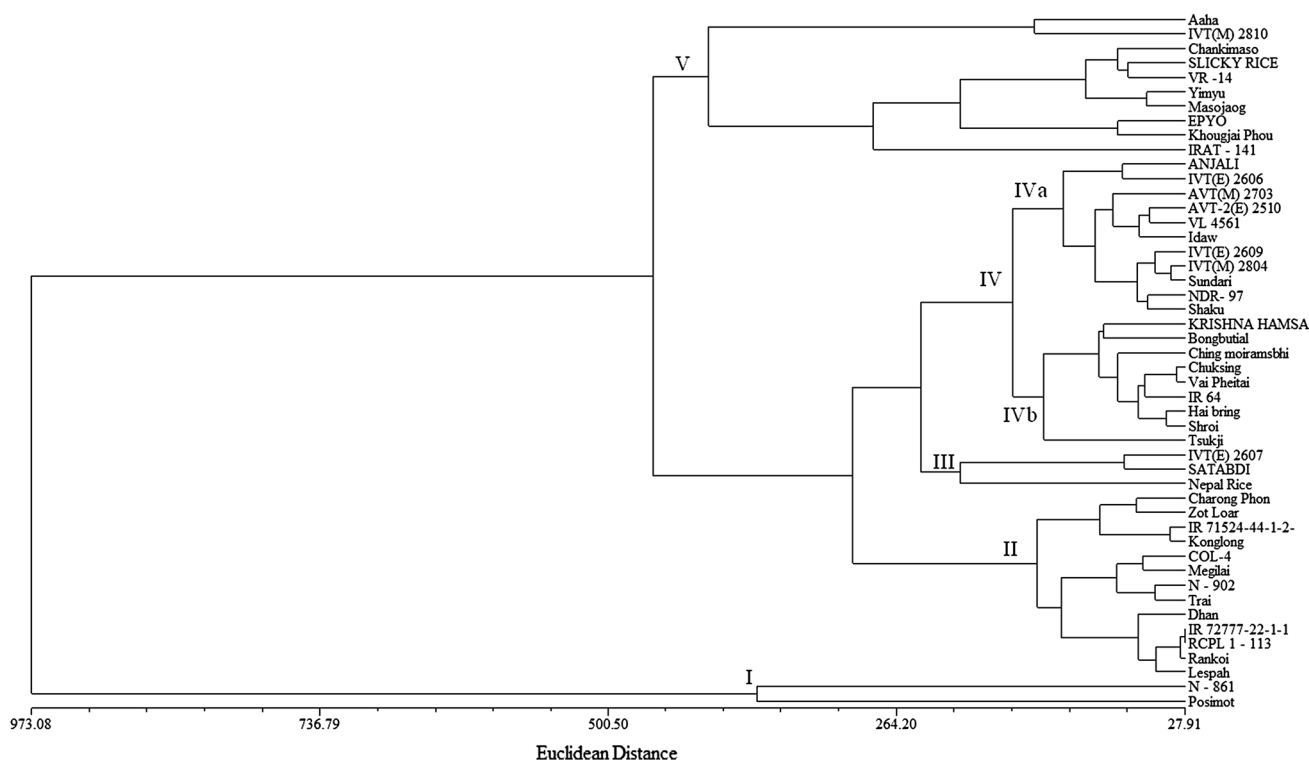


Fig. 3 A cluster analysis of paddy genotypes based on field and Al related traits

flowering and days to maturity have more weighting in principal component axis II.

Cluster diagram using Ward's method based on agro-morphological traits of forty eight rice genotypes proposed five clusters (Fig. 3). The cluster IV was the largest cluster having nineteen genotypes (39.59 %) which can further be divided into two sub-clusters, IVa (16.67 %) and IVb (22.92 %). Cluster I comprised of two genotypes, which represented 4.17 % of the total genotypes. It has been observed that the mean value of yield and its component traits was highest in cluster I (Table 5) followed by cluster V which comprised of ten genotypes (20.83 %). Cluster II and III represent 27.08 and 6.25 % of the total genotypes respectively. Cluster I was also the early maturing group and thus the most useful cluster. Genotypes in cluster II were short to intermediate in plant length and with medium panicle length but having low yield. The yield for genotypes in cluster III was very low and this cluster seemed to be susceptible for Al toxicity. Genotypes in cluster IVa were intermediate in plant length showing very late maturity and with low yield. Cluster IVb consists of dwarf genotypes with short panicle and low yield. Genotypes in cluster V were tall, late maturing and with a good yield performance. Some genotypes such as Charong Phon, IR 71524-44-1-2-8, Trai (cluster II), Ching Moiramsbhi, Sundari, shaku, Anjali

(cluster IV), Aaha, IVT(M)2810, Maojaog, IRAT-141 (cluster V) found good regarding the Al related traits. These genotypes may be useful in future crop improvement programme. Cluster I consists of two genotypes N-861 and Posimot, both being tall, tolerant to Al toxicity and having good yield. Based on their distance, a hybridization programme needs to be initiated to develop a superior line by selection among segregating generations or mapping population for further QTL related studies.

Conclusion

The yield and component traits under study have shown higher heritability, high to moderate value of GA over mean with significant association for all traits with single plant grain weight. The PCA in general confirmed the groupings obtained through cluster analysis. Majority of genotypes have shown decreased root growth in the presence of Al, except Posimot, Epyo, Aaha and VR-14. For agro-morphological and yield related traits, N-861, Khougjai Phou, Posimot and Epyo were found promising. Based on above findings the authors were able to assess the variability present among rice genotypes and identified responsive genotypes both for tolerance to Al toxicity as

Table 5 Comparison of clusters for agronomic and Al related traits

Cluster	I			II			III			IVa			IVb			IV			V		
	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max
DFE	104.50	96.00	113.00	112.90	101.67	127.00	112.56	81.00	129.00	107.88	116.37	111.70	111.70	96.00	131.33	112.80	98.00	129.00	112.80	98.00	129.00
DM	136.00	127.00	145.00	144.51	132.33	157.67	145.33	116.00	160.00	139.09	148.22	143.20	143.20	126.00	163.00	143.67	131.00	160.00	143.67	131.00	160.00
PH	126.50	126.00	127.00	99.05	77.67	119.67	75.11	54.00	101.33	62.91	97.26	78.37	78.37	46.33	91.33	108.50	71.00	135.00	108.50	71.00	135.00
PWPP	32.00	24.00	40.00	11.64	7.00	15.00	3.11	2.67	4.00	5.03	7.70	6.23	6.23	1.67	11.00	16.30	12.33	26.00	16.30	12.33	26.00
SW	61.00	41.00	81.00	21.74	13.33	35.00	10.78	8.67	12.67	10.85	15.78	13.07	13.07	3.33	15.00	29.07	16.00	58.67	29.07	16.00	58.67
PL	24.50	22.00	27.00	20.54	12.67	25.67	15.89	12.00	21.00	14.94	19.78	17.12	17.12	10.00	18.33	22.67	14.33	27.33	22.67	14.33	27.33
EBT	11.50	8.00	15.00	6.95	4.67	11.00	6.44	5.67	7.33	6.12	5.96	6.05	6.05	2.33	12.67	8.27	3.00	14.00	8.27	3.00	14.00
NHG	1,144.00	1,098.00	1,190.00	449.92	371.00	560.33	95.33	36.00	187.00	153.06	269.93	205.65	205.65	66.33	228.67	673.63	421.00	876.00	673.63	421.00	876.00
NCG	782.00	602.00	962.00	272.69	173.00	372.00	324.78	275.00	422.00	118.39	199.59	154.93	154.93	35.33	187.67	350.67	214.67	644.33	350.67	214.67	644.33
SF	25.50	19.00	32.00	9.44	7.00	12.67	1.56	1.00	2.33	3.58	6.33	4.82	4.82	1.67	6.67	13.77	9.00	21.67	13.77	9.00	21.67
TW	62.50	57.00	68.00	57.51	44.00	74.00	20.67	12.00	31.00	47.85	57.74	52.30	52.30	32.67	60.00	65.67	45.00	76.33	65.67	45.00	76.33
RDRW	22.00	17.00	27.00	20.33	14.67	25.00	13.33	10.33	17.67	18.67	19.89	19.22	19.22	10.67	26.00	19.67	10.00	26.00	19.67	10.00	26.00
RDRL	89.67	77.33	102.00	85.33	44.33	127.33	68.00	61.33	75.00	88.21	89.11	88.62	88.62	66.00	114.67	91.27	62.67	122.00	91.27	62.67	122.00
SPGW	74.83	53.67	96.00	62.18	33.67	73.00	54.78	36.33	65.33	61.06	60.41	60.77	60.77	40.67	76.67	65.70	44.00	86.33	65.70	44.00	86.33

DEF days to fifty percent flowering, DM days to maturity, PH plant height, PWPP panicle weight/plant, SW straw weight, PL panicle length, EBT ear bearing tillers, NHG no of healthy grain, NCG no of chaffy grain, SF spikelet fertility, TW test wt, RDRL relative difference for root length, RDRW relative difference for root dry weight, SPCGW single plant grain weight

well as yield related traits, which provide enough scope for further breeding work.

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