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GENETIC VARIABILITY AND DIVERSITY ANALYSIS OF RICE FOR YIELD CHARACTERISTICS ACROSS SUBMERGENCE STRESS AND NORMAL CONDITION

Prajwal Pradhan¹, Bimal Das², Deepak Kumar², Bandan Thapa^{4*}, Soumendra Chakraborty¹,
Suwendu Kumar Roy¹, Lakshmi Hijam¹ and Avijit Kundu³

¹Department of Genetics and Plant Breeding, Uttar Banga Krishi Viswavidyalaya, Pundibari-736 165, Coochbehar, West Bengal, India.

²College of Agriculture (Extended campus), Uttar Banga Krishi Viswavidyalaya, Majhian-733 133, Dakshin Dinajpur, W. B., India.

³Regional Research Station, Uttar Banga Krishi Viswavidyalaya, Pundibari - 736 165, Coochbehar, West Bengal, India.

⁴Regional Research Station, Hill Zone, Uttar Banga Krishi Viswavidyalaya, Kalimpong - 734 301, West Bengal, India.

*Corresponding author E-mail : bandhan.thapa@gmail.com

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ABSTRACT

The experiment were based on forty five rice genotypes in a randomized complete block design with three replicates (2021-2022) across submergence and normal condition to estimate genetic diversity. Significant variable responses were found among the twelve agro-morphological and yield traits. A slight variation between PCV and GCV was found. Traits such as grain yield plant⁻¹, grain yield, flag leaf length, test weight and plant height showed high heritability coupled with high genetic advance as per cent of mean suggesting that selection for the improvement of these traits may be rewarding. Following Mahalonobis D² analysis, forty five rice genotypes were grouped into ten clusters in both conditions. Important traits contributed to maximum divergence were flag leaf length, test weight and plant height found to be important consideration to select parent. Among the genotypes studies SS-1, Kamini, Hinchekalma, Marichbot, Sadakalam could be selected as parent to develop high yielding submergence tolerant cultivar.

Key words : Genetic diversity, Heritability, Rice, Submergence stress, Yield.

Introduction

Rice is one of the most important cereal crop and widely grown staple food crop for more than half of the world population. Maximum production as well as consumption of rice occupied in Asian country and India being the second most producers in the world. Rice plant can withstand in diverse ecosystem varying from foot hill to high altitude, deep water to submerged situation. Rice production is affected by different biotic and abiotic stresses, among which submergence has been considered as the 3rd most important constraint for decrease in rice productivity (Sarkar and Bhattacharjee, 2011). In flash flood-prone rice growing environment submergence stress usually persists for a week to months and considered as one of the most important factor for crop failure (Septiningsih and Mackill, 2018). Submergence due to

flash floods mainly affects the rain-fed lowlands which can acts as a fragile ecosystem. Submergence stress leads to anoxia condition, loss of oxygen for the plants, resulting in impaired respiration and physiological metabolism. Rice seedlings can withstand anaerobiosis for certain duration (Banerjee and Roychoudhury, 2019; Banerjee *et al.*, 2018). Eventhough, the rice crop can withstand anoxia condition, excessive or prolonged flooding leads to partial or complete submergence of the seedlings. Submergence stress initially affects the growth and development of the plant and later results in yield loss. Being complex and polygenic trait, seed yield is affected by many of its component characters (Renukadevi and Subbalakshmi, 2006). In rice different factor responsible for submergence tolerance include genotype and environment (Prasanna and Ramarao,

2014), different phenotypic characteristic and major QTL Sub1A (Xu *et al.*, 2006; Khasna *et al.*, 2020; Septiningsih *et al.*, 2009). Selection of ideal genotypes under stress environment is vital for development of high yielding stress tolerant variety. Evaluation of genetic variability along with diversity present in base population is the important requirement for successful breeding approaches (Jasim *et al.*, 2018). In this regards, estimation of genetic diversity could be useful to identify the parents possessing high variability as well as adaptability of crop plants to varied environments with special reference to changing climatic conditions and helps to develop varieties related to submergence stress tolerant. Multivariate analysis specifically cluster analysis with Euclidean distance is a valuable statistical approach for determining the genetic diversity of germplasm collections (Tiwari *et al.*, 2022). Previously, many researchers had successfully used morph-physiological traits to classify and estimate genetic diversity in rice germplasm using multivariate analyses (Nachimuthu *et al.*, 2014). Therefore, present investigation was carried out to understand the genetic variability and diversity analysis for genetic improvement of rice for submergence tolerance.

Table 1 : Description of genotypes under investigation.

Genotype code	GenotypeName	ICNo	Source	Variety status/ Remarks
G1	BhashaManik		Fulia, Nadia	Landraces
G2	Hinchekalma		CRRS, Hooghly	Pure line
G3	Sadamota	IC399078	Fulia, Nadia	Landraces
G4	Kalomocaha		Tapan, DakshinDinajpur	Landraces
G5	Jaldubi		Fulia, Nadia	Landraces
G6	Indurshal	IC646599	Fulia, Nadia	Landraces
G7	TilakKachari		Tapan, DakshinDinajpur	Landraces
G8	Patikalam		Fulia, Nadia	Landraces
G9	Sadakalam		Fulia, Nadia	Landraces
G10	Maguri		Fulia, Nadia	Landraces
G11	Pateni	IC277313	Fulia, Nadia	Landraces
G12	Narkel Chari		Fulia, Nadia	Landraces
G13	Chamarmoni		Tapan, DakshinDinajpur	Landraces
G14	Majuli		Fulia, Nadia	Landraces
G15	Phulpagli		Fulia, Nadia	Landraces
G16	Khara		Tapan, DakshinDinajpur	Landraces
G17	DesiMansuri	IC597679	Fulia, Nadia	Pure line
G18	Narayan Kamini		Fulia, Nadia	Landraces
G19	Talmuli		Fulia, Nadia	Pure line
G20	Magurshal	IC597675	Fulia, Nadia	Landraces
G21	Kamini	IC594030	Raiganj, Uttar Dianjpur	Landraces
G22	Talmugur	IC594020	Raiganj, Uttar Dianjpur	Landraces
G23	Putikhali		Fulia, Nadia	Landraces

Table 1 continued...

Materials and Methods

Location

The experiments was conducted in two condition i.e. submerged stress condition and normal condition during *Kharif* seasons of 2021 and 2022 at Instructional Farm, Regional Research Station (Old Alluvial Zone), UBKV, in the district Dakshin Dinajpur, West Bengal, India with the latitude 25°19' N and longitude 88°46' E. Soil type was sandy loam with a pH of 5.6 of the experimental field.

Experimental Materials and Planting procedure of genotype

In this experiment, forty five rice genotypes were evaluated for estimation of genetic diversity (Table 1). Nursery beds prepared in which each genotype seedlings were nurtured. By maintaining the spacing at 20 cm × 20 cm (row to row and plant to plant), 25 days old 2-3 seedlings were transplanted in 2 m² plots for each genotype following randomized complete block design with three replications. Under submergence stress environment, stress was created by maintaining 1m stagnant water level for 14 days level at vegetative growth

Table 1 continued...

G24	Marichbot		Fulia, Nadia	Landraces
G25	Nagra	IC399080	Fulia, Nadia	Landraces
G26	Hogla		Fulia, Nadia	Released variety
G27	Hanseswari	IC261546	Fulia, Nadia	Released variety
G28	CR Dhan -500		Fulia, Nadia	Released variety
G29	Bhudev		Fulia, Nadia	Released variety
G30	Sabitri		CRRS, Hooghly	Released variety
G31	SS-1		CRRS, Hooghly	Released variety
G32	Sashi		CRRS, Hooghly	Released variety
G33	Samba Masuri sub -1		CRRS, Hooghly	Released variety
G34	Bhagirathi		Tapan, DakshinDinajpur	Released variety
G35	Golok		Raiganj, Uttar Dianjpur	Released variety
G36	Bipasha		Tapan, DakshinDinajpur	Released variety
G37	Sabita	IC261556	Fulia, Nadia	Released variety
G38	Biraj		Tapan, DakshinDinajpur	Released variety
G39	Sujala		Fulia, Nadia	Released variety
G40	Puspa		Majhian, DakshinDinajpur	Released variety
G41	Rani Dhan		Majhian, DakshinDinajpur	Released variety
G42	Dinesh		CRRS, Hooghly	Released variety
G43	Pratiksha		CRRS, Hooghly	Released variety
G44	Dhiren		CRRS, Hooghly	Released variety
G45	Ranjit	-	CRRS, Hooghly	Released variety

(30 days after transplanting) of plants. Whereas, evaluation of genotypes under normal condition was provided with irrigation as required basis and well management practises. Chemical fertilizer (NPK) was applied at 40:30:30 kg ha⁻¹ and necessary intercultural operation occurred in both the environmental condition.

Agro-morphological traits

Ten randomly selected plants were taken for observations in each replication for both submerged stress condition and normal field condition. Observation were recorded for different agro morphological traits such as days to 50% flowering (DF), Days to maturity (DM), Flag leaf length (FLL), Plant height (PH), Tiller per plant (TPP), Panicle number plant (PNPP), Panicle length (PL), Test weight (TW), Number of grain per panicle (NGP), Grain length/ breadth ratio (LBR), Grain yield per plant (GYPP) and Grain yield/ha (GY) were recorded.

Statistical analysis

The observed pooled mean data over the years was used to determine genetic variability parameter such as genotypic and phenotypic variance, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (H%), genetic advance (GA) and genetic advance % of mean (GAM) for both submerged

stress condition and normal field condition by using R software. From the pooled data in both conditions the genetic divergence among the genotypes was estimated by using Mahalanobis D² statistics (Mahalanobis, 1936); and intercluster and intracluster generalized distances (D²) were measured where forty five genotypes are classified in different clusters.

Results and Discussion

Genetic variability of yield traits of different genotypes in submergence stress and normal condition

Genetic variability of yield and yield component traits among forty five rice genotypes over two years (pooled) replicated data in both submergence stress and normal condition were presented in Tables 2a and 2b. In both the situation it was revealed that a wide range and significant variance were recorded for most of the traits under observation. The maximum GV and PV in both the condition were found in NGPP, PH, FLL and DM. The magnitude of PCV was marginally higher than GCV for all the traits and it suggested that there is influence of environment on phenotypic expression of each traits (Adhikari *et al.*, 2018). The traits showing maximum difference between GCV and PCV in both submergence stress and normal condition were PNPP and TPP. Traits

Table 2a : Genetic variability of yield traits of different genotypes in submergence condition.

Characters	Range	General mean	GV	PV	EV	GCV	PCV	h ² (%)	GA	GA (% of mean)
FF	117.17-132	124.58	18.83	17.26	1.57	3.33	3.48	91.69	8.20	6.57
FLL	40.33-92.55	66.44	151.08	149.27	1.82	20.21	20.33	98.80	25.02	41.38
DM	153.33-179.5	166.41	54.24	45.78	8.47	4.05	4.40	84.39	12.80	7.66
PH	116.86-254.51	185.68	1146.28	1112.04	34.24	17.36	17.62	97.01	67.66	35.22
TPP	8.75-15.67	12.21	3.58	2.86	0.72	13.99	15.65	79.89	3.11	25.76
PNPP	7.08-13.58	10.33	3.55	2.72	0.83	16.53	18.88	76.68	2.98	29.81
PL	16.03-26.6	21.31	3.72	3.13	0.59	8.86	9.65	84.19	3.35	16.74
TW	14.13-31.67	22.9	14.45	14.07	0.38	17.87	18.11	97.35	7.62	36.33
NGPP	63.87-169.23	116.55	756.36	669.44	86.92	22.83	24.27	88.51	50.14	44.25
LBR	2.37-4.68	3.52	0.184	0.219	0.036	13.51	13.84	95.33	0.95	27.18
GYPP	3.78-29.08	16.43	25.40	23.99	1.41	43.36	44.62	94.44	9.80	86.82
GY	0.786-3.753	2.269	0.47	0.42	0.05	30.35	31.99	90.00	1.27	59.31

Table 2b : Genetic variability of yield traits of different genotypes in normal condition.

Characters	Range	General mean	GV	PV	EV	GCV	PCV	h ² (%)	GA	GA (% of mean)
FF	113.67-129.83	121.74	19.47	20.42	0.95	3.85	3.96	94.72	9.46	7.72
FLL	37.98-90.2	64.09	148.40	150.17	1.77	20.85	20.97	98.84	24.89	42.70
DM	146.83-173	159.91	45.78	54.24	8.47	4.21	4.58	84.39	12.80	7.97
PH	102.6-220.4	161.5	891.39	915.98	24.58	16.81	17.07	97.03	55.51	34.12
TPP	9.5-20.83	15.16	4.62	5.21	0.59	19.50	20.47	90.72	5.40	38.26
PNPP	8.58-18.42	13.5	3.87	4.34	0.46	19.69	20.67	90.80	4.96	38.65
PL	16.97-26.51	21.74	3.37	3.60	0.24	9.55	9.84	94.22	3.86	19.10
TW	15-32.56	23.78	14.51	14.93	0.41	17.71	18.04	96.38	7.84	35.82
NGPP	78.3-256.92	167.61	1014.92	1048.64	33.72	27.27	27.50	98.34	80.13	55.70
LBR	2.37-4.55	3.46	0.184	0.219	0.036	12.34	13.49	83.64	0.80	23.25
GYPP	5.55-38.61	22.08	27.93	28.80	0.87	37.28	37.85	97.02	11.63	75.66
GY	1.431-4.322	2.87	0.40	0.43	0.03	22.59	23.19	94.89	1.30	45.33

like GY and GYPP showed maximum variation between GCV and PCV in submergence stress condition which indicates the high influence of environment in expression of trait. In submergence stress condition, maximum value for both GCV and PCV was recorded in GYPP (43.36 and 44.62) followed by GY (30.35 and 31.99), NGPP (22.83 and 24.27) and FLL (20.21 and 20.33); whereas in normal condition, maximum value for both GCV and PCV was recorded in GYPP (37.28 and 37.85) followed by NGPP (27.27 and 27.50), GY (22.59 and 23.19) and FLL (20.85 and 20.97). In both the condition the minimum value for both GCV and PCV was recorded in the traits like FF and DM, which indicates very low amount of genetic variability among these traits (Tables 2a and 2b). In submergence stress condition broad sense heritability were high (>80%) for all the traits observed except PNPP(76.68) and TPP(79.89); whereas in normal condition broad sense heritability were high (>80%) for

all the characters studied. The success of a crop improvement program depends on the wide genetic variability and high heritability of the traits (Shrestha *et al.*, 2022). High genetic advance as % of mean (GAM) was observed for GYPP (86.82) followed by GY (59.31), NGPP (44.25) and FLL (41.38) in submergence stress and it was maximum for GYPP (75.66), NGPP (55.70) and GY (45.33) in normal condition. GAM was minimum for FF and DM in both environments. The assessment of genetic variability among the morphological and yield component traits considered first step for plant breeding programme (Wang *et al.*, 2020) in stress and normal environment. In this study, all the traits were slightly influenced by environmental factors which suggested selection would be rewarding for future breeding programs (Rahman *et al.*, 2014; Hasan-Ud-Daula and Sarker, 2020; Debsharma *et al.*, 2023). In submergence stress condition maximum variability responses was recorded

Table 3a : Clustering of 45 rice genotypes in stress condition.

Cluster No.	Genotype numbers in cluster	Names of Genotypes
I	24	Sujala, Puspa, Sabitri, Dhiren, Indurshal, Phulpagli, Talmugur, Bhudev, Pateni, Pratiksha, Desimansuri, Sashi, BhashaManik, Samba Masuri Sub -1, Kalomocaha, Bipasha, Patikalam, Dinesh, TilakKachari, Ranidhan , Bhagirathi, Sadamota, Majuli, Narayan Kamini.
II	2	Marichbot, Sadakalam
III	5	Biraj, Jaldubi, Talmuli, Magarshal,Ranjit
IV	5	Chamarmoni, Khara, Nagra, Narkel Chari, CR-dhan-500
V	2	Hogla, Sabita
VI	3	Maguri, Golok, Putikhali
VII	1	SS-1
VIII	1	Hanseswari
IX	1	Kamini
X	1	Hincheckalma

Table 3b : Clustering of 45 rice genotypes in non-stress condition.

Cluster No.	Genotype numbers in cluster	Names of Genotypes
I	20	Sujala, Puspa, Phulpagli, Sabitri, Indurshal, Sashi, Pratiksha, TilakKachari, Dhiren, Bipasha, Bhudev, Talmugur, Pateni, SS-1, Samba Masuri Sub -1, DesiMansuri, Rani Dhan, Marichbot, Sadakalam, Dinesh.
II	11	Bhagirathi, Biraj, Sabita, Ranjit, Magarshal, Sadamota, Talmuli, Majuli, Patikalam, Jaldubi, Narayan Kamini.
III	6	BhashaManik, CR Dhan -500, Narkel Chari, Nagra, Chamarmoni, Maguri.
IV	1	Kamini
V	2	Golok, Putikhali
VI	1	Khara
VII	1	Hogla
VIII	1	Kalomocaha
IX	1	Hanseswari
X	1	Hincheckalma

from GYPP, GY, NGPP, FLL and these traits could be useful for selection parents in stress environment. Heritability and genetic advances are the important genetic parameters for selection approaches (Sarker *et al.*, 2016) and this study reveals that traits like GYPP, GY, FLL and TW have high heritability and GA, suggesting that these traits are controlled by additive genes with minor environmental influence.

Estimation of genetic diversity for yield component traits under submergence stress and normal environment

Grouping of genotypes in different cluster is based on Mahalanobis D² analysis of yield and yield component

traits among forty five rice genotypes in both submergence stress and normal condition were presented in Tables 3a and 3b. In both the situation forty five genotypes were grouped into ten different clusters. Under submergence stress condition, maximum number of genotypes were grouped in cluster I (24 genotypes) followed by cluster III, IV (5 genotypes each) and Cluster VI (3 genotypes). Cluster VII, VIII, IX and X are mono genotypic having only one genotype each cluster. Whereas in normal condition, the maximum number of genotypes are grouped in cluster I (20 genotypes) followed by cluster II (11 genotypes), Cluster III (6 genotypes) and Cluster IV, VI, VII, VIII, IX and X are mono genotypic. Cluster having a single genotype shows high degree of divergence as

Table 4a : Inter and Intra cluster (Diagonal) average distance of 45 rice genotypes in submergence stress condition.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	281.96	425.76	487.36	432.14	748.06	971.43	602.76	723.00	942.7	725.4
II		344.1	778.54	787.12	792.97	1426.72	497.40	653.06	1751.88	550.73
III			282.82	397.68	576.85	456.91	1030.53	634.56	641.93	948.84
IV				224.06	792.02	559.65	1013.88	545.50	495.75	941.67
V					140.67	814.05	710.35	657.78	1520.43	819.34
VI						293.37	1887.63	614.89	562.10	1566.46
VII							0	1388.65	2147.72	435.71
VIII								0	1248.17	1047.59
IX									0	2003.34
X										0

Table 4b : Inter and Intra cluster (Diagonal) average distance of 45 rice genotypes in non stress condition.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	310.92	666.66	921.21	933.57	1518.61	1550.33	967.45	761.42	693.58	1249.06
II		381.36	545.02	462.09	637.67	1112.01	701.22	1089.49	564.97	918.05
III			325.14	621.03	794.58	662.07	1465.91	931.61	678.80	823.48
IV				0	556.79	1368.27	1029.53	1551.48	813.91	1314.49
V					459.47	1413.58	922.35	1889.68	869.44	1444.33
VI						0	2340.86	918.62	1239.36	1253.88
VII							0	1946.62	739.32	1653.03
VIII								0	1117.18	1371.39
IX									0	1379.14
X										0

compared to other genotypes (Chamundeswari, 2016 and Venkatesan *et al.*, 2016).

Intra and inter cluster distance in both the situation were presented Tables 4a and 4b. The highest inter cluster distance was found between cluster VII and IX (2147.72) followed by cluster IX and cluster X (2003.34) in submergence stress and the lowest inter cluster distance was found in cluster III and IV (397.68); whereas in normal condition it was maximum between cluster VI and VII (2340.86) followed by VII and VIII (1946.62) and lowest in between cluster II and IV (462.09). The maximum intercluster distance (between cluster VII and IX) shows wider genetic diversity and these clusters would yield desirable segregants with the accumulation of favourable genes in segregating generations (Devi *et al.*, 2017), whereas minimum intercluster distance (between cluster III and IV) shows that the genotypes closely related each other and hybridizing such genotypes may result lowering heterosis. The greater the distance between two clusters expresses maximum divergence (Singh and Narayanan, 2013). Hence, based on cluster distance for yield traits, it is important to select the genotype *viz.* SS-1, Kamini and Hincchekalmain order to develop the variety with wide variability and submergence

tolerance. These genotypes could be used as parents in future breeding programmes (Amegan *et al.*, 2020; Bekis *et al.*, 2021).

The highest intra cluster distance were recorded in cluster II (344.1) followed by cluster VI (293.37) and cluster III (282.82) in submergence stress and cluster V (459.47) followed by cluster II (381.36) and cluster III (325.14) in normal condition. The genotypes that belong to this particular cluster exhibit the highest intra-cluster distance and can be considered for future breeding programmes, considering they possess a significant level of genetic divergence within the genotypes. The maximum cluster distance between the clusters shows wider genetic diversity between the genotypes (Ahmed *et al.*, 2015). In this study, average inter cluster distance were found higher than average intra cluster distance in both submergence stress and normal condition which reveals that there is wider genetic diversity among the forty five rice genotypes (Debata *et al.*, 2020; Kumari *et al.*, 2015; Subudhi *et al.*, 2009; Mohanty *et al.*, 2010). In respect with cluster mean value, under submergence stresses the results showed that cluster IX has the highest mean value performance for three traits such as DM (176.33), PH (243.27), PL (22.27); cluster VII for PNPP

Table 5a : Cluster mean performance of 45 rice genotypes in stress condition.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	Contribution %
FF	124.77	119.33	123.47	129.10	119.58	130.00	119.67	127.17	128.50	117.83	2.12
FLL	54.55	45.20	73.15	65.50	67.98	85.68	44.36	64.57	78.86	47.17	39.59
DM	166.00	165.17	169.23	172.73	163.67	172.78	158.67	167.00	176.33	154.00	0.30
PH	183.06	177.09	201.46	222.63	141.29	232.50	117.30	235.76	243.27	200.78	14.14
TPP	11.97	11.13	13.30	12.72	13.25	9.78	13.25	9.92	10.58	14.50	0.20
PNPP	9.82	8.42	10.83	11.07	11.63	7.86	12.83	9.00	8.25	10.00	0.20
PL	20.16	19.30	19.55	22.02	17.61	17.47	18.95	20.97	22.27	19.15	0.40
TW	19.79	24.91	20.34	20.45	28.44	23.27	20.48	31.67	14.13	22.72	18.88
NGPP	107.07	90.02	111.58	150.17	90.18	119.41	156.98	101.83	114.79	128.50	2.62
LBR	3.58	4.19	3.80	3.01	3.03	3.34	3.37	3.62	2.70	3.22	11.01
GYPP	9.47	10.96	12.47	13.72	12.06	13.00	17.72	7.31	10.79	29.08	6.86
GY	1.86	2.20	2.31	2.72	2.56	2.38	3.00	1.88	2.47	2.73	3.63

Table 5b : Cluster mean performance of 45 rice genotypes in non-stress condition.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	Contribution %
FF	121.53	121.94	126.78	125.83	127.75	128.50	119.33	115.33	121.83	114.33	3.838
FLL	48.07	66.87	64.53	76.51	85.53	65.53	66.63	50.13	62.22	46.65	28.28
DM	157.43	162.09	165.75	169.83	165.17	164.83	166.00	168.17	160.50	147.50	0.10
PH	147.99	162.84	194.04	196.80	180.08	181.77	123.81	172.97	191.17	179.60	10.50
TPP	13.94	15.02	12.51	11.75	11.94	18.08	18.25	14.50	9.75	20.08	0.50
PNPP	12.77	13.48	11.78	9.82	10.17	16.83	16.58	13.33	8.58	17.17	0
PL	20.27	20.03	20.40	22.21	17.56	26.51	17.22	19.50	21.47	18.70	2.62
TW	20.84	22.24	21.36	15.00	24.85	22.94	31.11	19.32	32.56	24.23	11.01
NGPP	128.82	139.62	182.04	115.58	137.27	256.92	78.30	235.12	128.68	180.20	26.36
LBR	3.54	3.65	3.27	2.75	3.26	3.12	2.99	3.48	3.53	3.26	0.30
GYPP	12.76	17.63	18.54	15.16	16.37	14.02	14.89	5.55	10.66	38.61	15.45
GY	2.58	3.19	3.47	2.63	2.67	2.28	3.15	1.43	3.11	4.16	1.01

DF = 50% flowering (days); DM = Days to maturity (days); FLL = Flag leaf length (cm); PH = Plant height (cm); TPP = Tiller per plant; PNPP = Panicle number plant; PL = Panicle length (cm); TW = Test weight (gm), NGP = Number of grain per panicle; LBR = Grain length/ breadth ratio; SYPP = Seed yield per plant (gm) and GY = grain yield/ha (t ha⁻¹).

(12.83), NGPP (156.98) and GY (3.00); Cluster VI for FF (130.00) and FLL (85.68); Cluster X for TPP (14.50) and GYPP (29.08); Cluster II for LBR (4.19) and Cluster VIII for TW (31.67) (Table 5a). Under normal condition Cluster X has the highest mean value performance for TPP (20.08), PNPP (17.17), GYPP (38.61) and GY (4.16); Cluster VI for FF (128.50), PL (26.51) and NGPP (256.92); Cluster IV for DM (169.83) and PH (196.80); while cluster II, V and IX for LBR (3.65), FLL (85.53) and TW (32.56), respectively (Table 5b). The genotypes belong to diverse clusters and a high cluster mean value of different traits may be directly used for adaptation under submergence stress condition, or inter crossing may be recommended to produce the wide spectrum of variability (Nisar *et al.*, 2017; Bose and Pradhan, 2005;

Sridhar *et al.*, 2016). In submergence stress, the highest contribution towards the divergence was observed for FLL (39.59), followed by TW (18.88), PH (14.14) and LBR (11.01) but the traits like DM, TPP, PNPP and PL show comparatively very less contribution towards the divergence of the cluster. Whereas, under normal condition divergence were maximum for traits like FLL (28.28), followed by NGPP (26.36) and GYPP (15.45). In this regard, the traits (FLL, TW and PH) contributed to maximum divergence could be considered desirable traits to select genotypes under submergence stress environment.

Conclusion

The present study provides the information about the

genetic variability present among the genotype studied under stress environment. This variation present in the population could be used as a great tool for the selection of parents based on the Diversity analysis of different agro-morphological and yield traits for future breeding programme. The wide genetic variability were found among forty five genotypes which were divided into ten clusters in both submergence stress as well as normal condition and shows large variable cluster distance. In submergence stress the highest inter cluster distance was shown between VII and IX (2147.72) and in non stress condition it was shown in cluster VI and VII (2340.86). Hence, genotypes falling in these clusters (SS-1, Kamini and Hinchekalma) can be used in future hybridization programs to develop high yielding as well as submergence tolerant varieties.

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