Genetic divergence studiesof submergence tolerant rice genotypes

Notes: The words with red colour are meaning the words after correction.

Abstract

The present investigation was carried out with24 rice genotypes including both indigenous and exotic collections/varieties/lines under both normal transplanted condition and in submerged condition and observation for various morphophysiological, quantitative and qualitative traits by usingrandomized block design at the Research Farm of 'Tirhut College of Agriculture, Dholi, Dr Rajendra Prasad Central Agricultural University, during *Kharif* season of 2019.All the 24 genotypes grouped into 3 clusters using D^2 statistics.Intra cluster distance was at most in case of Cluster II while highest inter cluster distance was detected between Cluster III and Cluster II. Cluster III contains maximum yield attributing traits so it can be used for hybridization programme of above-mentioned traits.Crop Growth Rate at 30DAS showed maximum contribution towards total divergence while minimum contribution was exhibited by Number of Fertile Spikelet.

Introduction

Rice (*Oryza sativa* L.,2n=24) basically a monocotyledonous, short day angiospermplant which is being placed with genus 'Oryza' of Gramineae (Poaceae) family. It is semi aquatic plant in nature and can be grown over a vast range of water condition like long term flooded area to dry hilly regions. The remarkable diversity of this crop made it adaptable to various condition of climatic factors like temperature, humidity, rainfall etc. There are also less favourable situations for growth and development of rice in case of rainfed upland and rainfed low land. Rice is the staple food considered in more than 100 countries for which it is referred as 'Global Grain'. It provides more than 20% direct calory intake. Particularly in Asia, it is the principal food for them who earns a minimum wage or their family. Green Revolution and lesser price of rice is really a blessing for such people An annual production of 497.6million tonnes (2019-2020) with acreage of 161.1 million hectare is forecasted out of which, only Asia will contribute 90% of total production. (United States Department ofAgriculture,2019). In the year 2018-19 there was production of 60lakh metric tonnes in India with a productivity of 4517kg/ha and for the session 2019-20 it is estimated to produce 114 lakh metric tonnes of rice. As per the ranking China is the largest producer of rice followed by India. If we consider the states of India, Eastern region like Bihar, Odisha, Chhattisgarh, Madhya Pradesh, Uttar Pradesh, West Bengal found to be greater producer of rice. Taking into account the situation of Bihar, it is the fifth largest producer of rice which contribute 7% of total land(3.34million ha) and almost 7% of total production(8.1million tonnes) having a productivity of 24kg/ha, during 2017-2018(Directorate of Economics and Statistics,2017-2018). The essential goal of plant breeding is to assess the variable germplasm. Genetic diversity of course plays a crucial role in breeding programme since the progeny which is obtained from the diversified parent may exhibit higher heterosis and may provide a good variability in the segregated population. Besides this diversity also causes new recombination in a gene pool. Notably a better classification of the genotypes will ultimately help the breeder for identification of best suitable parent with broad genetic diversity from which some of the selected individuals can be used for hybridization programme.

Material and method

The study was carried out at the Research Farm of Tirhut College of Agriculture, Dholi, Dr Rajendra Prasad Central Agricultural University, Bihar. For successful cultivation of crop as well as to complete the experiment, every necessary action was provided by Department of Plant Breeding and Genetics, TCA Dholi, Dr. Rajendra Prasad Central Agricultural University. The experimental material used 24 rice genotypes including both indigenous and exotic collections/varieties/lines planted in both normal transplanted condition and in submerged condition for screening of submergence against flash floods. Out of 24 genotypes 8 are from IRRI,8 are from RPCAU itself.There are 2 check among those lines namely ChehirangSub1(Indonesia) and IR 64 Sub1(IRRI,Philippines).Observation recordedfor Days to 50% Panicle Emergence,Seedling Vigor, Plant height, Leaf Area, No. of Pubescence per Unit Area,No of Effective Tillers per plant,No. of Spikelet per Panicle,No of Fertile Spikelet per Panicle, Days to maturity, Scoring of Submergence Tolerance, Root Length,Root Volume, Crop Growth Rate at 15 DAS, Crop Growth Rate at 30 DAS,1000 seed weight (g), Harvest index (%), Grain yield per plant(g).For scoring of Submergence Tolerance, all the genotypes are sown with three replications and they are completely submerged for 7 days in seedling stage(15DAS). After a week field was drained completely(21DAS) and after 7 days they were scored according to score of “Standard

Evaluation(SES) for Rice”,5th Edition(2013) by IRRI. The twenty four genotypes were assigned into different clusters by Tocher’s method.

Result and discussion

Genetically diverse parents are separated by estimation of genetic divergence. For getting transgressive segregants, hybridization should be done between efficient parents which will result new recombinants in the gene pool. The Mahalanobis D^2 was found to be the best tool for estimating the genetic divergence of 24 rice genotypes. Assemblage of genotypes into diverse clusters provides genetic diversity between the genotypes. That diversity may be resulted due to many factors like history of collection, heterogeneity, selection under unlike environment, and genetic drift. Cluster distance represent though the genotypes lies in the same cluster they also have genetic diversity among themselves. Twenty-four rice germplasms were grouped into three clusters by using Tocher’s method. The distribution pattern of the rice cultivars, cluster mean of the traits, intracluster, and inter-cluster divergence (D^2) and contribution percentage of traits towards genetic divergence were structured within the Tables 1, 2, 3, and 4.

Clustering pattern indicated that twenty out of twenty-four germplasms belong to the same cluster i.e. cluster I. On the other hand, three belong to cluster II and cluster III contain 1 germplasm.Comparable clustering patternon the D^2Mahalanobis was reported by Sankar *et al*. (6),Banumathy*et al*. (1),Chakravorty and Ghosh (3). Intra and inter-cluster distances among the genotype i.e. D^2 values have been shown in the Table ??. Intra-cluster distance was highest in case of cluster II (10.92) which comprised of three germplasms followed by cluster I (9.60). Cluster III showing 0.00 intra cluster distance. Inter- cluster distance was highest between cluster II and III (17.24) followed by cluster I and II (16.27) and cluster I and III (13.00).

Highest cluster mean of the traits like Days to 50% Panicle Emergence, SeedlingVigor,Plant height,Leaf Area,No. of Effective Tillers per plant, No. of Spikelet per Panicle,Days to maturity,Root Length, Root Volume, 1000Seed Weight,Harvest index, Grain yield per plantlies in Cluster III only. Cluster III contains maximum yield attributing traits so it can be used for hybridization programme of above-mentioned traits. Comparable findings reported bySudeepthi*etal*(4), Dev *et al*(5).Theresults obtained for per Percentage

Contribution towards Genetic Divergence was found maximum for Crop Growth Rate at 30DAS followed by Days to 50% Panicle Emergence, Leaf Area, Crop Growth Rate at 15DAS,1000 Seed Weight and Number of Pubescence/Unit Area.As these characters have maximum contribution towards total divergence, they should be given top priority than others in order to improve the rice genotypes.Similar type finding was previously recorded by Bose and Pradhan (6),Singh *et al*.(2),Chandramohan*et al*. (4) and Singh *et al*. (9)

References

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Table 1: Assignment of 24 rice genotypes into 3 clusters as per the D^2 statistics

CLUSTERS	NO. OF GENOTYPES	GENOTYPES INCLUDED
I	**20**	**IR 88234 STG 11-1-1-1-1,IR 88243 17-1-1-3,IR 88762 SUB 51-3-1-3,IR 88789 SUB 64-2-2-3,IR 89262 SUB 5-2-3-2,IR 14D 201,RAU 1526 IR 99642,RAU 1530-IR 15M 1689,RAU 1531 IR 95133,RAU 1524 IR 97433,RAU 1532 IR 99647,RAU 1533 IR 91143,RAU 1534 IR 82745,RAU 1482-4-1,NDR 9066,NDR 9077,CN 2124, CHEHIRANG,LALAT,IR 8828-33-5-2.**
II	**3**	**IR 87439-BTN-145-2-1, CHEHIRANG SUB 1 (CHECK),IR 64 SUB 1(CHECK)**
III	**1**	**PSBRc 68**

Table 2: Mean of cluster for 17 morphophysiological characters among the genotypes in Rice.

Character		Mean of cluster			Total mean
		I	II	III	
1	D50F	82.79	80.43	101.15	88.12
2	SV	13.54	16.20	18.87	16.20
3	PH	112.62	105.30	115.57	111.16
4	LA	23.12	22.42	23.86	23.13
5	NPUA	69.08	91.72	86.47	82.42
6	NETP	15.77	17.87	19.40	17.68
7	NSPP	146.53	185.01	205.50	179.01
8	NFSPP	130.05	167.50	190.95	162.83
9	DM	112.74	112.11	126.42	117.09
10	SST	4.33	3.44	3.67	3.81
11	RL	36.84	37.92	42.42	39.06
12	RV	36.84	38.67	45.73	40.41
13	CGR 1	0.25	0.56	0.15	0.32
14	CGR 2	0.56	1.01	0.45	0.67
15	1000SW	28.13	32.02	34.19	31.47
16	HI	39.86	43.18	46.30	43.11
17	GYPP	41.64	53.67	61.32	52.21

:- D50PE = Days to 50% Panicle Emergence, SV=Seedling Vigor, PH = Plant height (cm), LA=Leaf Area, NPUA=No. of Pubescence per Unit Area, NETP=No.of Effective Tillers per plant, NSPP=No. of Spikelet per Panicle, NFSP=No. of Fertile Spikelet per Panicle, DM = Days to maturity,SST=Scoring of Submergence Tolerance, RL=Root Length, RV=Root Volume, CGR-15=Crop Growth Rate at 15 DAS, CGR-30=Crop Growth Rate at 30 DAS,1000 SW = 1000 seed weight (g), HI = Harvest index (%), GYPP= Grain yield per plant(g).

Table 3:Average intra & inter-cluster distances among twenty-four rice genotypes studied

CLUSTERS	I	II	III
I	9.60	16.27	13.00
II		10.92	17.24
III			0.00

Table 4 Contribution percentage of 17 character towards total divergence in Rice.

SN	Character	Times ranked first	Contribution %
1	D50F	72	26.09 %
2	SV	5	1.81 %
3	PH	1	0.36 %
4	LA	42	15.22 %
5	NPPUA	13	4.71 %
6	NETP	4	1.45 %
7	NSPP	3	1.09 %
8	NFSP	0	0.00 %
9	DM	2	0.72 %
10	SST	0	0.00 %
11	RL	3	1.09 %
12	RV	1	0.36 %
13	CGR_15	22	7.97 %
14	CGR_30	94	34.06 %
15	SW	13	4.71 %
16	HI	0	0.00 %
17	GYPP	1	0.36 %