

Indexing of IRRI-Global Rice Array Genotypes for Earliness to Meet the Challenges of Climate Change

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ABSTRACT: Early-maturing rice genotypes can help the farmers to sow the first season crop during late onset of monsoon and/or delayed release of irrigation water from reservoir. This scenario is the most common problem now-a-days in the north Indian hills. In this context, indexing of 11 exotic rice lines selected from the IRRI-Global Rice Array Antenna Panel, and a local check (Govind) were done to identify early maturing genotypes. The field experiment of present study was done at the N.E.B., Crop Research Centre of GBPUA&T, Pantnagar during *kharif* season of two consecutive years 2019-2020. The observations were recorded on six morphological traits and data obtained was subjected to statistical analysis. The Analysis of Variance of both seasons indicated that the mean sum of square due to genotype were highly significant for all studied trait indicating the preponderance of genetic variability in the experimental material. In the year 2019, *URAIBOOL::IRGC 52785-1* and *IR 126182-1-1-1* were found to be similar to the local check in terms of days to 50% flowering. Similarly, in the year 2020, *URAIBOOL::IRGC 52785-1*, *IRRI 104* and *Jamir* were found to be similar to local check for days to 50% flowering. The genotype *URAIBOOL::IRGC 52785-1* (averaging 81 days over two years for days to 50% flowering) and *IRRI 104* (averaging 84.5 days over two years) were found as the early maturing genotype in both seasons though none of the lines were found to be significantly early than the local check.

Keywords: Rice genotypes, Early maturing, IRRI, Global Rice Array, Antenna Panel.

INTRODUCTION

Rice is one of the most important cereal crop which is being cultivated globally, the crop has come a long way and improved a lot in terms of production, productivity, insect-pest resistance, quality and abiotic stress tolerance aspect (Kushwaha, 2016). Historically, rice was cultivated widely in the riverine valleys of Southern and Southern-east Asia about 10,000 years ago (Gnanamanickam, 2009) and it is believed to have originated probably in India. But, numerous archaeobotanical surveys states that the Chinese Yangtze river valley is the area of rice domestication (Fuller *et al.*, 2007 and Zheng *et al.*, 2007). Findings regarding cyclic and periodical changes in climatic conditions in the Yangtze river valley area, supports the probability of asian rice domestication and diversification in that area (Wang *et al.*, 1999). In the genus of *Oryza*, there are two cultivated species and more than 20 wild species and the wild species having evolved in a wider range of environments over millions of years (Stebbins, 1981). Domesticated rice comprises two species of food crops, *Oryza sativa* and *Oryza glaberrima*. These plants are native to tropical and subtropical Southeast Asia and south-eastern Africa respectively, (Crawford and

Shen, 1998). *Oryza sativa* has three major division: the *Indica*, *japonica* and *javanica*. *Indica* rice varieties are grown widely in Asia (Ricepedia, 2020).

There is a need for continuous improvement in order to tackle the major challenges ahead like- global changing climate scenario, increasing world population, always evolving pathotypes of insects and other pathogens and some other major bottlenecks. Rice genome was the first crop genome to be sequenced which helped the researchers in underpinning of the major as well as the minor QTLs governing the traits which are of relevance to crop breeders. Domestication led to rapid genetic erosion and loss of variability so there is a need to study properly the evolution of rice and excavate more and more wild relatives. Such wild relatives can then be scouted to find numerous genes of interest, which we can transfer in our cultivated varieties today for an overall improvement of the rice cultivars that are being grown today and try to improve yield. Around 33% yield variation in rice can be attributed to climate variability globally (Ray *et al.*, 2015).

In order to address the challenges of climate change, there is a need to develop new varieties of rice which can adapt to future climates as well as can handle the consequences of pest and disease pressures. Lack of

water availability severely affects rice yield. In the *Tarai* and the hilly areas of northern India, rainfed or direct seeded rice is mainly practiced. The present-day varieties often faces the problem of terminal drought leading to yield loss and thus affecting the life and livelihood of rice-growing farmers. Also, the onset of winters is early in the above areas. Moreover, early maturing genotypes can ensure good yield in shorter duration and also will allow timely sowing of other *rabi* crops. Hence the present study focusses on identification and indexing of early-maturing genotypes from the exotic lines of the IRRI-Global Rice Array, Antenna Panel. Global Rice Array is a rice flagship project launched by IRRI. The main goal of this flagship project is to help breeders all around the globe to scout out desirable genes from the rich genepool and subsequently incorporate such genes into their locally adapted varieties.

MATERIAL AND METHODS

A. Plant material and field trial

The experimental material comprised of 11 genotypes of rice selected from Antenna Panel of the Global Rice Array of IRRI and a local check Govind (Table 1, Fig. 1). The field experiment was done at the Norman E. Borlaug Crop Research Centre of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar (29.5° N latitude and 79.3°E longitude). The experimental material was grown in Randomized Block Design (RBD) with three replications in both seasons. Field evaluation and phenotyping were carried out during *kharif* season of year 2019 and 2020. Each genotype was sown in plots and each plot consisted of four rows of 2m length following intra and inter-row

spacing of 15 cm and 20 cm respectively. Recommended cultural practices were practiced to ensure a good crop stand. The climatic conditions during both the seasons are represented by Fig. 2 and 3.

Table 1: List of 12 genotypes of rice including 11 genotypes from Antenna Panel of the Global Rice Array of IRRI and 1 local check.

Sr.No.	Genotype
1.	URAIBOOL::IRGC 52785-1
2.	IR84984-83-15-481-B
3.	IRRI 104
4.	N 22::IRGC 19379-1
5.	IR 126182-1-1-1
6.	Jamir
7.	Manaw Thukha
8.	OM4900
9.	MTU1010
10.	IR 64
11.	IR10F360
12.	Govind



Fig. 1. IRRI GRA trials being conducted in GBPUAT, Pantnagar, *Kharif*-2020.

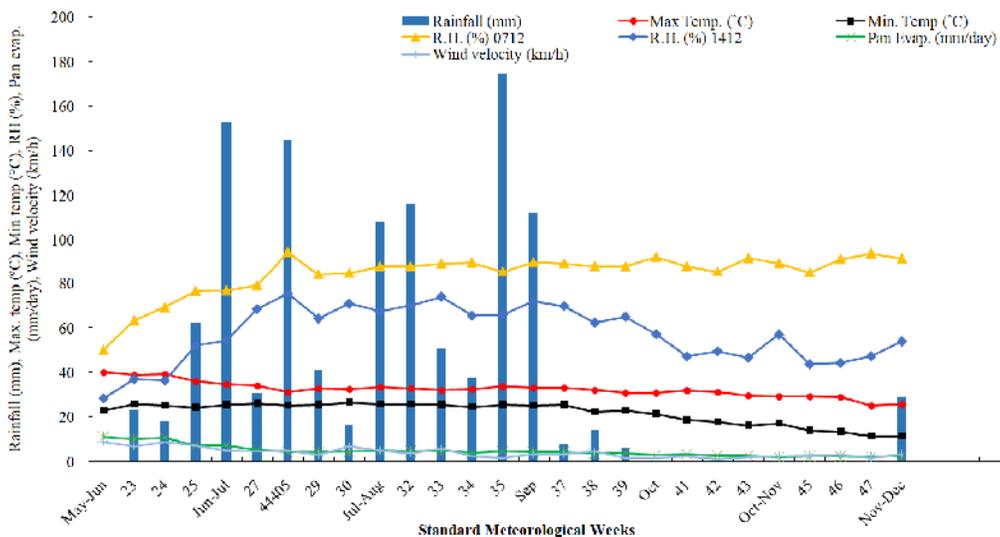


Fig. 2. Weekly meteorological data during *Kharif* 2019-20.

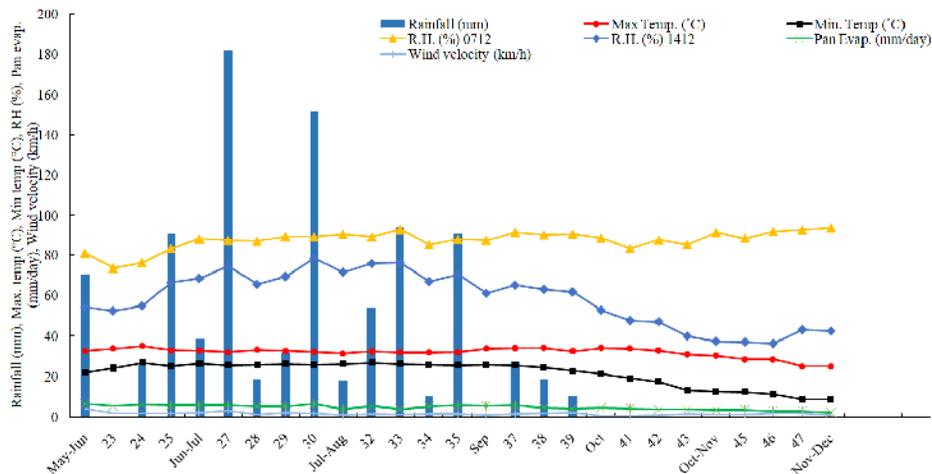


Fig. 3. Weekly meteorological data during *Kharif* 2020-21.

B. Observations Recorded

The observations were recorded on six traits viz., Days to 50 percent flowering, plant height at maturity (cm), number of tillers per plant at maturity, panicle length (cm), grains per panicle, thousand grains weight (g) and grain yield per plant (g). Five competitive plants from each plots were randomly selected for recording observations on various traits (except days to 50 percent flowering which was recorded on the plot basis).

C. Statistical analysis

The analysis of variance for six characters was carried out as given by Fisher (1920). The statistics data were analysed using the INDOSTAT software (IndoStat Inc. Hyderabad, India).

RESULTS AND DISCUSSION

The major goal of any plant breeding programme is the generation and exploitation of genetic variability for crop improvement. For selection to be effective there must be presence of sufficient amount of genetic

variability for a trait in any crop plant species. The ANOVA of both seasons (2019 and 2020) for six traits indicated that mean sum of squares were highly significant (Table 2) indicating the preponderance of genetic variability in the experimental material. The similar findings for these traits were also reported earlier by Ismaila *et al.*, (2015) and Bhatt *et al.*, 2017. Days to maturity, Days to 50% percent flowering or days to heading - are good indicators of earliness. Many researchers attempted hybridization programmes in order to develop extra-early maturing genotypes in rice. The first step of any such crop improvement programmes in terms of earliness includes the identification and indexing of early-maturing genotypes from the available resources and then either use them directly as cultivars or use as pollen parents in hybridization programmes. Before heading to hybridization programmes there is a need to identify the gene action involved. Many similar researches were designed and carried out in this line.

Table 2: ANOVA for 12 early genotypes over two years.

Source of Variation	Year	degree of freedom	Mean Sum of Squares					Yield (Kg/h)
			Days to 50% flowering (days)	Plant Height (cm)	Tillers per Plant	Panicle Length (cm)	1000 grain weight (grams)	
Replication	2019	2	11.965	7.076	0.009	0.036	0.699	8121.998
	2020	2	15.186*	62.291**	0.096	0.221	0.014	4486.503
Genotypes	2019	11	358.617**	1972.290**	5.182**	28.487**	116.073**	9956768.576**
	2020	11	78.614**	1049.215**	20.432**	29.423**	16.323**	6886890.839**
Error	2019	22	5.053	8.126	0.167	0.486	0.295	11257.605
	2020	22	2.699	6.127	0.155	0.396	0.435	13288.366

The predominance of non-additive gene action (Devi *et al.*, 2015) and additive gene action (Upadhyay and Jaiswal, 2015) were reported in crosses involving early-maturing genotypes with other improved cultivars by early workers. In some advanced studies, Fujino and Sekiguchi (2005) reported that two QTLs (namely-

qDTH-7-1 and qDTH-7-2), both residing on chromosome 7 is responsible for very early heading in *Hoshinoyume*-derived population. They also found epistatic interactions between them and that the recessive alleles of these two identified genes is mainly responsible for the earliness in rice via early heading.

In the present study as listed in Table 3, days to 50% flowering among all 12 genotypes in the year 2019, ranged from 80.000 days (*URAIBOOL::IRGC 52785-1*) to 112.000 days (*IR10F360*) and in 2020, ranged from 82.000 days (*URAIBOOL::IRGC 52785-1* and *Govind*) to 96 days (*MTU1010* and *IR 64*). Coefficient of variation for this character was 2.441 in 2019 and 1.861 in 2020. Plant height among all 12 genotypes in the year 2019, ranged from 78cm (*URAIBOOL::IRGC 52785-1*) to 134.33 cm (*IR84984-83-15-481-B*) and in 2020, ranged from 78.33 days (*URAIBOOL::IRGC 52785-1*) to 150cm (*N 22::IRGC 19379-1*). So, from the data indexed over two seasons it can be seen that

URAIBOOL::IRGC 52785-1 genotype is early in maturity as well as dwarf in stature. Number of tillers per plant among all 12 genotypes ranged from 14 to 18 in 2019 and 12 to 20 in 2020. Panicle length among all 12 genotypes in 2019 ranged from 15.67 cm (*Manaw Thukha*) to 27.33 cm (*URAIBOOL::IRGC 52785-1*) whereas in Kharif-2020 ranged from 18 cm (*MTU1010*) to 30 cm (*IR10F360*). So, it is also found that *URAIBOOL::IRGC 52785-1* possesses long panicles in both the growing seasons. 1000 grain weight among all 12 genotypes ranged from 17.68 g to 38.50 g in 2019 and in 2020 it ranged from 18.2 to 26 grams.

Table 3: Mean and CD value for 12 genotypes and six traits.

Genotypes	Days to 50% flowering (days)		Plant Height (cm)		Tillers per Plant		Panicle Length (cm)		1000 grain weight (grams)		Yield (Kg/h)	
	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020
URAIBOOL::IRGC 52785-1	80	82	78	78.33	16	12	27.33	25	27.08	20.4	2489	1638
IR84984-83-15-481-B	91	86	134.33	114.33	15	13	22.67	28	38.50	18.2	2400	4063
IRRI 104	85	84	93.33	83.67	14	13	24.67	27	21.05	21.2	2151	4288
N 22::IRGC 19379-1	88	86	132	150	15	14	21	22	22.66	19.2	2329	3388
IR 126182-1-1-1	81	94	79.33	109	16	14	26.67	25	20.92	26	1156	6000
Jamir	85	84	128.33	116	18	15	23.67	22	21.11	23	1244	4413
Manaw Thukha	110	88	115.67	110	14	13	15.67	25.67	17.68	22.6	2151	4288
OM4900	97	91	111	109.33	14	19	25	25	22.47	21.8	6791	3537
MTU1010	96	96	118.33	108.33	15	14	25.33	18	26.02	24.2	3484	5388
IR 64	99	96	107.67	96	17	14	22	26.33	35.89	23.4	5884	4963
IR10F360	112	90	93.67	124	15	20	25	30	22.43	20.8	1520	6100
Govind	81	82	102.33	98	17	18	23.67	24	25.16	25	4549	7500
CD	3.831	2.800	4.859	4.221	0.696	0.671	1.188	1.073	0.926	1.124	180.831	196.467

In the year 2019, *URAIBOOL::IRGC 52785-1* and *IR 126182-1-1-1* were found to similar to the local check in terms of days to 50% flowering having a grain yield of 2489 kg/h and 1156kg/h respectively. Similarly, in the year 2020, *URAIBOOL::IRGC 52785-1*, *IRRI 104* and *Jamir* were found to be similar to local check for days to 50% flowering with a grain yield of 1638 kg/h,

4288 kg/h and 4413 kg/h respectively. So, from the field data it can be concluded that *URAIBOOL::IRGC 52785-1* is an early genotype in both the years. *URAIBOOL::IRGC 52785-1* took 80 days in 2019 and 82 days in 2020 to attain the stage of 50% flowering as depicted in Fig. 4.

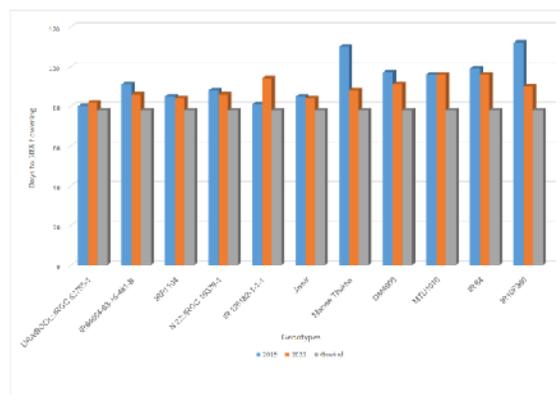


Fig. 4. Days to fifty percent flowering of early genotypes in comparison to local check- Govind over two years. Roy & Pandey *Biological Forum – An International Journal* 13(3): 105-110(2021) 108

CONCLUSIONS

Global Climate Change, water scarcity, labour shortage, declining water-table level predicted severe shortfall in rice production (Monaco *et al.*, 2016). In order to address the challenges of climate change, there is a need to develop new varieties of rice which can adapt to future climates as well as can handle the consequences of pest and disease pressures. The GRA was designed in this line where there are two type of panels – Antenna panel and reference panel. The Antenna panel is like the eye of the breeder which facilitates in indexing of rice genotypes for superior traits in all aspects of crop improvement. It can be concluded from above study that *URAIBOOL::IRGC 52785-1* and *IRRI 104* are early genotype out of all the exotic lines evaluated and that early line identified can be used to transfer earliness in our local high yielding varieties or can be used as a cultivar for the hills where there is problem of ripening of grains due to early advent of winters and growing these kinds of early genotypes may prove to be rewarding. Identification and indexing of early genotypes will further aid in timely sowing of other rabi crops.

FUTURE SCOPE

The identified early lines can further be included in studies to figure out the predominance of additive or non-additive gene action. If there is preponderance of additive gene action, recombination and selection approach of crop improvement can be adopted. Crossing of very-early maturing rice genotypes with other improved varieties can be attempted. The early maturity if governed by additive gene action will be realized in F₁ crosses and could eventually be fixed in the advanced generations of the crosses performed (Arunachalam *et al.*, 2020). Thus, indexing of exotic lines to identify genotypes which are early can thus be a game-changer in this changing climate regime. Hence, the future scope of this kind of research is immense as high rice yielders with a shorter life cycle can help in better crop rotation with other crops and thus increase the overall productivity of hilly areas of Northern India.

Conflict of Interest. The author declares that he has no competing interest.

AUTHOR'S CONTRIBUTION

Data recorded, research Conceptualised and the manuscript is Written by D. Roy. The Global Rice Array- Antenna Panel experimental material was made available from International Rice Research Institute, Los Banos, Phillipines by Dr. Indra Deo Pandey, Project-In-Charge.

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