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Research Article

Deciphering genetic diversity in 'Antenna Panel' genotypes of IRRI's Global Rice Array-IV for yield traits in Indo-Gangetic Plains

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Abstract
International Rice Research Institute (IRRI) has launched a flagship project-4 consisting of 58 rice genotypes 'Antenna Panel' (a panel of diverse genotypes having various beneficial genes introgressed) from the Global Rice Array-IV (GRA-IV). Exploring diversity provides an opportunity for plant breeders to develop resilient crops and analysis of diversity is important for any crop improvement programme. Mahalanobis's distance matrix thus obtained was further subjected to clustering by the UPGMA hierarchical agglomerative clustering method to decipher the degree of genetic divergence in the 'Antenna Panel' genotypes of IRRI's Global Rice Array-IV. On the basis of D^2 values, rice genotypes were grouped into eleven clusters. Cluster I was the largest and contained the maximum number of genotypes. The inter-cluster distance ranged from 5.8 between cluster I and cluster VIII to 18.8 between cluster V and cluster X. The highest inter cluster distance was recorded between clusters V and X (18.80) followed by clusters II and V (17.78). The intra cluster distance was found to be maximum in cluster II (5.20) followed by cluster V (5.01), and cluster I (4.25). The character days to 50% flowering (33.1%) showed a maximum contribution followed by plant height (30.2%), grain yield (10.3%), the number of grains per panicle (10.00%), panicle length (7.3 %), the number of tillers per plant (4.8%) and 1000-grain weight (4.3%). If a superior genotype with an ample amount of genetic divergence and well adapted in India's Indo-Gangetic Plains can be selected, from these global databases then it can be of great help to break the stagnation of yield by improving the genetic potential of the existing rice varieties through hybridization and exploitation of heterosis. In this context, if hybridization is attempted between the genotypes included in the cluster V (SUPA, ZANTON::IRGC 31248-1 and URAIBOOL::IRGC 52785-1) and cluster X (Hokkai 188, M202) greater heterosis can be expected.

Keywords: Rice genotypes, Genetic Divergence, IRRI, D^2

INTRODUCTION

Rice accounts for nearly 75% of Asia's staple dietary needs and feeds approximately more than 3 billion mouths of the global population (FAOSTAT, 2019). The UN says the world population will be a whopping 10.9 billion by the end of the century i.e., 2100 and by simple extrapolation, the world's need for rice is bound to be increased. In India, more than half of the population is directly or indirectly dependent on rice for their calorie demands (Pathak *et al.,* 2019). Globally, India holds the second rank among all the rice producing countries in the world after China (FAOSTAT, 2019). The sustainability of the rice production system in India is of huge importance in ensuring the global food supply. In recent years, rice production in the Indian sub-continent is facing

several challenges, mainly in the form of degrading crop environment and changing climatic conditions (Wassmann *et al.,* 2009). Besides, most of the Indian varieties have already touched the yield ceiling in the past few years and thus resulting in declining factor productivity as well as yield stagnation (Akter *et al*., 2014). International Rice Research Institute (IRRI) has launched their flagship project-4 consisting of the 'Antenna Panel' (a panel of diverse genotypes having various beneficial genes introgressed) from the Global Rice Array-IV (GRA-IV), which is a new concept to help researchers stay ahead of climate change and understand the G×E interactions in a better way. Such an enormous project can help to boost the crop improvement of rice across the globe so better adapted varieties can be bred at a faster rate. Most of the complex traits *viz.,* grain yield in rice are polygenic in nature and are highly affected by micro and macro environmental conditions (Vaezi *et al.,* 2019). Having an idea of the amount of genetic divergence before starting any hybridization programme can be useful for obtaining high-yielder offsprings. Mahalanobis's (1936) D^2 statistics are used in this study to decipher the degree of genetic divergence in the 'Antenna Panel' genotypes of IRRI's Global Rice Array-IV. If a superior genotype with stable characters, well adapted in India's Indo-Gangetic Plains can be selected, from these global databases, then it can be of great help to break the stagnation of yield by improving the genetic potential of the existing rice varieties.

MATERIALS AND METHODS

Field experiments for the current study were conducted during rainy seasons (July to October) in 2019 at the N. E. Borlaug Crop Research Centre of G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India. The experimental site is situated in the Tarai region of the Himalayan foothills (29.0°N; 79.5°E; 242.9 m above MSL) and enjoys a hot-humid summer

Table 1. List of 58 genotypes from Antenna Panel of the Global Rice Array of IRRI

S.No.	Genotype	S.No.	Genotype
1	IRRI 154	30	ManawThukha
2	MINGHUI 63	31	BR28
3	ZHENSHAN 97 B	32	TN1
4	IR 64	33	IR6
5	IRBB 66	34	GSR IR2-9-R1-SU3-Y2
6	IR 78222-20-7-148-2-B-B-B-B	35	zanton::IRGC 31248-1
7	IR 69726-116-1-1	36	URAIBOOL::IRGC 52785-1
8	IRRI 147	37	Hokkai 188
9	SANHUANGZHAN NO 2	38	IR 126182-1-1-1
10	IR77186-122-2-2-3	39	IR10F360
11	IR77298-14-1-2-10	40	Sahel 108
12	SAMBHA MAHSURI + SUB 1	41	Sahel 134
13	SUPA	42	Sahel 177
14	IRRI 104	43	Giza 178
15	N 22::IRGC 19379-1	44	Moroberekan
16	MTU1010	45	DJ123
17	SWARNA	46	Oryzica 1
18	NANHI	47	FEDEARROZ 50
19	JASMINE 85	48	TEQING
20	KINANDANG PATONG	49	MG 2::IRGC 79837-1
21	SADRI	50	UPL RI 7::IRTP 9897-C1
22	OM4900	51	CT11891-2-2-7-M
23	IR 95042:13-B-7-11-15-3	52	Oryzicasabana 10
24	IR 93340:14-B-21-17-12-1RGA-1-B-B	53	Oryzicasabana 6
25	IR 93354:34-B-5-1-23-1RGA-1-B-B	54	Oryzica Llanos 5
26	KhaoHlan On	55	ChhomrongDhan
27	IR13F167	56	NSIC Rc240
28	IR84984-83-15-481-B	57	Jamir
29	M202	58	IR10M300

and cool-dry winters. The meteorological data during the experimental period. The soil of the site belongs to the order Mollisols, silty clay loam in texture, high in organic carbon (0.76%), low to medium in available nitrogen, medium in available phosphorus and potassium with a near neutral pH of 7.2. The genetic matevrials for the experiment were part of the 'Antenna Panel' component of the GRA-IV (**Table 1**). A total of 58 genotypes were transplanted on 22nd July of the growing season and harvested between the 2nd to 3rd week of November. Four rows of 2 m length were transplanted in each plot and replicated twice. Standard agronomic practices were practised to raise a healthy crop stand in all three years. The various characters were recorded *viz.*, days to 50 % flowering, plant height at maturity (cm), the number of tillers per plant at maturity, panicle length (cm), thousand grains weight (g) and grain yield (kg/ ha).

The data recorded for various yield and attributing attributes was subjected to estimation of genetic diversity using the Mahalanobis D^2statistics (Mahalanobis, 1936). The clusters were prepared as suggested by Rao (1952). Mahalanobis's distance matrix thus obtained was further subjected to clustering by the UPGMA hierarchical agglomerative clustering method. R statistical 77 software packages such as "Biotools" (Da Silva and da Silva, 2017), the contribution of each variable towards diversity was calculated using function "singh" from the same package (Singh, 1981). Further, to create illustrations and graphs, R-statistical software packages "ggplot2" (Wickham, 2016), "dendextend" (Galili, 2015) and "circlize" (Gu *et al.,* 2014) were used.

RESULTS AND DISCUSSION

On the basis of D^2 values, 58 rice genotypes were grouped into eleven different clusters (**Table 2 and Fig. 1 and 2**). The cluster I was the largest and contained the maximum number of genotypes i.e.,30 followed by cluster III (9) and cluster VIII (4), while the cluster IV, cluster VI, cluster IX and cluster XI each contained one genotype, respectively. Cluster I contained genotypes *viz.,* IRRI 154, MINGHUI 63, IR 64, IRBB 66, IR 69726-116-1-1, IRRI 147, SANHUANGZHAN NO 2, IR77186-122-2-2-3, IR77298-14-1-2-10, IRRI 104, MTU1010, JASMINE 85, IR 95042:13-B-7-11-15-3, IR 93340:14-B-21-17-12-1RGA-1-B-B, IR 93354:34-B-5-1-23-1RGA-1-B-B, BR28, TN1, IR6, IR10F360, Sahel 108, Sahel 134, Sahel 177, Giza 178, Oryzica 1, FEDEARROZ 50, UPL RI 7::IRTP 9897-C1, CT11891-2-2-7-M, Oryzicasabana 10, Oryzica Llanos 5, IR10M300. Cluster III contained genotype IR 78222-20-7-148-2-B-B-B-B, N 22::IRGC 19379-1, NANHI, KINANDANG PATONG, IR84984-83-15-481-B, Moroberekan, Oryzicasabana 6, Chhomrong Dhan and Jamir, while the cluster VIII contained genotype OM4900, GSR IR2-9-R1-SU3-Y2, TEQING and MG 2::IRGC 79837-1. Attempting a hybridization programme between parents derived from most divergent clusters is expected to maximize heterosis (Souroush *et al*., 2004).

The inter-cluster distance ranged from 58 between cluster I and cluster VIII to 18.8 between cluster V and cluster X (**Table 3**). The highest inter cluster distance was recorded between cluster V and X (18.80) followed by cluster II and V (17.78), cluster II and VI (15.37), cluster VI and X (14.71), cluster IX and X (14.59), cluster VII

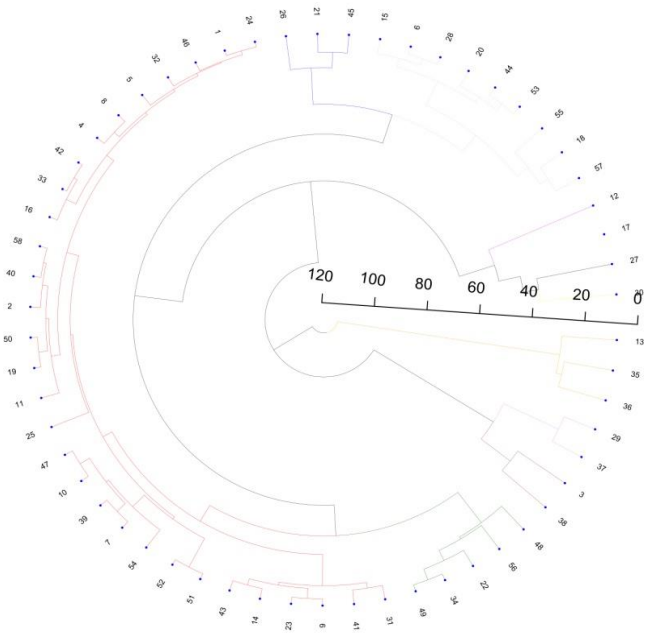

Fig.1. Clustering of genotypes based on Mahalanobis distance value (refer Table 1 for genotypes name)

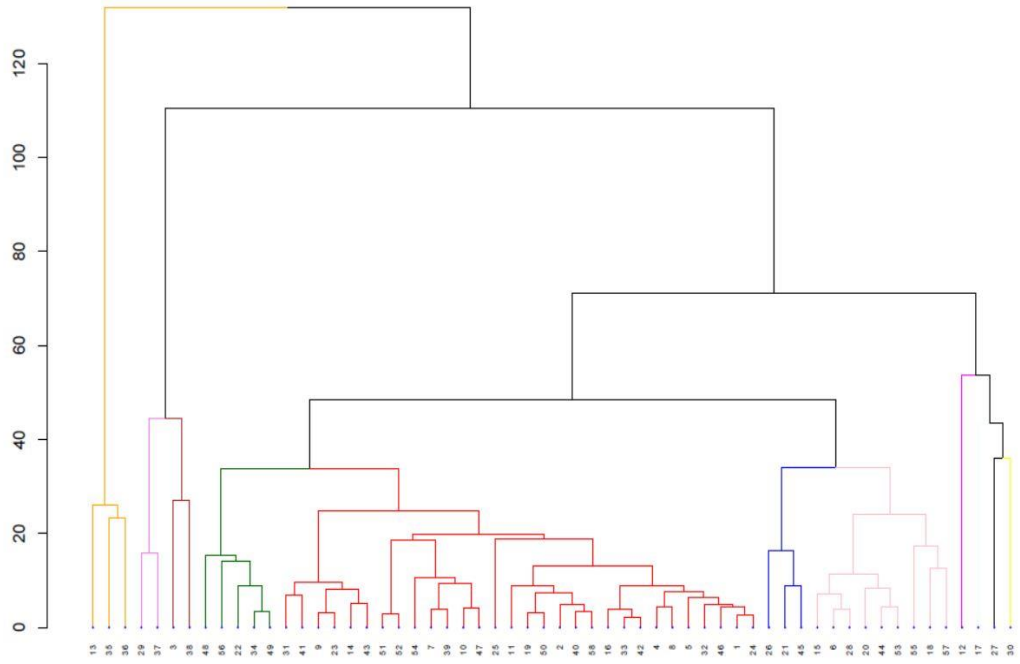

Fig. 2. Clustering of genotypes based on UPGMA (refer to Table 1 for genotypes name)

Table 2. Clustering pattern among 'Antenna Panel' genotypes of Global rice Array-IV

Cluster number	Number of genotypes	Genotypes
I	30	IRRI 154, MINGHUI 63, IR 64, IRBB 66, IR 69726-116-1-1, IRRI 147, SANHUANGZHAN NO 2, IR77186-122-2-2-3, IR77298-14-1-2-10, IRRI 104, MTU1010, JASMINE 85, IR 95042:13-B-7-11-15-3, IR 93340:14-B-21-17-12-1RGA-1-B-B, IR 93354:34-B-5-1-23-1RGA-1-B-B, BR28, TN1, IR6, IR10F360, Sahel 108, Sahel 134, Sahel 177, Giza 178, Oryzica 1, FEDEARROZ 50, UPL RI 7::IRTP 9897-C1, CT11891-2-2-7-M, Oryzicasabana 10, Oryzica Llanos 5, IR10M300
II	2	ZHENSHAN 97 B, IR 126182-1-1-1
III	9	IR 78222-20-7-148-2-B-B-B-B N 22::IRGC 19379-1 NANHI KINANDANG PATONG IR84984-83-15-481-B Moroberekan Oryzicasabana 6 ChhomrongDhan Jamir
IV	1	SAMBHA MAHSURI + SUB 1
V	3	SUPA zanton::IRGC 31248-1 URAIBOOL::IRGC 52785-1
VI	1	SWARNA
VII	3	SADRI, KhaoHlan On, DJ123
VIII	4	OM4900 GSR IR2-9-R1-SU3-Y2 TEQING MG 2::IRGC 79837-1
IX	1	IR13F167
X	2	Hokkai 188, M202
XI	1	ManawThukha

and X (14.47) and cluster VI and VII (14.18). The intra cluster distance was found to be maximum in cluster II (5.20) followed by cluster V (5.01), cluster I (4.25), cluster III (4.15), cluster X (3.97), cluster VII (3.72), and cluster VIII (3.53). All other clusters (cluster IV, cluster VI, cluster XI and cluster XI) showed zero intra-cluster distance. Hence, the higher inter-cluster distances as compared to intra-cluster distances suggested the presence of a sufficient amount of genetic divergence among the 'Antenna Panel' genotypes of Global rice Array-IV under study. This indicated that if hybridization is attempted between the genotypes included in the cluster V (SUPA, ZANTON::IRGC 31248-1 and URAIBOOL::IRGC 52785-1) and cluster X (Hokkai 188, M202), a lot of variations could be obtained in the segregating generations and the selection for desirable genotypes can be practised. The hybridization between different genotypes included in the most divergent clusters to get desirable segregants for yield and other traits is also advocated earlier by Satapathy and Panigrahi (2014), Singh *et al.* (2015) and Verma *et al.* (2018).

Hence, from cluster analysis, it is revealed that a higher inter-cluster distance than the intra-cluster distance indicated the high genetic diversity among the genotypes. The maximum intra-cluster distance was observed in cluster II which indicated the existence of wide genetic divergence in comparison of the other clusters hence the genotypes belonging to such clusters having a high degree of divergence and they could produce more segregating breeding material. The maximum inter-cluster distance was obtained between clusters V and X, which indicated that the genotypes belonging to these clusters could be used as parental material under a hybridization programme for getting desirable/ transgressive segregants (Devi *et al*., 2017).

The cluster mean values for all the characters are provided in **Table 4**. The cluster mean for days to 50% flowering ranged from 735 to 133 days. The cluster X (73.5 days) was found to be the earliest flowering cluster followed by cluster II (74.3 days), Cluster VII (93.3 days), cluster III (94.3 days), cluster VIII (99.1 days), cluster I

Table 3. Inter and intra–cluster distances in 'Antenna Panel' genotypes of Global rice Array-IV

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**4.25**										
II	8.93	**5.20**									
III	6.05	9.63	**4.15**								
IV	7.34	13.67	9.87	**0.00**							
V	11.32	17.78	9.80	11.23	**5.01**						
VI	9.45	15.37	11.27	7.39	11.35	**0.00**					
VII	8.80	12.08	5.84	12.75	9.44	14.18	**3.72**				
VIII	5.80	11.34	7.24	6.97	10.54	11.60	8.87	**3.53**			
IX	6.95	13.60	7.23	7.96	6.98	6.29	8.60	8.34	**0.00**		
X	9.98	6.67	10.84	13.15	18.80	14.71	14.47	12.54	14.59	**3.97**	
XI	7.05	12.81	6.79	6.58	8.81	6.88	10.14	8.31	6.01	11.69	**0.00**

Table 4. Cluster mean for different characters in 'Antenna Panel' genotypes of Global rice Array-IV

Cluster	DTF	PH	TPP	PL	GPP	GW	YLD
I	100.2	99.6	16.7	25.6	303.2	25.7	3596.4
II	74.3	80.7	15.4	25.1	164.0	33.7	1451.1
III	94.3	127.8	15.6	23.9	273.1	28.5	1800.0
IV	118.0	81.0	17.8	23.0	651.5	13.5	3582.2
V	123.8	161.1	14.0	27.2	389.8	30.9	2130.4
VI	133.0	78.8	17.8	22.8	188.5	20.6	1817.8
VII	93.3	158.2	18.1	28.9	308.2	29.1	1952.6
VIII	99.1	113.7	16.2	26.3	535.4	26.6	5498.7
IX	121.5	120.8	18.0	27.7	203.5	26.7	2560.0
X	73.5	62.4	15.0	15.2	183.0	20.9	1611.1
XI	111.0	108.7	13.7	18.3	332.0	18.5	1573.3

DTF= Days to 50% flowering, PH=Plant height (cm), TPP= Number of tillers per plant, PL=Panicle length (cm), GPP= Number of grains per panicle, GW= 1000-grain weight (g), YLD= Grain yield (kg/ha)

(100.2 days), cluster XI (111.00 days) and cluster IV (118.00 days). These results indicated the genotype present in cluster X (73.5 days) can be used as donors for early maturity in rice. The cluster means for plant height ranged from 62.4 to 161.1 cm. The cluster X (62.4 cm) was found to have the lowest height followed by cluster VI (78.8 cm), cluster II (80.7 cm), cluster IV (81.0 cm), cluster I (99.6 cm), cluster XI (108.7 cm), cluster VIII (113.7 cm) and maximum for cluster V (161.1 cm). The dwarf plant height is a desirable character in rice as it results in less lodging and ultimately generates more yield hence cluster X can be used as donors for dwarf plant height in rice. The cluster means for the number of tillers per plant ranged from 13.7 to 18.1. Cluster VII (18.1) was found to have the highest number of tillers per plant followed by cluster IX (18.0), cluster VI and IV (17.8), cluster I (16.7), cluster VIII (16.2), cluster III (15.6), cluster II (15.4) and minimum for cluster XI (13.7). These results again indicated that cluster VII can be used as donors for more number of tillers per plant in rice. The cluster means for panicle length ranged from 15.2 cm to 28.9 cm. Cluster VII (28.9 cm) was found to have the larger panicle length followed by cluster IX (27.7 cm), cluster V (27.2 cm), cluster VIII (26.3 cm), cluster I (25.6 cm), cluster 2 (25.1 cm), cluster III (23.9 cm) and minimum for cluster X (15.2 cm). These results indicated the genotypes included in cluster VII can be used as donors for bigger panicle lengths in rice. The cluster means for the number of grains per panicle ranged from 164.0 to 651.5. Cluster IV (651.5) was found to have the highest number of grains per panicle followed by cluster VIII (535.4). The more number of grains per panicle is directly related to high yield in rice and hence, the genotype SAMBHA MAHSURI + SUB 1 present in cluster IV can be used as a donor for more number of grains per panicle in rice. The cluster means for 1000-grain weight ranged from 13.5 to 33.7 g. Cluster II (33.7g) was found to have the highest 1000-grain weight followed by cluster V (30.9 g), cluster VII (29.10 g), cluster III (28.50 g), cluster IX (26.7g), cluster VIII (26.60 g), cluster I (25.7 g) and minimum for Cluster IV (13.5 g). Thus cluster II can be used as donors for more 1000-grain weight in rice. The cluster means for grain yield ranged from 1451.1 to 5498.7 kg/ha. The cluster VIII (5498.7 kg/h) was found to have the highest grain yield followed by cluster I (3596.4 kg/h), cluster IV (3582.2 kg/h), cluster IX (2560.00 kg/h), cluster V (2130.4 kg/h), cluster VII (1952.6 kg/h), cluster VI (1817.8 kg/h) and minimum for cluster II (1451.1 kg/h). Thus the genotype included in cluster VIII can be used as donors for higher grain yield in rice. The preponderance of genetic divergence in rice cultivars has also been reported by several rice breeders *viz.,* Rajesh *et al*. (2010); Ashok *et al*. (2017) Dey *et al*. (2018); Devi *et al*. (2019) and Singh *et al.* (2020).

Table 5. Contribution of different characters towards total divergence

S.No.	Source	Per cent contribution
1	Number of days to 50% flowering	33.1
2	Plant height	30.2
3	Number of tillers per plant	4.8
4	Panicle Length	7.3
5	Number of grains per Panicle	10.0
6	1000-grain weight	4.3
7	Grain yield	10.3

The contribution of different characters toward the divergence is presented in **Table 5**. The character days to 50% flowering (33.1%) showed a maximum contribution followed by plant height (30.2%), grain yield (10.3%), the number of grains per panicle (10.00%), panicle length (7.3 %), the number of tillers per plant (4.8%) and 1000-grain weight (4.3%). Thus, the characters plant height, the number of days to 50% flowering was found as major contributing characters while the characters- the number of tillers per plant (4.8%) and 1000-grain weight (4.3%) showed a negligible contribution towards the genetic divergence. Plant height as a major contributor to genetic divergence was also documented by Kavurikalpana *et al.* 2018**.**

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