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).

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
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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 climate.

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    | NANNHI                        | 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    | CT1891-2-2-7-M       |
| 23    | IR 95042:13-B-7-11-15-3       | 52    | Oryzicasabana 10     |
| 24    | IR 93340:14-B-21-17-12-IRGA-1-B-B | 53    | Oryzicasabana 6      |
| 25    | IR 93354:34-B-5-1-23-IRGA-1-B-B | 54    | Oryzicasabana 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 materials 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 D²statistics (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 D² 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

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

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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, NAHNI, KINANDANG PATONG                              |
|               |                     | IR84984-83-15-481-B, Moroberekan, Oryzicasabana 6, ChhomrongDhan, Jamir  |
| IV            | 1                   | SAMBHA MAHSURI + SUB 1, SUPA                                               |
| V             | 3                   | zanton::IRGC 31248-1, URAIBOOL::IRGC 52785-1                              |
| VI            | 1                   | SWARNA                                                                     |
| VII           | 3                   | SADRI, KhaoHlan On, DJ123, OMY900                                          |
| VIII          | 4                   | GSR IR2-9-R1-SU3-Y2, TEQING, MG 2::IRGC 79837-1                           |
| IX            | 1                   | IR13F167                                                                   |
| X             | 2                   | Hokkai 188, M202                                                           |
| XI            | 1                   | ManawThukha                                                                |

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

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| 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 |

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 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)
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 (539.4). 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 (33.7 g) was found to have the highest 1000-grain weight followed by cluster V (30.9 g), cluster VII (29.1 g), cluster III (28.50 g), cluster IX (26.7 g), 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/ha) was found to have the highest grain yield followed by cluster I (3596.4 kg/ha), cluster IV (3582.2 kg/ha), cluster IX (2560.00 kg/ha), cluster V (2130.4 kg/ha), cluster VII (1952.6 kg/ha), cluster VI (1817.8 kg/ha) and minimum for cluster II (1451.1 kg/ha). 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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