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# Genetic diversity analysis for various agromorphological, yield and yield related traits in wheat (*Triticum aestivum* L.)

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## Abstract

**Thirty diverse wheat genotypes were used to assess the genetic diversity for various agromorphological, grain yield and yield related traits. The analysis of variance showed highly significant differences among the test genotypes for grain yield and its contributing components viz., days to 50% flowering, days to 75% maturity, number of tillers per plant, plant height (cm), biological yield (g), harvest index (%), grain yield per plant (g) and 1000 grain weight (g). High heritability along with high genetic advance and high phenotypic coefficient of variation (PCV) were recorded for biological yield per plant (g) and 1000 grain weight (g). It indicated substantial contribution of additive gene action in the expression and thus selection would be effective for genetic improvement of these traits. On the basis of multivariate analysis, 30 genotypes were grouped into '13' clusters based on genetic divergence ($D^2$) value. The compositions of clusters revealed that the Cluster II and Cluster IV had the highest number of genotypes (9) followed by Cluster I (2). The highest intra-cluster distance was observed in cluster IV (2.05) followed by cluster II (1.98) and cluster I (1.12) and in the remaining clusters, there was only one genotype each, thereby the intra-cluster distance was zero. Cluster I (HS 507 and HPW 368) showed maximum values for biological yield per plant. Cluster III (E 9) showed minimum values for days to 75% maturity and cluster XIII showed minimum value for days to 50% flowering. Cluster VI (Roelfs F 2007) showed maximum values for tillers per plant. Cluster XI (HPW 373) showed maximum values for harvest index and cluster XII having variety Baj#1 showed maximum value for grain yield per plant and 1000-grain weight. The highest inter-cluster distance of 5.18 was observed between cluster VIII (TC1-7) and X (TC 1-24) followed by cluster VI (Roelfs F 2007) and X (TC 1-24) with a distance of 4.92 indicating that genotypes in these clusters have wide genetic diversity and thus can be used in hybridization programme for improving grain yield.**

**Key words:** Wheat genotypes, Genetic diversity, Genetic parameters, Yield traits.

Wheat (*Triticum aestivum* L.) is the world's most extensively grown cereal crop and staple food for over 10 billion people. In India, wheat is the second most important cereal crop next only to rice (Thapa *et al*. 2019) and the country holds second position in area and production after China. The crop has been grown in about 30 million hectares (14% of global area) to produce 99.70 million tones of wheat with average productivity of 3371 kg/ha (Sendhil *et al.* 2019). To feed the growing population, there is an immediate and urgent need to increase wheat production (Saini *et al*. 2019). This can be achieved by enhancing the production of wheat by developing improved varieties through involving parents with high genetic divergence. The knowledge of genetic variability for yield and its contributing components helps in the improvement of grain yield and planning of effective breeding programme. The creation and utilization of genetic diversity is essential to overcome the problems of narrow genetic base and for generating precise information on the nature and degree of genetic diversity in selecting the parents for targeted hybridization

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The cluster analysis is an appropriate method to determine the extent of genetic distance of genotypes from each other. Therefore, information on the genetic diversity for grain yield is important to meet the diversified goal of plant breeding such as breeding for increasing yield, wide adaptation and desirable yield related traits (Lal *et al.* 2009). Therefore, the present study was undertaken to identify genetically diverse wheat genotypes to be used as donors for improving grain yield and other yield contributing components in wheat.

## Materials and Methods

The experimental material comprised 30 diverse genotypes of wheat comprising advanced breeding material selected from CIMMYT germplasm, elite lines and two checks *viz.,* HPW 349 and HPW 368. These were evaluated in a randomized block design (RBD) with three replications during 2017-18 at CSKHPKV, Rice and Wheat Research Centre, Malan. The test genotypes were grown in two metre long rows spaced 20 cm apart, following standard package and practices for irrigated conditions (*http://www.hillagric.ac.in/extension/dee/pdf_files/Rabi_28-8-09. PDF*). The observations were recorded on five randomly selected plants in each replication for days to 50% flowering, days to maturity, number of tillers per plant, plant height (cm), biological yield per plant (g), harvest index(%), grain yield per plant (g) and 1000 grain weight (g)**.** The analysis of variance (ANOVA) was done following Panse and Sukhatme (1985). The PCV and GCV were calculated by the method suggested by Burton and De Vane (1953). Heritability and genetic advance as percent of means for each character were calculated following Johnson *et al.* (1955). The genetic diversity was studied through cluster analysis using $D^2$ statistics suggested by Mahalanobis (1936) and they were grouped into various clusters based on $D^2$ value suggested by Rao (1952). The detail of the material used in present investigation along with its pedigree is given in Table 1.

## Results and Discussion

### Analysis of variance

The analysis of variance (ANOVA) indicated highly significant differences among the genotypes for days to 50% flowering, days to 75% maturity, number of tillers per plant , plant height, biological yield per plant, harvest index, grain yield per plant and 1000 grain weight (Table 2) revealing the existence of sufficient genetic variability in the present set of breeding material for all the traits under study. The characters which have sufficient genetic variability suggested that a crossing programme involving diverse genotypes may lead to an overall improvement in wheat crop. As has been reported in the present study significant differences among the genotypes for different morphological and quality traits were also reported by Singh *et al.* (2014), Tewari *et al.* (2015), and Kumar *et al.* (2016a) in wheat crop.

### Genotypic and phenotypic variability

The phenotypic coefficient of variation (PCV) was slightly higher than their corresponding genotypic coefficient of variation (GCV) for all the agro-morphological and quality traits among the genotypes indicating that the characters were less influenced by the environment, therefore selection on the basis of phenotype alone can be effective for the improvement of these traits (Table 2). Higher values of PCV and GCV indicated high variability among the genotypes. The higher values of PCV and GCV were recorded for biological yield (20.31% and14.80 %) followed by 1000 grain weight (19.36% and 14.70%), harvest index (17.89% and 12.54%), number of tillers per plant (15.13% and 6.98%), grain yield (11.59% and 8.63%), and plant height (7.03% & 5.75%) indicating better opportunity for improvement in these traits through selection. The highest estimates of PCV and GCV for grain yield per plant was reported by Arya *et al.* (2017). Taneva *et al*. (2019) also found that PCV was generally higher than the GCV for all the traits studied. As has been reported in the present study PCV and GCV ranged from 1.98 to 33.03% and 1.75% to 32.03%, respectively, has also been reported by Verma *et al.* (2014) whereas PCV and GCV ranged from 0.81% to 9.07% and 0.50% to 8.08%respectively in studies by Kumar *et al.* (2017). High value of PCV and GCV for grain yield and tillers per plant were also reported by Singh *et al.* (2013), Singh *et al.* (2014) and Kumar *et al.* (2016a). A close examination of phenotypic and genotypic coefficient of variation indicated better opportunity for improvement in grain yield based on the selection of above traits in wheat crop.

### Estimates of heritability (broad sense) and genetic advance

The estimates of high heritability (>50%) coupled with high genetic advance (>20%) was observed for biological yield per plant and 1000 grain-weight whereas, high heritability coupled with low genetic advance was observed for days to 75% maturity, plant

**Table 1. Pedigree of the wheat genotypes used in the present investigation**

| Sr. No. | Genotype | Pedigree |
|---|---|---|
| 1 | VL 907 | DYBR 1982-83842ABVD 50/VW9365//PBW 343 |
| 2 | TC1- 7 | SDSS12B00678S-0B-0B-271Y-0B<br>JAL95. 4.3/3/KACHU#1/ KIRITAT1// KACHU |
| 3 | TC1- 10 | SDSS12B00678S-0B-0B-79Y-0B<br>JAL95.4.3/3/KACHU#1/KIRITAT1//KACHU |
| 4 | TC1- 17 | SDSS12B00678S-0B-0B-456Y-0B<br>JAL95.4.3/3/KACHU#1/KIRITAT1//KACHU |
| 5 | TC1- 19 | SDSS12B00678S-0B-0B-46Y-0B<br>JAL95.4.3/3/KACHU#1/KIRITAT1//KACHU |
| 6 | TC1- 24 | SDSS12B00678S-0B-0B-487Y-0B<br>JAL95.4.3/3/KACHU#1/KIRITAT1//KACHU |
| 7 | TC1- 23 | Early SDSS12B00678S-0B-0B-473Y-0B<br>JAL95.4.3/3/KACHU#1/KIRITAT1//KACHU |
| 8 | TC1- 25 | Early SDSS12B00678S-0B-0B-488Y-0B<br>JAL95.4.3/3/KACHU#1/KIRITAT1//KACHU |
| 9 | TC1- 27 | SDSS12B009277-04-0B-0B<br>IG41514 /5 /SERI.1B/ KAUZ/HEVO/3/AMAD*2/4/ KIRITATI/6/FRET2*2 /4 /<br>SN1/TRAP#1/3/KAUZ*2/.. |
| 10 | HS 507 | KAUZ/MYNA/VUL//BUC/FLK//4/MILAN |
| 11 | E-1 | KACHU<br>CMSS 97M03912T-040Y-020Y-030M-020Y-040M-4Y-3M-0Y |
| 12 | E-2 | BAJ#1<br>CGSSS 01Y00134S-099Y-099M-099M-13Y-0B |
| 13 | E-6 | SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITAT 1<br>CGSSB00198T-099T0PY-099M-099NJ-14WGY-0B |
| 14 | E-8 | HPW 234+LR34/PRINIA*2//KIRITAT1<br>CGSS05B00244T-099T0PY-099M-099NJ-10WGY-0B |
| 15 | E-9 | WHEAR/KRONSTAD F2004<br>CGSS04Y00106S-099Y-099M-099Y-099M-13WGY-0B |
| 16 | E-11 | CNDO/R143/ENTE/MEXI.2/3/AEGILOPS SQUARROSA(TAUS)/4/WEAVER/5/..<br>CMSS04M01331S-0T0PY-099ZTM-099Y-099M-3WGY-0B |
| 17 | E-12 | KAUZ//ALTAR84/AOS/3/PASTOR/4/MILAN/CUPE//SW89.3064/ 5/KIRITAT1<br>CMSS04MO1386S-0T0PY-099ZTM-099Y-099M-2WGY-0B |
| 18 | E-13 | SW89.5277/BORL95//SKAUZ/3/PRL/2*PASTOR/4/HEILO<br>CMSS04M01483S-OT0PY-099ZTM-099Y-099M-1WGY-OB |
| 19 | E-14 | PRL/2*PASTOR//PBW343*2/KUKUNA/3/ROLF07<br>CGSS04B00025T-099Y-099ZTM-099Y-099M-8WGY-0B |
| 20 | E-21 | QUAIU #1<br>CGSS01B00046T-099Y-099M-099M-099Y-099M-29Y-0B |
| 21 | E-23 | VOROBEY<br>CMSS96Y02555S |
| 22 | E-24 | ROELFS F2007<br>CGSS00B00169T-099TOPY-099M-099Y-099M-9CEL-0B |
| 23 | E-25 | NAVOJOA M 2007<br>CMSS97404045S-040Y-050M-040SY-030M-14SY-010M-0Y-OMEX |
| 24 | GS 7038 | SOKOLL/3/PASTOR//HXL7573/2*BAU*2/4/NAVJ07 |
| 25 | GS 6012 | KACHU/6/YAR/AE.SQUARROSA<br>(783)/4/GOV/AZ//MUS/3/SARA/5/MYNA/VUL//JUN |
| 26 | GS 5031 | PRL/2*PASTOR//KACHU |
| 27 | HPW 373 | MILAN//BUC/CHRC/3/METSO |
| 28 | HPW 349 | OASIS/SKAUZ//4*BCN/3/2*PASTOR/4/KAUZ*2/YACO//KAUZ |
| 29 | HPW 368 | NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR |
| 30 | HS 562 | OASIS/SKAUZ//4*BCN/3/2*PASTOR |

height and grain yield per plant (Table 3). Similar findings pertained to high heritability with high genetic advance in wheat were earlier reported by Singh *et al. (*2013), Singh *et al. (*2014), Meena *et al. (*2014) and Kumar *et al. (*2016a). High heritability along with high genetic advance and high coefficient of variability (PCV and GCV) for biological yield and 1000 grain weight inferred good scope for improving these traits through selection. The traits viz., days to maturity, plant height and grain yield per plant that showed high heritability but moderate to low genetic advance and coefficient of variation whereas productive tillers showed moderate heritability, genetic advance and coefficient of variation which may be due to non-additive gene action and therefore, simple selection may be suitable. In this case hybridization followed by selection of desirable transgressive segregants would be a better option for improving such traits.

**Table 2. Analysis of variance (ANOVA) for eight agro- morphological and yield traits in wheat**

| Character | Replication (df=2) | Treatments (df=29) | Error (df=58) |
|---|---|---|---|
| Days to 50 % flowering | 31.93 | 11.19** | 4.00 |
| Days to 75%maturity | 19.21 | 35.28** | 5.67 |
| Plant height (cm) | 33.41 | 93.43** | 16.68 |
| No. of tillers per plant | 1.24 | 0.47* | 0.26 |
| Biological yield per plant (g) | 18.24 | 19.15** | 4.80 |
| Harvest index(%) | 217.72 | 133.77** | 39.06 |
| Grain yield per plant(g) | 0.39 | 1.35** | 0.28 |
| 1000 grain weight (g) | 8.92 | 164.12** | 35.93 |

**Table 3. Estimates of genetic parameters for 8 morphological and yield traits in wheat**

| Character | Mean | Range | PCV (%) | GCV (%) | Heritability $h^2bs$ (%) | Genetic Advance(as % of mean) |
|---|---|---|---|---|---|---|
| Days to 50% flowering | 110.50 ± 1.16 | 106.00-114.00 | 2.30 | 1.40 | 37.32 | 1.76 |
| Days to 75% maturity | 139.72 ±1.36 | 134.33-145.00 | 2.82 | 2.26 | 64.17 | 3.73 |
| Plant height (cm) | 92.74 ±2.16 | 82.71-104.79 | 7.03 | 5.75 | 66.96 | 9.69 |
| Tillers per plant | 3.80 ± 0.29 | 3.00-4.67 | 15.13 | 6.98 | 21.30 | 6.64 |
| Biological yield per plant (g) | 15.19 ± 1.22 | 12.00-19.89 | 20.31 | 14.80 | 53.11 | 22.22 |
| Harvest index (%) | 46.82 ± 3.45 | 32.28-54.97 | 17.89 | 12.54 | 49.11 | 18.10 |
| Grain yield per plant (g) | 6.89 ± 0.31 | 5.90-8.27 | 11.59 | 8.63 | 55.37 | 13.22 |
| 1000- grain weight (g) | 45.78 ± 3.33 | 34.54-56.10 | 19.36 | 14.70 | 57.62 | 22.98 |

**Cluster analysis**

The results of genetic diversity among 30 diverse wheat genotypes for various morphological and quality traits are presented in Table 4. Thirty genotypes were grouped into thirteen clusters by non-hierarchical Euclidean cluster statistics. The genotypes within a cluster had small or low $D^2$ values than those between the clusters. The compositions of clusters revealed that Cluster II and Cluster IV had the highest number of genotypes (9) followed by Cluster I (2). The grouping of genotypes based on multivariate analysis has also been reported earlier in wheat by Singh *et al.* (2014), Verma *et al.* (2014), Tewari *et al.* (2015), Kumar *et al.* (2016b) and Vora *et al.* (2017). The inter cluster distance was higher than the intra cluster distance indicating wide genetic diversity among the genotypes belonging to different clusters (Table 5).

The highest inter-cluster distance was between cluster VIII and X (5.18) followed by cluster VI and X (4.92). which indicated that genotypes in these clusters have wide genetic diversity and thus can be used in wheat breeding programme for improving grain yield. The inter-cluster values indicating close relationship indicated that hybridization among the genotypes of these clusters would not yield good level of segregation. Highly divergent genotypes would yield broad spectrum of transgressive segregation in the subsequent generations enabling further selection and improvement.

**Table 4. Distribution of 30 wheat genotypes among clusters on the basis of $D^2$-analysis.**

| Cluster no. | Genotypes |
|---|---|
| I | **2** (HS507, HPW 368) |
| II | **9** (E-12, GS 5031, E-6, E-13, E-8, TC1-19, E-14, TC1- 23, E-21) |
| III | **1** (E-9) |
| IV | **9** (TC1-27, E-1, HS 562, GS 7038, TC1F4 25, TC1- 10, E-23, TC1 - 1, TC1- 17) |
| V | **1** (GS 6012) |
| VI | **1** (E-24) |
| VII | **1** (E-25) |
| VIII | **1** (TC1- 7) |
| IX | **1** (E-11) |
| X | **1** (TC1- 24) |
| XI | **1** (HPW 373) |
| XII | **1** (E-2) |
| XIII | **1** (VL907) |

**Table 5. Average intra and inter-cluster distance**

| Cluster | I | II | III | IV | V | VI | VII | VIII | IX | X | XI | XII | XIII |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | **1.12** | | | | | | | | | | | | |
| II | 3.36 | **1.98** | | | | | | | | | | | |
| III | 3.59 | 2.33 | **0.00** | | | | | | | | | | |
| IV | 2.94 | 2.70 | 2.71 | **2.05** | | | | | | | | | |
| V | 2.59 | 2.74 | 3.61 | 2.72 | **0.00** | | | | | | | | |
| VI | 3.65 | 3.54 | 3.21 | 2.61 | 3.76 | **0.00** | | | | | | | |
| VII | 3.12 | 2.33 | 3.12 | 2.65 | 2.08 | 3.59 | **0.00** | | | | | | |
| VIII | 4.37 | 3.51 | 3.74 | 3.12 | 4.36 | 2.60 | 4.28 | **0.00** | | | | | |
| IX | 3.09 | 2.37 | 2.73 | 2.65 | 2.88 | 3.13 | 3.48 | 2.38 | **0.00** | | | | |
| X | 3.95 | 2.58 | 2.89 | 3.60 | 3.30 | 4.92 | 2.10 | 5.18 | 3.99 | **0.00** | | | |
| XI | 3.67 | 3.24 | 3.89 | 2.89 | 3.36 | 2.31 | 3.11 | 2.21 | 2.82 | 4.55 | **0.00** | | |
| XII | 3.58 | 3.23 | 1.95 | 2.79 | 3.78 | 3.96 | 3.45 | 4.60 | 3.68 | 3.18 | 4.70 | **0.00** | |
| XIII | 3.41 | 3.62 | 4.09 | 2.73 | 3.56 | 3.53 | 3.18 | 3.52 | 3.72 | 4.46 | 3.33 | 3.77 | **0.00** |

The low genetic diversity and selection of parents within the cluster having higher mean values for a particular character may also be useful for further improving wheat genotypes for grain yield. The highest intra-cluster distance was observed to be in cluster IV (2.05) followed by cluster II (1.98) and cluster I (1.12) and in the remaining clusters, there was only one genotype in each, thereby the intra-cluster distance was zero. Therefore, the highest intra-cluster divergence was in cluster I however, it was low, hence, the chances of developing superior genotypes among parents within clusters would be very low. It is logical to attempt crosses between the genotypes falling in different clusters based on inter-cluster distance to develop improved genotypes for increased grain yield in wheat.

Cluster I (HS 507 and HPW 368) showed maximum values for biological yield per plant. Cluster III (E 9) showed minimum values for days to 75% maturity and cluster XIII showed minimum value for days to 50% flowering . Cluster VI (Roelfs F 2007) showed maximum values for tillers per plant and cluster VIII ( TC1-7) showed maximum value for plant height (Table 6). Cluster XI (with genotype HPW 373) showed maximum values for harvest index and cluster XII having variety Baj#1 showed maximum value for grain yield per plant and 1000-grain weight. The highest inter-cluster distance of 5.18 was observed between cluster VIII (TC1-7) and X (TC 1-24) followed by cluster VI having high tiller no (Roelfs F 2007 ) and cluster X (TC 1-24) with a distance of 4.92 indicated that genotypes in these clusters have wide genetic diversity and thus can be used in hybridization programme for improving grain yield. Selection of genotypes from these clusters may be used as potential donors for further hybridization programme to develop genotypes with high yield potential in wheat. The maximum contribution towards genetic divergence was exhibited by plant height (24.83%) followed by days to 75% maturity (20.92%), biological yield per plant (17.93%) and 1000-grain weight (15.17%) (Table 7). The traits viz; days to 50% flowering, tillers per plant, harvest index and grain yield per plant had low percentage of contribution to total genetic divergence, therefore these traits may be used as selection parameters in segregating generations.

## Conclusion

The present results suggested that analysis of variance (ANOVA) showed significant differences among the genotypes for all morphological and yield traits. Cluster XI with genotype HPW 373 showed maximum values for harvest index. Based on high yield and harvest index this genotype has been recently released for its cultivation in the state of Himachal Pradesh. Cluster XII including variety Baj#1 showed maximum value for grain yield per plant and 1000-grain weight. Looking at the disease resistance and quality aspect Baj #1 is a PVS variety and has been released in North Western Plain Zone in India during 2010 (Mondal *et al*. 2020). This variety can be exploited in breeding programme or may be released as direct variety in the state of Himachal Pradesh. The traits with sufficient variability suggested that hybridization programme involving diverse genotypes may lead to transgressive segregants leading to overall genetic improvement in wheat crop. Hybridisation between variety TC1-7 and TC 1-24 and Roelfs F 2007 ( having high tiller number) and TC 1-24 belonging to different cluster groups may lead to variability. Inter cluster distance indicated sufficient genetic diversity between and within clusters, hence, it would be desirable to choose the donor from different clusters.

**Conflict of interest:** There is no conflict of interest among the authors.

**Table 6. Cluster means and contribution of individual characters to the divergence among 30 genotypes of wheat**

| Traits | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII | Cluster VIII | Cluster IX | Cluster X | Cluster XI | Cluster XII | Cluster XIII | Mean | Min. | Max. |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | 111.17 | 109.33 | 109.67 | 111.19 | 114** | 114** | 111.67 | 109.33 | 110 | 109 | 114** | 109.33 | 107* | 110.75 | 107 | 114 |
| Days to 75% maturity | 139.67 | 136.63 | 134.33* | 142.22 | 142.33 | 143.67 | 142.33 | 140.67 | 136 | 136.33 | 144.33 | 137.67 | 145** | 140.09 | 134.33 | 145 |
| Plant height | 90.17 | 92.26 | 94.56 | 92.46 | 85.11 | 104.22 | 88.44 | 104.79** | 95.67 | 82.71* | 101.78 | 86.78 | 95.44 | 93.41 | 82.71 | 104.79 |
| Tillers per plant | 3.61 | 3.95 | 3.89 | 3.79 | 3.78 | 4.22** | 3.78 | 4 | 4 | 3.78 | 3.44 | 3.33 | 3.00* | 3.74 | 3.00 | 4.22 |
| Biological yield per plant | 21.02** | 13.68 | 14.94 | 16.05 | 16.35 | 13.54 | 11.33 | 14.33 | 17.89 | 12 | 11.18* | 18.22 | 16.33 | 15.14 | 11.18 | 21.02 |
| Harvest index | 30.84* | 48.46 | 50.64 | 46.76 | 37.08 | 53.39 | 52.61 | 53.63 | 39.65 | 54.97 | 57.2** | 45.48 | 41.27 | 47.08 | 30.84 | 57.2 |
| Grain yield per plant | 6.26 | 6.52 | 7.51 | 7.37 | 6.06 | 7.22 | 5.9* | 7.61 | 7.07 | 6.42 | 6.39 | 8.27** | 6.63 | 6.86 | 5.9 | 8.27 |
| 1000-grain weight | 46.8 | 44.11 | 59.92 | 47.55 | 37.58 | 52.72 | 44.58 | 35.44 | 37.23 | 49.36 | 32.5* | 63.34** | 42.14 | 45.64 | 32.5 | 63.34 |

**Table 7. Contribution of individual characters to the divergence among 30 genotypes of wheat**

| Traits | Times Ranked 1st | Contribution % |
|---|---|---|
| Days to 50% flowering | 22 | 5.06 |
| Days to 75% maturity | 91 | 20.92 |
| Plant height (cm) | 108 | 24.83** |
| Tillers per plant | 18 | 4.14* |
| Biological yield per plant (g) | 78 | 17.93 |
| Harvest index(%) | 25 | 5.75 |
| Grain yield per plant(g) | 27 | 6.21 |
| 1000-grain weight | 66 | 15.17 |

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