

Cluster Analysis and Evaluation Genetic Variation to Determine the Best Crosses in Bread Wheat (*Triticum aestivum* L.) Cultivars in Isfahan Province

Saeed Salehi^{1*}, Ghorban Noormohammadi² and Seyyed Mohammad Javad Mirhadi²

¹Young Researchers and Elite Club, Sanandaj Branch, Islamic Azad University, Sanandaj, Iran.

²Department of Agronomy, Science and Research Branch, Islamic Azad University, Tehran, Iran.

doi: <http://dx.doi.org/10.13005/bbra/1496>

(Received: 18 October 2014; accepted: 30 November 2014)

Indirect selection in early generations through traits having heritability higher than yield as well as correlated significantly with seed yield is one of the most important breeding procedures. Production of new cultivars adaptable to different environments also has importance for wheat breeders. Cross among new cultivars and selection of superior genotypes among their progenies based on suitable traits is efficient breeding procedures. Therefore in order to determination of the most yielding bread wheat genotypes identification of the traits affective on seed and protein yield as well as parents of the best crosses an experiment was conducted 2012-2013. Assessment of variation is important in wheat breeding programs to choice the best parents. Genetic improvement of wheat depend on genetic variability existence in germplasm. On the other hand, wheat (*Triticum aestivum* L.) is the major cereal crop in Iran on which the food security rests. Therefore, in order to evaluate and classify bread wheat genocultivars, eighteen cultivars were sown in randomized complete block design with three replications. Cluster analysis using ward's method grouped these cultivars in four clusters. Similarity between results of principal component and cluster analysis were observed for classification of genocultivars. Cluster analysis showed the efficacy of crossing between genocultivars 4 and 8 from cluster 4 with genocultivars 11 from cluster 1 to heighten genetic variation and transgressive segregation via genes having additive effects specifically in segregating generations. Overall, crosses among cultivars having maximum genetic distance can be resulted higher transgressive segregation and genetic gain of selection. Increasingly, cross between genocultivars 5 and 1 as well as selection among their progenies have the best result to produce new cultivars and hybrid seed.

Key words: Bread wheat, genetic variation, hybrid seed, cluster analysis, ward method.

The purpose of plant breeding, genetic improvement of a varieties in the best way possible. Obviously, the economic Value for it depends on a cultivars of different traits. so how to choose multiple characteristic is always plant breeders

consideration¹. Although there is positive correlation between yield and number of it's yield components, there is negative relationship between yield components so, yield components can't improve seed yield in cereal². If divided simple correlation between characteristics according to analysis method into direct and indirect effect so we can clear effective characteristic role on yield and do indirect choosing methods for improving seed yield³. Plant breeders are trying to identify

* To whom all correspondence should be addressed.
E-mail: ss136555@yahoo.com

new ways to increase efficiency in the production of new varieties¹. Various algorithms have been used in studying of genetic diversity in cluster analysis of which, UPGMA and Ward's methods are the most popular approaches. Of the algorithms, UPGMA, Ward's, SLINK, and CLINK, applied for cluster analysis and exploring genetic diversity and grouping of plant materials in the past, the UPGMA is the most valid method in accordance with the relationship of family based on their genetic material⁴. Chaining effect in UPGMA model is considered as the major drawback on application of this approach in cluster analysis and results in confusions in interpretation of the results⁴. In order to benefit transgressive segregation, genetic distance between parents is necessary⁵. The higher genetic distance between parents, the higher heterosis in progeny can be observed. Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production. One of the important approaches to wheat breeding is hybridization and subsequent selection. Parents' choice is the first step in plant breeding program through hybridization. Usually before calculating the genetic distance, the variables are standardized so that all variables are of similar 18 standardization decreases the differences among groups. The results of cluster analysis and PCA may have relative differences with each other. Therefore, before using cluster analysis, the principle components may be avoided. On the other hand, when the two first principal components account for high variation percentage, grouping according to these two components, may be avoided. On the other hand, when the two first principal components account for high variation percentage, grouping according to these two components, can certainly be a useful method to find the clusters⁶. Ward's approach is similar to UPGMA method but it without having chain effect issues. Results of using PCA showed that this method is limited when the pattern of variation is not based on a 0 and 1 scores. Therefore, combined PCA and other techniques can be appropriately used for grouping⁴. The cluster analysis is an appropriate method for determining family relationships. The main advantage of using PCA over cluster analysis is that each genotype Cultivars can be assigned to

one group only⁷. The main objective of this study is to capture the potential genetic diversity between wheat genotype Cultivars grown in Iran by using cluster analysis based on ward's method. Shafa-e-Din Banadaki (1992) in his study shows that genetic diversity and geographical diversity on wheat related to Five central province of Iran report that all of parts regarding to all of characteristic there is meaningful differences and by using cluster analysis of studied cities we divided it into 9 cluster and stated that genetic diversity is comply with geographical diversity and by total average shows that most of characteristics have proper diversity⁸. Analysis of Noori (1993) with genetic diversity and geographical diversity of local wheat in west of Iran there is meaningful differences at 1% level between different places so by cluster analysis mentioned places divided into 6 cluster⁹. Murphy *et al.*, (1986) used cluster analysis and principal component analysis to classify wheat lines to select landraces, cultivars and hybrids in wheat breeding populations showed¹⁰. Fang *et al.*, (1996) based on the characteristics of maturity, plant height, spike length, number of grains per spike, grain weight per spike and grain yield a 120 spring wheat varieties were divided into 5 groups by cluster analysis¹¹. Mohammadi *et al.*, (2002) using cluster analysis of 600 lines of native plants using the UPGMA method, WARD were classified into 6 clusters¹². As a result of regression analysis stage and favorable conditions of water stress on spring wheat cultivar and seed weight, biological yield and seed filling rate and strong positive correlation between the harvest index and biological yield most important components of seed weight respectively¹³. The highest amount of protein in the Parsi and in line 11 was the lowest. The higher protein yield in the Parsi due to the high percentage of protein. In line 11, low protein content and seed yield both a substantial decrease in protein yield¹⁴.

MATERIALS AND METHODS

Test at research field of Kabutar Abad station at Isfahan province in 2013 culture year had been done. At this test 16 wheat line with 2 witness Cultivars had been analysis. Experiment in a randomized complete block design with 3 replications was conducted. The experimental plot consisted of 6 rows of plants with a 2 m long and

20 cm between the lines (rows), respectively. Distance of plants on planted rows is 4 cm and distance of trial parts is 40 cm and repeated distance is 2m. Soil analysis had been done at Sharivar and after field preparation and primary in fertilizer use according to soil. Water and trial culture at end of October had been studied. Seed rate with regard to one hundred Seed weight used according to 400 seed per square meter. Preparation process of soil contains plough at the end of March and disking and dividing had been done correctly.

Culture treatment

Irrigation had been done during 1 to 5 of November, so during the winter season necessary works had been done and during spring weed control and insects had removed and during growing stages all of required analysis such as options, Tillering stage, plant height falling seed, date of growing and physiological Maturity had analyzed and measured and after that seed characteristic and bakery quality analyzed.

Sampling method for the studied traits

Sixteen traits viz ; seed yield (Kg/ha), spike weight (g), spike harvest index (%), plant harvest index (%), number of seed/spike, biological yield (Kg/ha), number of spikelet/spike, spike yield (g), 1000-seed weight (g), spike length (cm), plant height (cm), peduncle length (cm), grain filling duration, grain filling rate (Kg/ha/day), protein percentage (%) and protein yield (Kg/ha) were measured on 25 normal plants randomly selected from each plot after border effect eliminating.

Protein percentage

For determining protein percentage of first total amount of Nitrogen of seed measured by cajeldal method so obtained numbers by cajeldal system multiply at 5.7 to measuring protein percent, because there is 17.55 g Nitrogen at 100 gr protein and protein amount of seed define according to 13-14 moisture percent of mentioned method for determine seed protein percentage is according to st no 105.2 I.C.C.

Protein yield

Protein yield is product of protein percentage at seed yield.

Pedancle length

For measuring pedancle length we use a ruler so we sample 50 Cultivars from each line and by a ruler pedancle length measured pedancle thickness measured by Collis , in nex step from

each line 2 line planted ant 20 cm fill then by a measure weigh of seeds measured and weight of seeds measured separately.

Spike length, spike weight, spikelet number and seeds weight/spike

For measuring spike length, spike weight and it's weight at spike at first 5 sample had chosen per each line and by digital scale with confidence level of 0.02 determined.

After that spike length measured by a ruler and number of spikes determined finally, numbered spike weighted by scale.

Statistical Analysis

The center of each plot lines by removing the marginal effects of our target population. Analysis of variance, Duncan's method compared to the 5% level, correlation analysis, stepwise regression analysis, path analysis method and Davy Liu . Data analysis based on principal component analysis and rotation varimax and cluster analysis is based on Euclidean distance and Ward's method of analysis is that the numbers of this research was conducted. The statistical analysis using SAS statistical software, SPSS, was PATH2. Graphs were plotted using the Excel software.

RESULTS AND DISCUSSION

There were significant differences between wheat geno Cultivarss for all traits measured. By incision the dendrogram at 12.5 unit distance, the genoCultivarss categorized into four groups. Using discriminant analysis revealed that in this case 10% of the members of the second group were classified into the first Group. Then cutting point was determined at distance 12.5 and four clusters was obtained, in which the members completely belonged to the same group (Fig 1).

Four components were extracted from the

Table 1. Eigen value, percent of variance and cumulative variance of extracted components

Components	Eigen value	Variance (%)	Cumulative variance (%)
1	3.01	32.29	32.29
2	2.95	20.14	52.43
3	2.73	19.18	71.61
4	2.61	12.85	84.46

15 studied traits by PCA analysis. These four components that explained 84.64% of total variation were used for clustering genoCultivarss (Table 1). In fact, with this method, 15 variables were reduced to four components. Using the discriminant analysis the best incision point was determined at distance 12.5. By incision at distance 12.5, four distinct clusters were formed (Fig 1). Cluster one, comprised 5, 6, 12, 13, 18, 11, 16, 15 and 17 cultivars. Cluster two, involved onle one cultivar namely 14. Cultivars 9 and 10 were grouped in the cluster three. Finally, cluster four comprised 2, 7, 4, 8, 3 and 1 cultivars. Amongst, cultivar 11 from cluster one had the highest genetic potential for improving seed and protein yield especially in normal conditions. On the ther hand, cultivars 4 and 8 showed the potential for cultivation in stress environments hence crosses between cultivars 11 from cluster one with cultivars 4 and 8 from cluster four could be efficient in improvement bread wheat yield and other traits (Fig 1). Principal component analysis is suitable multivariate technique in identify and determination of independent components that are effective on plant traits separately. Because of that, traits effective in every component were identified and components also entitled based on traits having Eigen values greater than others. Therefore, correlation and principal component analysis helps breeders to genetic improvement traits such as yield that have low heritability specifically in early generations via

indirect selection for traits effective on this^{15,16,17}. Narouee Rad (2006) determined the genetic diversity of wheat landraces in the west of Iran and by using cluster analysis, six clusters were determined for different areas¹⁸. Feng *et al.*, (1996) clustered 120 geno Cultivarss of durum wheat into five groups based on maturity date, plant height, spike length, number of seed per spike, 1000-seed weight and spike seed yield¹⁹. Genetic diversity could be the result of geographical impact through evolution and hence traits could be considered as a function of variety^{20,21}. Estimation of genetic distance is one of appropriate tools for parental selection in wheat hybridization programs. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase^{22,23}. Some appropriate methods, cluster analysis, PCA and factor analysis, for genetic diversity identification, parental selection, tracing the pathway to evolution of crops, center of origin and diversity, and study interaction between the environment are currently available^{24,4,25}. In conclusion, Similirity between results of principal component and cluster analysis were observed for classification of genoCultivarss. Overall, crosses among cultivars having maximum genetic distance can be resulted higher transgressive segregation and genetic gain for selection among their progenies. In present study revealed the efficacy of crossing between genoCultivarss 4 and 8 from

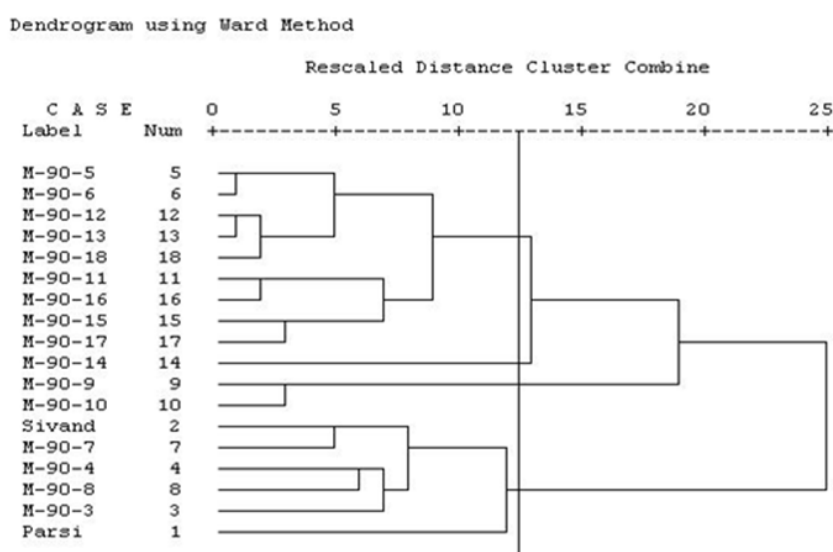


Fig 1. Dendrogram of cluster analysis based on ward's method on the measured traits in bread wheat cultivars

cluster 4 with genoCultivars 11 from cluster 1 to heighten genetic variation and transgressive segregation through genes having additive effects specifically in segregating generations.

CONCLUSION

1. Genetic variety between wheat line that help us to chose and genetic improvement of different characteristic in quality and quantity level.
2. Line 9 online late maturity and has a higher yield than the control (Persian and Seyvan) is. So this line to grow in water (without stress) is advisable. However, for conditions of drought stress lines 4 and 8 can be introduced. Because it was premature lines and have a high rate of seed filling.
3. Filling rate of seeds has more effect on seed yield and at the same time has positive correlation by seed yield and it seems that filling rate of seeds is the best measure of indirect choosing of seed to improving their yield.
4. Number of each spike per squar meter had direct effect but it's indirect effect see from filling seed way so is a proper measure for improving seeds yield especially if indirect effects had been consider to direct effects had been consider to direct effect of this property .
5. Filling term of seed although has positive and direct effect on seed yield, has negative direct effect on seeds filling that cause negative coronation coefficient so it isn't correct choice .
6. There isn't meaningful difference regarding protein percent line average of wheat,so there is humeral differences highest and lowest portion percent is in Parsi Cultivars and no:11 line.
7. Peduncle length, number of seeds spike are improving yield components in spike yield so we can use these characteristic in mentioned characteristic improve.
8. Peduncle diameter, days to flowering, days to maturity, plant height constituted factor increases photosynthesis and therefore increase the amount of resources that could lead to improved reservoir characteristics

in the extrusion, particularly for conditions of stress.

9. The confluence between lines 4 and 8 of 11 from cluster to cluster fourth line of qualitative and quantitative yield And most of the other characters in the two points are exactly opposite each other can, most source of genetic variation and transgressive segregation by genes with effects of increasing, especially in the separation of generations.

REFERENCES

1. Abuzari Gazafrodi., Genetic variation and correlation between morphological and electrophoretic data storage proteins in rice. MA thesis. Faculty of Agriculture. The University of Guilan, 2002.
2. Dewey RD; Lu KH. A correlation and path coefficient analysis of component of crested grass seed production. *Agron. J.* 1959; **51**: 515-18.
3. Rabiei B; Valizadeh M; Ghareyazie B; Moghaddam. Evaluation of selection indices for improving rice grain shape. *Field Crops Research.* 2004; **89**: 359-367.
4. Mohammadi SA, Prasanna BM., Analysis of Genetics diversity in crop plants: salient statical tools and considerations. *Crop Sci* 2003; **43**: 1235-1248.
5. Joshi BK, Mudwari A, Bhatta MR, Ferrara GO. Genetic diversity in Nepalese wheat cultivars based on agromorphological traits and coefficients of parentage. *Nep Agric Res J* 2004; **5**: 7-17.
6. Fotokian M, Shahnejat bushehri A, Taleie A. Cluster analysis based on PCA in rice genoCultivarss. Paper presented at the 6rd international conference of Statistics, University of Tarbiat modares, Iran, 2002.
7. Mohammadi SA. Statistical methods in genetics. Paper presented at the 6rd international conference of Statistics, University of Tarbiat modares, Iran, 2002.
8. Shaf-e-din benadaky S. Genetic variety analysis of local wheat in central part of Iran ,agriculture university Tehran, university, 1992.
9. Noori F., Genetic verities analysis local wheat of Iran of ,Tehran university agriculture university, 1993; 135.
10. Murphy J P; Cox T S and Rodgers D M . Cluster analysis of red winter wheat cultivars based upon coefficient of parentage. *Crop Sci.*

- 1986; **26**: 672-676.
11. Fang X W, Xiong E H, Cao Y, Cai S B and Zhu W., Cluster analysis of elite wheat germplasm. *Jiangsu Agric. Science* 1996; **4**: 14-16.
12. Mohammadi MM, Ghanadha RVA, Taleei A. Assessment of genetic diversity in native Iranian bread wheat lines using multivariate statistical methods. *Seed and Plant Journal* 2002; **34**.
13. Naderi A, Dezfuli H., Razaee M., Effective characteristic study and seed weight and determining physiologic parameter effect on seed. Yield in proper and stress conditions. Abstracts of Crop Science Congress. Mazandaran University. 2002; 121.
14. Salehi S, Noormohammadi G, Mirhadi M J, Ghandi A., Assessment of protein yield criteria through correlation regression and path analysis in bread wheat (*Triticum aestivum* L.) cultivars. *J. IJFAS*. 2013; **2**(S):1298-1301.
15. Royo C, Miloudi MM, Fonze ND, Arraus JL, Pfeiffer WH, Slafer GA., Durum wheat breeding current approaches and future strategies. Vol 1: Food Product press. Newyork; London; Oxford. 2005; 1984.
16. Leilah AA, Al-Khateeb SA., Statistical analysis of wheat yield under drought conditions. *J. Arid. Environments*. 2005; **61**: 483-496.
17. Dogan R., The correlation and path coefficient analysis for yield and some yield components of durum wheat (*Triticum turgidum* var. durum L.) in west Anatolia conditions. *Pak. J. Bot.* 2009; **41**(3): 1081-1089.
18. Narouee Rad M., Evaluation of genetic diversity and factor analysis for morphologic traits of wheat landraces of Sistan-Baloochestan. J Pajouhesh-va-Sazandegi in Persian, abstract in English 2006; **73**: 50-58.
19. Feng L, Sebastian S, Smith S, Cooper M., Temporal trends in SSR allele frequencies associated with long-term selection for yield of maize. *Maydica* 2006; **51**: 293-300.
20. Pirayeshfar B, Jalal kamali MR, Najafian G, Keshavarz A, Nourinia A, Lotfinejad L., The quality of bread wheats produced in Iran during 2003-04 cropping season. Proceeding of the 9th Iranian Congress of Crop Sciences. Univ. of Tehran, Abureyhan campus, 2006.
21. Akram Z, Ajmal S, Munir M., Estimation of correlation coefficient among some yield parameters of wheat under rainfed conditions *Pakistan J. Bot.* 2008; **40**(4): 1777-1781.
22. Samiee M., The quality of Iranian wheats. Self Sufficiency and Research Center for Milling; Baking and Related Industries Publications. Affiliated to the Iranian Ministry of Industry; Tehran. 2004; 56.
23. Islam MR., Genetic diversity in irrigated rice. *Pak J Biol Sci* 2004; **2**: 226-229.
24. Nazan D., Genetic analysis of grain yield per spike and some agronomic traits in diallel crosses of Bread wheat (*Triticum aestivum* L.). *Turk. J. Agric. For.* 2008; **32**: 249-258.
25. Eivazi AR, Naghavi MR, Hajheidari M, Pirseyedi SM, Ghaffari MR, Mohammadi SA, Majidi I, Salekdeh GH, Mardi M., Assessing wheat (*Triticum aestivum* L.) genetic diversity using quality traits, amplified fragment length polymorphisms, simple sequence repeats and proteome analysis. *Ann Appl Biol* 2007; **152**: 81-91.