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Estimation of Genetic Diversity of Sunflower Single Cross Hybrids Using Principal Components Analysis

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Abstract: In order to study genetic diversity of sunflower single cross hybrids through the using principal components analysis, a North Carolina Design I experiment was conducted in a randomized complete block design in three replications at Agricultural and Natural Research Station of Khoy. In 2005, six fertility restorer male lines crossed with 18 cytoplasmic male sterility female lines. Each male line crossed with 3 different female lines to make 2 sets with 9 hybrids in each set. In 2006, Single cross F_1 hybrids were planted for studying genetic diversity. Data were collected from agronomic traits including: flowering initiation, seed filling period, maturity, plant height, head diameter, 1000 seed weight, seed numbers per head, harvest index, oil content, seed yield and oil yield. Survey results showed that three first components explained variability of the all data (77.20%). Traits including seed numbers per head, harvest index, oil content, seed yield and oil yield were the main parts of first component, while second component affected mainly by flowering initiation, maturity and plant height. Seed filling period, head diameter, seed yield and oil yield were the important parts of third component. Totally, first component with high amount of total variance and high correlation with traits including seed yield, oil yield, seed numbers per head, oil content and harvest index could be appropriately useful in grouping and selecting of superior single cross hybrids.

Key words: Diversity, hybrid, principal components analysis, sunflower, traits, flowering initiation

INTRODUCTION

In recent years, lots of sunflower single cross and three-way-cross hybrids have been produced in the country, Iran and selection of the best of them in regional preliminary experiments is very important. Multivariate statistical methods that can create relationship between cultivar traits can help to grouping cultivars and easy selection of them on the basis of biplot and triplot diagrams. Principal components analysis method through the summarizing preliminary correlated varieties in the form of independent and limited components provides the possibility of genotype grouping in the 2D or 3D space (Moghaddam *et al*., 1994). Spranaaij and Bos (1993) due to giving acceleration to the genotypes selection from the aspect of traits like seed yield use principal components analysis, used this for the reduction selection cost and know this very useful in the preliminary stage of cultivars selection. Kroonenberg *et al.* (1995) know this method with three-way-cluster analysis to the separating of genotypes in limited bunches for the manipulation, also Cheres and Knapp (1998) have used the efficient grouping of this method for the evaluation of genetic diversity in sunflower germplasm and determination of ancestral relationship. De La Vega *et al.* (2001) have used principal components analysis for determination of interaction among different sunflower cultivars with cultural media and consideration of indirect selection possibility of yield in such media. Ghaffari (2003) used this method for rapid screening among 121 sunflower cultivars and hybrids that logical cultivars grouping through the influence from agronomic traits could be used as an efficient factor in superior and early mature hybrid selection. Zeinalzadeh and Ghaffari (2005) have used this method for the survey of genetic diversity of sunflower genotypes and in their experiment, commercial cultivars such as Azargol, Record, Armavirski and Hysun33 well-distinguished from three-way-cross hybrids through the high seed and oil yield by first component. In biplot and triplot diagrams, designed on the basis of achieved facts from principal components analysis, traits influence on the genotype grouping in different vector forms and the position of every genotype on the basis of selected component type are shown. Length of any vector shows the weight of that in creation of distinguished groups and is correlated with the amount of component for the related traits.

Through, the designing of a vertical line from a genotype location to trait vector, genotypes can be compared. In effect, the more there is distance of

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conjunction of line with origin, there is more diversion of genotype yield from others (Chapman *et al.*, 1997). Angle among the vectors in such diagrams shows the correlation of them (Kroonenberg, 1997). This kind of relationship among the agronomic traits and related vectors in formed diagrams is grouping experimental genotypes logically and orientally. This method can be used as an agent for surveying of genetic diversity of evaluated materials and also for selection of superior genotypes in preliminary experiments. The aim of this study is for the use of principal components analysis and obtained biplot and triplot diagrams and for surveying of genetic diversity and selection of superior sunflower single cross hybrids, which are under study and for determination of relationship among traits.

MATERIALS AND METHODS

This experiment was conducted at Agricultural and Natural Resources Research Station of Khoy, Iran (44°58'N, 38°33'E) in 2004 and 2005. The minimum, average and maximum annual temperature of this station are respectively-30, 12.5 and 42°C and the average annual rainfall is 292.6 mm. Plant material of this experiment are sunflower single cross hybrids obtained from crosses of 6 male restorer lines (R-line) with 18 female cytoplasmic male sterile (CMS or A line) lines, which have been produced at Agricultural and Natural Resources Research Station of Khoy in 2003 (Fig. 1). In each set, three R lines crossed with different three CMS lines and on aggregate developed nine hybrids in each set. Hybrids containing common male parent are counted as half-sib family. Mating had been done as a nested design in North Carolina Design I plan, as such, CMS lines have been nested inside restorer lines. F_1 hybrids obtained from crosses have been planted for the principal components analysis and surveying of genetic diversity in 2005.

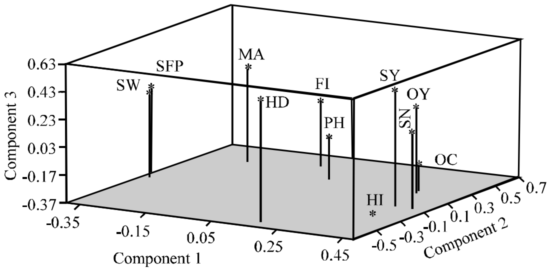

Fig. 1: 3D Diagram of first three component weights for agronomic traits on sunflower single cross hybrids. FI: Flowering Initiation; SFP: Seed Filling Period; MA: Maturity; PH: Plant Height; HD: Head Diameter; SW: 1000 Seed Weight; SN: Seed Number per Head;HI: Harvest Index;OC: Oil Content; SY: Seed Yield; OY: Oil Yield

Surveyed traits are: flowering initiation, seed filling period, maturity, plant height, head diameter, 1000 seed weight, seed numbers per head, harvest index, oil content, seed yield and oil yield. Correlation among the varieties has been done through the use of SPSS software and principal components analysis through the use of Statgraphics and biplot and triplot diagrams are designed.

On the basis of characteristics of every hybrids and direction and angle of related vectors, the position of 18 hybrids in biplot and triplot diagrams have been clarified and on the basis of that the range of existed diversity and methods of obtained grouping have been considered. Hybrids characteristics are shown in these charts.

Hybrid name	R-line	A-line
A	R_{43}	CMS_{28}
B		CMS_{128}
C		CMS_{346}
D	R_{27}	CMS_{330}
E		CMS_{78}
F		CMS_{328}
G	R_{34}	CMS_{336}
H		CMS_{52}
I		CMS_{148}

Hybrid name	R-line	A-line
J	R_{56}	CMS_{344}
K		CMS_{260}
L		CMS_{32}
M	R_{25}	CMS_{222}
N		CMS_{96}
O		CMS_{356}
P	R_{32}	CMS_{356}
Q		CMS_{196}
R		CMS_{376}

RESULTS AND DISCUSSION

Results of this study showed that three first components explained 77.20% of total variability of the all data (Table 1). Each component is a linear composition of primary eleven variables and consists of their variances. Therefore, diversity of evaluated genotypes from the eleven traits aspect could be explanted with few numbers of new components that have no correlation with each other and this matter can be presented in a 2D or 3D space (Moghaddam *et al.*, 1994). Portion of each three components was approximately 46, 18 and 12%, respectively. Greatness of these numbers influences good separation of genotypes and shows high valuable relations. If there would be correlations or similarities among genotypes, these components can provide suitable grouping and separate same genotypes in distinct groups.

Table 1: Variance of components in principal components analysis method

Component number	Eigen value	Variance percentage	Cumulative percentage
1	5.10	46.40	46.40
2	2.01	18.32	64.73
3	1.37	12.47	77.20
4	0.99	9.03	86.24
5	0.74	6.72	92.96
6	0.38	3.49	96.46
7	0.20	1.88	98.35
8	0.13	1.19	99.54
9	0.03	0.32	99.86
10	0.01	0.12	99.99
11	0.00	0.00	100.00

Table 2: Structure of first three components for agronomic traits

Traits	Component 1	Component 2	Component 3
Flowering Initiation (FI)	-0.05	0.57	0.09
Seed Filling Period (SFP)	-0.32	-0.01	0.32
Maturity (MA)	-0.23	0.50	0.29
Plant Height (PH)	0.06	0.36	-0.06
Head Diameter (HD)	0.16	-0.44	0.49
1000 Seed Weight (SW)	-0.35	0.03	0.23
Seed Number per head (SN)	0.41	0.06	0.17
Harvest Index (HI)	0.32	0.00	-0.37
Oil Content (OC)	0.35	0.28	-0.16
Seed Yield (SY)	0.37	0.07	0.46
Oil Yield (OY)	0.40	0.14	0.31

Equation of every three first components has been shown in Table 2. For example equation of first component is:

$$Z1 = -0.05\ FI - 0.32\ SFP - 0.23\ MA + 0.06\ PH + 0.16\ HD - 0.35\ SW + 0.41\ SN + 0.32\ HI + 0.35\ OC + 0.36\ SY + 0.40\ OY$$

Data are standard in Table 1 and 2. Therefore, amounts of them show their weights in comprising of related component. It's considerable that seed numbers per head, harvest index, oil content, seed and oil yield are main parts of first component. Thus, this component can provide a great grouping among genotypes from the aspects of seed and oil yield and separate high yielded hybrids from low yielded ones (Table 2). Second component was more affected by flowering initiation, maturity and plant height. Therefore, separation of hybrids by these traits can be performed through a diagram, which forms one of vectors of this component.

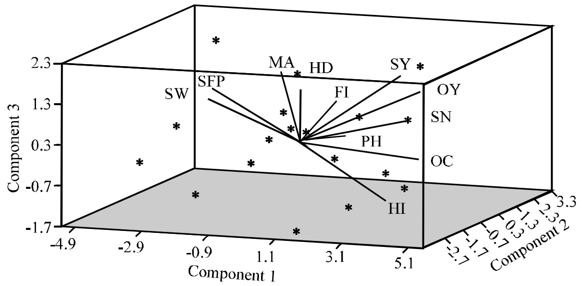

Fig. 2: 3D diagram for position of sunflower genotypes and trait vectors in principal components analysis method. FI: Flowering Initiation; SFP: Seed Filling Period; MA: Maturity; PH: Plant Height; HD: Head Diameter; SW: 1000 Seed Weight; SN: Seed Number per Head; HI: Harvest Index; OC: Oil Content; SY: Seed Yield; OY: Oil Yield

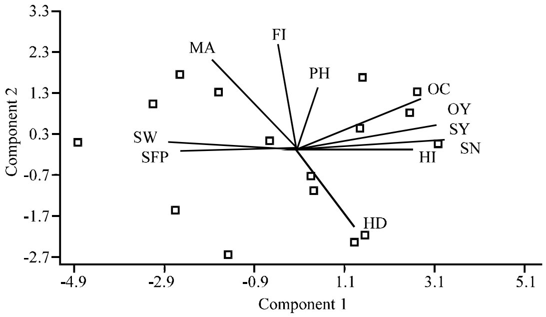

Fig. 3: Biplot for position of sunflower genotypes and trait vectors in principal components analysis method. FI: Flowering Initiation; SFP: Seed Filling Period; MA: Maturity; PH: Plant Height; HD: Head Diameter; SW: 1000 Seed Weight; SN: Seed Number per Head;HI: Harvest Index;OC: Oil Content; SY: Seed Yield; OY: Oil Yield

Seed filing period along with head diameter, seed and oil yield are main part of third component and it can be useful in grouping of hybrids from these traits aspects (Table 2). Five traits, seed and oil yield, seed numbers per head, oil content and harvest index, which located extremity right direction of diagram indicate great portion of these traits in comprising of first component. Amounts of Table 2 can be easily understood, also. Regarding to Table 2, it appears that using first and second components are suitable to separate early mature and high yielded hybrids. Ghaffari (2003) and Zeinalzadeh and Ghaffari (2005) were reported the same results. According to diagram drawn based on first and second components, position of each genotype can be determined and then, selection from the point of yield, oil content and maturity can be applied. On the other hand, it should be reminded that because of high correlation of flowering initiation time with maturity, use of flowering initiation data can be effective in selection of early mature hybrids (Ghaffari, 2003).

Through, the doing of principal components analysis and grouping of genotypes on the basis of quantity of two first components, it has been clarified that genotypes on the basis of trait's weight in every component get special position in correlation with agronomic traits vector and are scattered according to the correlation of considered traits with components and according to the quantity of under study trait (Fig. 2 and 3).

This kind of genotype scattering in provided vectors can provide at least the possibility of fast omission or selection of main parts of genotypes and this can be useful in preliminary evaluations. Because used genetic materials of each experiment are different, genotypes orientation around the related vectors of agronomic traits will depend on the obtained correlations in every experiment and trait's weight in the formation of every component. Because of that the method of selection in every experiment will be different from another one. Use of this method is not limited to sunflower crop and like other multivariate methods it can be used in other products.

CONCLUSION

In this research on the basis of general waypoint, it can be reached to this conclusion that the first component obtained from principal components analysis with having 46.40% of the total variance and high correlations with traits like seed numbers per head, harvest index, oil content, seed yield and oil yield, can be used in an efficient way in fast selection and screening of genetic materials in the initiative stages. Genotypes, which are in the half-right of biplot diagram and around the related vector to the seed yield, besides of having high seed yield, have high oil yield, oil content and number of seed per head. Selection on the basis of these genotypes with short maturity period is beneficial in reaching to the most important aims of production of sunflower hybrids seed programs.

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REFERENCES

Chapman, S.C., J. Crossa and G.O. Edmeades, 1997. Genotype by environment effects and selection for drought tolerance in tropical maize, two mode pattern analysis of yield. Euphytica, 95: 1-9.

Cheres, M.T. and S.J. Knapp, 1998. Ancestral origins and genetic diversity ofcultivated sunflower: Coancestry analysis of public germplasm. Crop Sci., 38 (6): 1476-1482.

De La Vega, A.J., S.C. Chapman and A.J. Hall, 2001. Genotype by environment interaction and indirect selection for yield in sunflower. I. Two-mode pattern analysis of oil and biomass yield across environments in argentina. Field Crop Res., 72: 17-38.

Ghaffari, M., 2003. Use of principal component analysis method for selection of superior hybrids in sunflower. Seed and Plant J., 19 (4): 513-527.

Kroonenberg, P.M., 1997. Introduction to Biplot for G×E Tables, Research report, No. 51, Center for statistics. The University of Queensland. Brisban. Australia.

Kroonenberg, P.M., K.E. Basford and A.G.M. Ebskamp, 1995. Three-way cluster analysis and component analysis of maize variety trials. Euphytica, 84: 31-42.

Moghaddam, M., S.A. Mohammadi and M. Aghaei, 1994. Introduction to multivariate statistical methods. Pishtaze Elm Press, Tabriz, Iran.

Spranaaij, L.D. and I. Bos, 1993. Component analysis of complex characters in plant breeding. Euphytica, 79: 225-235.

Zeinalzadeh, T.H. and M. Ghaffari, 2005. Evaluation of Genetic diversity of sunflower genotypes (*Helianthus annuus* L.) based on agronomic traits using principal component analysis. Proceedings of the First International Iranian Congress on Biological Sciences, Dec. 14-15, Islamic Azad University, Karaj Branch, Iran.