

Estimation of genetic diversity of sunflower single cross hybrids using principal component analysis

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ABSTRACT

In order to study genetic diversity of sunflower single cross hybrids through using principal component 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 were crossed with 18 cytoplasmic male sterile (CMS) female lines. Each male line was crossed with three different female lines to make two sets with nine hybrids in each set. In 2006, Single cross F₁ 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 3 first components explained variability of all the 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 was 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. In all, the first component with a large 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 appropriate and useful for grouping and selecting superior single cross hybrids.

Key words: genetic diversity sulfonylurea – hybrid sulfonylurea – principal components analysis – sunflower.

INTRODUCTION

In recent years, many sunflower single cross and three-way-cross hybrids have been produced in Iran, and a selection of the best of them in regional preliminary experiments is very important task. Multivariate statistical methods that can create relationships between cultivar traits, can help to group cultivars and make it easy to select them on the basis of biplot and triplot diagrams. The principal components analysis method, through the summarizing of 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). Some researchers, in order to accelerate the genotype selection for aspects of traits like seed yield have used principal components analysis, a method which is also useful for the reduction of the selection cost and in the preliminary stage of cultivar selection (Spranaaij and Bos, 1993). Kroonenberg et al. (1995) also used this method, with three-way-cluster analysis, for the separation of genotypes in limited bunches for their manipulation and 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 the determination of interaction among different sunflower cultivars with cultural media and for the consideration of indirect selection possibility of yield in these media and Ghaffari (2003) used this methodologies for rapid screening of 121 sunflower cultivars and hybrids, so that logical cultivar grouping through the influence from agronomic traits could be used as an efficient factor in superior and early mature hybrid selection. Finally, Zeinalzadeh-Tabrizi and Ghaffari (2005) have used this method for the survey of genetic diversity of sunflower genotypes. These authors employed 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 facts obtained from principal component analysis, trait 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 vector in the 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 further the distance of conjunction of the line with the origin, the more the diversion of genotype yield from others (Chapman et al., 1997). Any angle among the vectors in these diagrams shows their correlation (Kroonenberg, 1997). With this kind of relationship among the agronomic traits and related vectors in formed diagrams, is possible to group experimental genotypes logically. We can use this method as a way for surveying genetic diversity of evaluated materials and also for the selection of superior genotypes in preliminary experiments.

The aim of this study was the use of principal component analysis for the obtention of biplot and triplot diagrams, that can be used for surveying genetic diversity and selection of superior sunflower single cross hybrids under study, , and for the determination of relationships between traits.

MATERIALS AND METHODS

This experiment was conducted at Agricultural and Natural Resources Research Station of Khoy, Iran (44° 58' N, 38° 33' E) during 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 used in this experiment were sunflower single cross hybrids obtained from crosses of 6 male restorer lines (R line) with 18 female cytoplasmic male sterile (CMS or A) lines which have been produced at Agricultural and Natural Resources Research Station of Khoy in 2003. In each set, were included 3 R lines crossed with different 3 CMS lines and their developed 9 hybrids. Hybrids containing common male parent were 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. F₁ hybrids obtained from crosses were planted for the principal components analysis and to survey genetic diversity in 2005.

Surveyed traits were: flowering initiation, seed filling period, maturity, plant height, head diameter, 1000 seed weight, seed number per head, harvest index, oil content, seed yield and oil yield. Correlation among the varieties was done through the use of SPSS software and the principal components analysis employing Statgraphics, biplot and triplot diagrams being designed. On the basis of the characteristics of every hybrid, and the direction and angle of the related vectors, the position of 18 hybrids in biplot and triplot diagrams have been clarified, and, on that basis, the range of the existing diversity and methods of grouping obtained have been considered.

Hybrids characteristics are shown in charts below.

First Set		
Hybrid	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

Second Set		
Hybrid	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

Equation of every 3 first components has been shown in Table 2. For example, equation of first component is:

$$Z_1 = -0.05 \text{ FI} - 0.32 \text{ SFP} - 0.23 \text{ MA} + 0.06 \text{ PH} + 0.16 \text{ HD} - 0.35 \text{ SW} + 0.41 \text{ SN} + 0.32 \text{ HI} + 0.35 \text{ OC} + 0.36 \text{ SY} + 0.40 \text{ OY}$$

Table 1. Variance of components in principal component 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

Table 2. Structure of first 3 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

Through carrying out the principal components analysis and grouping the genotypes on the basis of the quantity of two first components, it was clarified that genotypes, on the basis of trait weight in every component, obtain a special position in correlation with the agronomic trait vector and are scattered according to the correlation of considered traits with components and according to the quantity of trait under study (Figs. 2 and 3).

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

In this study, on the basis of general waypoint we have reached the conclusion that the first component obtained from principal components analysis with 46.40 percent 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 the fast selection and screening of genetic materials in the initial stages. Genotypes which are in the right half of the biplot diagram and around the vector related to the seed yield, besides having a high seed yield, have a high oil yield, oil content and number of seed per head. Selection on the basis of these genotypes with a short maturity period is beneficial to the effort to achieve the most important aims of production of sunflower hybrids seed programs.

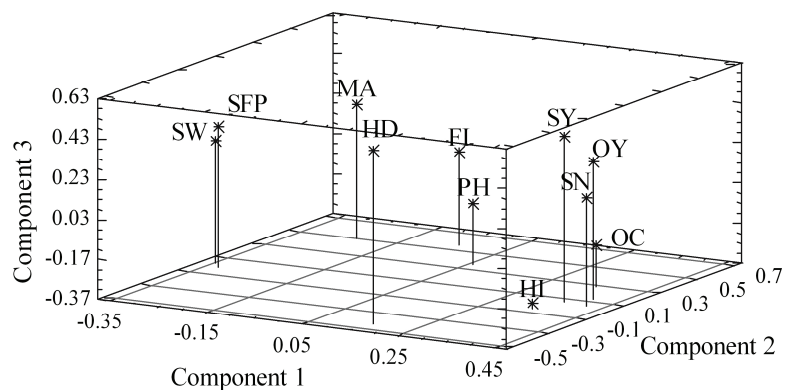


Fig. 1. Diagram of first three component weights for agronomic traits on sunflower single cross hybrids. Abbreviations are given in table 2.

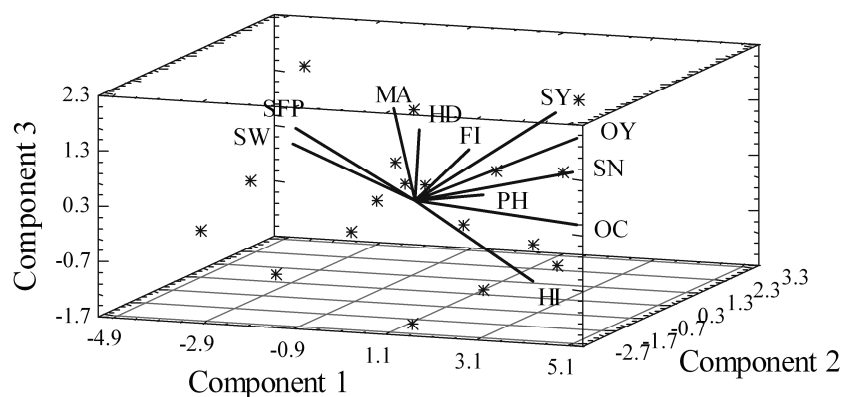


Fig. 2. 3D diagram for position of sunflower genotypes and trait vectors in principal component analysis method. Abbreviations are given in table 2.

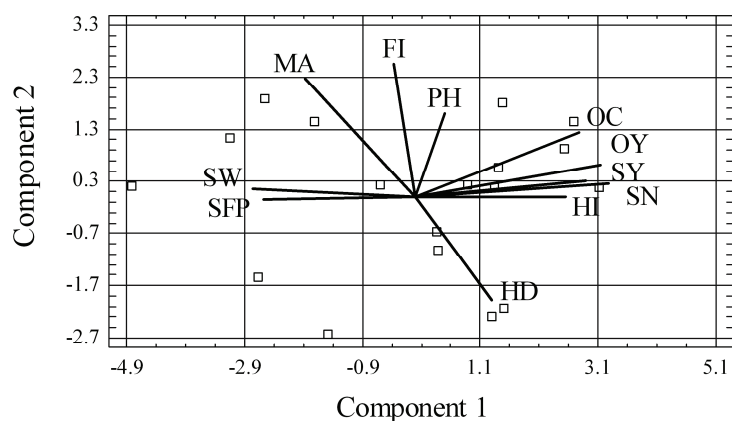


Fig. 3. Biplot for position of sunflower genotypes and trait vectors in principal components analysis method. Abbreviations are given in Table 2.

Table 3. Correlation among agronomic traits of sunflower single cross hybrids and components of principal component analysis

Traits	Flowering Initiation	Seed Filling Period	Days to Maturity	Plant Height	Head Diameter	1000 Seed Weight	No. of seeds per Head	Harvest Index	Oil Content	Seed Yield	Oil Yield
FI	1										
SFP	-0.115 ^{ns}	1									
MA	0.648 ^{**}	0.600 ^{**}	1								
PH	0.133 ^{ns}	-0.146 ^{ns}	0.113 ^{ns}	1							
HD	-0.379 ^{ns}	-0.142 ^{ns}	-0.479 [*]	-0.200 ^{ns}	1						
SW	0.142 ^{ns}	0.579 [*]	0.439 ^{ns}	0.143 ^{ns}	-0.064 ^{ns}	1					
SN	-0.043 ^{ns}	-0.548 [*]	-0.314 ^{ns}	0.079 ^{ns}	0.346 ^{ns}	-0.811 ^{**}	1				
HI	-0.073 ^{ns}	-0.641 ^{**}	-0.490 [*]	0.121 ^{ns}	0.083 ^{ns}	-0.572 [*]	0.583 [*]	1			
OC	0.073 ^{ns}	-0.523 [*]	-0.187 ^{ns}	0.339 ^{ns}	-0.002 ^{ns}	-0.651 ^{**}	0.717 ^{**}	0.614 ^{**}	1		
SY	0.034 ^{ns}	-0.417 ^{ns}	-0.200 ^{ns}	0.142 ^{ns}	0.529 [*]	-0.449 ^{ns}	0.863 ^{**}	0.388 ^{ns}	0.558 [*]	1	
OY	0.066 ^{ns}	-0.504 [*]	-0.221 ^{ns}	0.205 ^{ns}	0.388 ^{ns}	-0.561 [*]	0.903 ^{**}	0.493 [*]	0.750 ^{**}	0.965 ^{**}	1
Component 1	-0.107 ^{ns}	-0.735 ^{**}	-0.530 ^{**}	0.140 ^{ns}	0.376 ^{ns}	-0.788 ^{**}	0.932 ^{**}	0.727 ^{**}	0.790 ^{**}	0.820 ^{**}	0.896 ^{**}
Component 2	0.804 ^{**}	-0.016 ^{ns}	0.713 ^{**}	0.509 ^{**}	-0.623 ^{**}	0.050 ^{ns}	0.082 ^{ns}	0.005 ^{ns}	0.395 ^{ns}	0.095 ^{ns}	0.199 ^{ns}
Component 3	0.106 ^{ns}	0.381 ^{ns}	0.344 ^{ns}	-0.077 ^{ns}	0.580 [*]	0.275 ^{ns}	0.198 ^{ns}	-0.431 ^{ns}	-0.189 ^{ns}	0.535 [*]	0.364 ^{ns}

ns, * and **: Non significant, significant at 5 % and 1 %, respectively.

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