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Genetic analysis of agro-morphological traits in promising hybrids of sunflower (*Helianthus annuus* L.)

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ABSTRACT

The main objective underlying sunflower breeding programs is to develop high-yielding productive F_1 hybrid cultivars. This study was conducted to investigate the genetic control of some agro-morphological traits of new sunflower F_1 hybrids. For this purpose, fourteen inbred lines of sunflower were crossed with three male sterile inbred lines. Their hybrids (14 hybrids) were then evaluated against three control cultivars. The data thus obtained were analyzed using the nested model (North Carolina Design I) as a completely randomized block design (CRBD) with four replications. Analysis of variance showed that the hybrids were significantly different in all the traits studied, except for head and stem diameters. From among the hybrids evaluated, Cms19 × Rn1-81 was found to have the highest seed yield and oil content. Cluster analysis classified the hybrids into four different groups. Genetic analysis showed that days to maturity, seed weight, and oil content (%) were under the additive gene action. Breeding strategies based on selection could be suggested for the improvement of these traits. Head angle, head diameter, seed yield, and oil yield were under the dominance gene action; breeding based on hybridization methods is, therefore, proposed for these traits. Finally, both additive and dominance gene actions were observed to play important roles in the genetic control of plant height and stem diameter.

Key words: additive, dominance effect, evaluation of hybrids, oil content, sunflower, yield

IZVLEČEK

GENETSKA ANALIZA AGRO-MORFOLOŠKIH LASTNOSTI PRI OBETAJOČIH KRIŽANCIH NAVADNE SONČNICE (*Helianthus annuus* L.)

Glavni cilj žlahniteljskih programov navadne sončnice je razvoj visoko produktivnih F_1 hibridnih sort. V raziskavi smo preučevali genetsko kontrolo nekaterih agro-morfoloških lastnosti nekaterih novih F_1 hibridov navadne sončnice. V ta namen smo opravili križanja 14 inbridiranih linij navadne sončnice s tremi moško sterilnimi inbridiranimi linijami. Dobljeni križanci (14 hibridov) so bili ovrednoteni glede na tri kontrolne sorte. Tako pridobljeni podatki so bili analizirani z vgnezdenim modelom (North Carolina Design I) v bločni zasnovi s štirimi ponovitvami. Analiza variance je pokazala, da so bili križanci značilno različni v vseh preučevanih lastnostih, z izjemo premera koška in premera stebla. Izmed ovrednotenih križancev je imel križanec Cms19 × Rn1-81 največji pridelek semena in največjo vsebnost olja. Klastrska analiza je razvrstila križance v štiri skupine. Genetska analiza je pokazala, da so bile lastnosti, kot so število dni do zrelosti, masa semena in vsebnost olja (%), pod aditivno gensko kontrolo. Za izboljšanje teh lastnosti priporočamo žlahniteljsko strategijo zasnovano na selekciji. Lastnosti kot so naklon koška, premer koška, pridelek semena in pridelek olja so bile dominantno dedovane, zato za te lastnosti priporočamo žlahtnenje na osnovi križanja. Pri lastnostih kot sta višina stebla in njegov primer smo opazili pomembni vlogi tako aditivnega kot dominantnega delovanja genov.

Ključne besede: aditivno dominantni učinki genov, vrednotenje križancev, navadna sončnica, pridelek, vsebnost olja

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1 INTRODUCTION

Sunflower (*Helianthus annuus* L.) is widely grown in tropical, semi-arid, and arid regions such as Iran (Weiss, 2000). It is an important oil crop of high quality oil, good adaptation, and high seed yield (Razi and Asad, 1999; Hu et al., 2010). Sunflower oil contains approximately 12 % saturated fat and 64 % linoleic acid (an omega-6 essential fatty acid) (Weiss, 2000). The genotypes possessing self-incompatibility and cytoplasmic male sterility (CMS) offer the potential for hybrid production (Fick, 1987). Currently, the highest levels of sunflower cultivars belong to hybrid varieties grown in developed countries. The production of hybrid varieties of sunflower in Iran is accomplished by using CMS and restoring fertility (RF) lines. Hybrids of sunflower are more stable and highly self-fertile with a high yield performance and greater uniformity at maturity (Kaya and Atakisi, 2004). In some cases, the hybrid genotypes have been found to be superior in terms of seed yield to their parental lines. Shahsavari et al. (2010) observed significant differences in days to maturity, plant height, stem diameter, head diameter, seed weight, seed yield, and oil yield among twenty genotypes of sunflower including new hybrids and parental genotypes. Haq et al. (2006) also reported significant differences among sunflower hybrids with respect to their plant height, stem diameter, oil percentage, seed yield, and seed weight. Similarly, Razi and Assad (1999) reported significant differences in growth period, head diameter, seed weight, as well as oil and seed yields among the different genotypes of sunflower they studied. The creation of new sunflower hybrids with a high genetic potential for seed yield requires information about their mode of inheritance.

Various genetic mating designs have been used to generate improved plants. All such designs are meant to realize the following four main objectives: 1) to obtain information about the genetic control of the traits under study, 2) to generate a breeding population for use as a basis in the selection and development of potential varieties, 3) to provide estimates of genetic gain, and 4) to gain information about the parents used in the breeding programs (Acquaah, 2012). North Carolina Designs (I, II, and III) were developed by Comstock and Robinson (1948). Design I (NCDI) is commonly used for estimating the additive and dominance variances (Acquaah, 2012). The main advantage of this design is its ability to supply a test of significance for the additive genetic variance (Hill et al., 1998). The design has also been successfully used in obtaining estimates of genetic variance in sunflower. Knowledge of genetic factors helps researchers select appropriate breeding methods. The genetic components and heritability of seed yield and its components in sunflower hybrids have been identified by different genetic designs such as NCD-II (Alza et al., 1997) and line × tester (Ghaffari et al., 2011).

The present study was designed to evaluate both the mean performance of some new F_1 hybrids and the genetic control of such traits as stem diameter, head angle, and days to maturity in sunflower via the NCD-I genetic design.

2 MATERIALS AND METHODS

This research was conducted at the experimental research farm of Agricultural Research Institute of Isfahan, at Kabutar Abad region (51º 51′ longitude and 32º 31 latitude) in 2012–2013. The North Carolina Design I was used to prepare a new genetic population of sunflower hybrids with improved traits. Three lines of cytoplasmic male sterility (CMS14, CMS19 and CMS 522), as the female parents, and 14 new restorer inbred lines (Rn1-144, Rn1-56, Rn-14, Rn-1-128, Rn1-152, Rn1-60, Rn-864, Rn-1-76, Rn-1-130, Rn1-149, Rn1-4, Rn1-81, Rn4 and Rn-1-77), as the male parents, were separately planted in one row 4 m long in a small crossing plot at two different planting dates in 2012. The CMS and restore lines were prepared by oil seed research branch of Agricultural Research Center of Isfahan, Iran. A distance of 60 cm was left between the rows. Some plants in every line were covered with sheer before flowering time. For hand pollination, liberal amounts of pollen were applied on three plants of every male sterile on every second day of the flowering period for a total number of three times. The seeds of 14 F_1 hybrids with three control genotypes (‘Azargol’, ‘Allstar’, and ‘Haysan-33’) were evaluated in a completely randomized block design (CRBD) with four replications in 2013. Each experimental plot consisted of four lines in row of 5.5 m long each. The distances between and within the rows were set to 60 cm and 25 cm, respectively. The standard agronomic package of practices and suitable plant protection were adopted to raise healthy crops. Ten randomly selected plants were taken from the two middle rows of each experimental plot for evaluating their traits.

2.1 Traits studied

Seed and oil yields of each plot were calculated (kg/ha) after elimination of two margin lines. Seed oil (%) was determined using the seeds collected from ten random plants per plot by the NMR (Nuclear Magnetic Resonance, H20-18-25A) method. Plant height (cm) was measured as the distance between soil surface and stem attachment to the head. Head angle was defined as the receptacle orientation expressed at maturity as an angle in degrees. Analysis of variance was carried out using the SAS 9.1 software. Mean comparison was accomplished by the Least Significant Difference (LSD) test at a probability of 5% and cluster analysis was conducted using the Ward method with the SPSS software. Finally, the genetic population was subjected to genetic analysis using the SAS software. The variance components of NC-I are reported in Table 1.

Table 1: Analysis of variance and its components in North Carolina Design (I)

Source of Variation	D.F	Mean squares	Expected Mean Squares	Related covariance
Replication	r-1			
Female	f-1	M_3	σ^2+r $\sigma^2_{f/m}$+rm σ^2_f	σ^2+r (Cov F.S – Cov H.S)+ rm CovH.S)(
Female (male)	f(m-1)	M_2	σ^2+r $\sigma^2_{f/m}$	σ^2+r (Cov F.S – Cov H.S)
Error	mf-1) (r-1)	M_1	σ^2	σ^2

r, f, and m denote replication, female, and male, respectively

According to Table 1, dominance variance $(\sigma^2{}_D)$ and additive variance $(\sigma^2{}_A)$ would be calculated (as F=1) using the following Relation (Kempthorne, 1957):

$$\text{Cov (F.S)} = [(\frac{1+F}{2})\sigma^2{}_A + (\frac{1+F}{2})^2\sigma^2{}_D] \text{ and } \quad \text{Cov (H.S)} = (\frac{1+F}{4})\sigma^2{}_A$$

Broad-sense and narrow-sense heritability of the studied traits (Mahmud and Keramer, 1951) and degree of dominance (Kearsey and Pooni, 1996) were obtained using the following Relation:

$$H_b = \frac{\sigma_A^2 + \sigma_D^2}{\sigma_A^2 + \sigma_D^2 + \sigma_e^2}, \qquad H_n = \frac{\sigma_A^2}{\sigma_A^2 + \sigma_D^2 + \sigma_e^2}, \qquad \bar{d} = \sqrt{2\delta^2{}_D / \delta^2{}_A}$$

3 RESULTS AND DISCUSSION

Analysis of variance showed significant differences among the entries for all the studied traits (Table 2). Moreover, female and female (male) mean squares were significant for all the traits (Table 2). This indicates the existence of high variations among the parental genotypes. The control genotypes showed significant differences in all the traits studied, except for seed diameter and oil content. Comparison of F_1 hybrids vs. controls showed significant differences between the means of F_1 hybrids and the control genotypes (Table 2). Previous studies have also reported significant differences in growth period, plant height, seed weight, oil yield, and seed yield on F_1 hybrids of sunflower (Razi and Assad, 1999; Haq et al., 2006; Arshad et al., 2007).

Table 2: Analysis of variance and genetic components for agronomic traits in 14 promising F_1 hybrids and 3 control lines of sunflower with NCD-1

		Mean squares								
S.O.V	D.F	DM	PH	HA	HD	SD	SW	SY	OY	OC
Rep.	3	8.46	690.33^{**}	1421.6^{**}	7.238	6.94^{**}	154.74^{**}	800496^{*}	96358^{**}	1.77
Entries	16	89.1^{**}	915.5^{**}	1203.2^{**}	7.87^{*}	3.8^{**}	345.6^{**}	1855859.9^{**}	341647^{**}	14.5^{**}
Female	2	388.9^{**}	776.35^{**}	2059.6^{*}	14.19^{**}	7.4^{**}	659.67^{**}	1255622^{**}	203312^{**}	45.2^{**}
Female (Male)	11	40.8^{**}	160.2^{**}	653.27^{**}	5.72^{*}	1.5^{*}	90.3^{**}	344780^{*}	80274^{*}	9.5^{**}
Control	2	76.58^{**}	1982.33^{**}	3543.7^{**}	14.33^{**}	0.02	1195.88^{**}	7284571.5	1411360^{**}	2.46
Control *vs*. F_1	1	45.81^{**}	7368.43^{**}	842.21	5.95	29.45^{**}	969.18^{**}	8820790.9	1353993^{**}	31.5^{**}
Residual	48	5.31	72.6	269.62	2.8	0.58	24.31	105113	38774	2.1
Genetic estimates										
σ^2_A		12.43	21.22	50.23	0.30	0.21	20.33	32530	4394.2	1.38
σ^2_D		2	10.9	70.79	0.57	0.12	6.33	43651.7	8177.8	0.38
$\bar{d}$		0.56	0.99	1.67	1.95	1.08	0.78	1.63	1.92	0.74
h^2_b		91.57	64.44	64.22	60.57	69.81	81.43	75.34	56.46	77.10
h^2_n		78.86	43.10	26.65	31.28	43.86	62.10	31.74	19.1	60.43

**, *: Significant at 1% and 5%, respectively; ns: not significant

Abbreviations: DM: days to maturity, PH: Plant height, HA: Head angle, HD: Head diameter, SD: Stem diameter, SW: Seed weight, SY: Seed yield, OY: Oil yield, OC: Oil content.

$\bar{d}$ =average of dominance, h^2_b= broad-sense heritability, h^2_n: Narrow-sense heritability

3.1 Genetic components analysis

The genetic components of the studied traits were calculated and reported in Table 2. The variance of female (σ^2_f) (CMS lines) and female (male) ($\sigma^2_{f/m}$) (restorer fertility lines) were significant for all the studied traits, implying the important effects of both additive and dominance gene actions on the genetic control of the traits investigated. The variance among the CMS lines (female) for all the traits were greater than that among the male lines (restorer), indicating the possible existence of some degree of maternal effects for the genetic control of the studied traits (Ghaffari et al., 2011). Alza et al. (1997) reported that female variance was significant for seed weight and oil content.

3.2 Days to maturity

According to Table 2, $\sigma^2{}_A$ (12.43) is larger than $\sigma^2{}_D$ (2) for days to maturity (Table 2). Comparison of the variance components, the value of dominance ratio (0.56), and the high narrow-sense heritability (78.86) indicate the importance of the additive gene action for the genetic control of days to maturity. In agreement with our findings, Saeidi et al. (2009) reported that additive genetic effects had a greater contribution to the genetic control of days to maturity than did the non-additive ones. Wehner (1984) reported that dominance variance was greater than additive variance for days to germination as a phenological trait. Ghaffari et al. (2011) reported both additive and dominance gene actions to be effective in the genetic control of days to maturity.

3.3 Plant height

A major objective in sunflower breeding programs is to improve crops by reducing plant height. Genetic analysis in the present case showed that the value of $\sigma^2{}_A$ (22) was larger than that of $\sigma^2{}_D$ (10.9) for plant height (Table 2). Similar to the findings of Gaffari et al. (2011) and Ortegon et al. (1992), the dominance ratio (d=1) in the present study implied the importance of both additive and dominance gene actions in the genetic control of plant height. Also, Miller and Hammond (1991) reported that additive gene action played a more important role than the dominance one did.

3.4 Head angle and head diameter

Dominance variance ($\sigma^2{}_D$) was found to be greater than $\sigma^2{}_A$ for head angle and head diameter (Table 2). This indicates the predominant roles of the dominance over the additive gene action in the genetic control of these traits. Gangappa et al. (1997) reported that non-additive gene action was predominant for the genetic control of head diameter, which is in agreement with our results. Contrary to our results, however, Ghaffari et al. (2011) reported additive ones to be important for the genetic control of head diameter. To the best of our knowledge, no study has been reported on the genetic control of head angle in sunflower.

3.5 Stem diameter

Increasing stem diameter is another major objective in sunflower breeding programs. Analysis of genetic components showed that $\sigma^2{}_A$ (0.21) was greater than $\sigma^2{}_D$ (0.12) for stem diameter (Table 2). Comparison of variance components, dominance ratio (1.08), and medium narrow-sense heritability (43.86) implied the importance of both additive and dominance gene actions in the genetic control of stem diameter. These results confirm those reported by Miller and Hammond (1991).

3.6 Seed weight

According to Table 2, $\sigma^2{}_A$ (20.33) was greater than $\sigma^2{}_D$ (6.33) for seed weight (Table 2). The dominance ratio (0.78) and the high narrow-sense heritability (62.10) obtained in this study showed the predominant role of the additive over the dominance gene action in the genetic control of seed weight. This is in agreement with the findings of Ghaffari et al. (2011). However, Bajaj et al. (1997) reported the dominance gene action to be important for the genetic control of seed weight, which is not in agreement with our results**.** The differences between the results could be explained by differences in the genotypes used and the environmental effects in each study.

3.7 Seed and oil yield

The magnitude of $\sigma^2{}_D$ (as compared to $\sigma^2{}_A$), the dominance ratio, and the low value of narrow-sense heritability obtained in this study indicate the importance of the dominance gene action for the genetic control of the plant traits investigated (Table 2). The importance of dominance gene action for seed yield has also been reported elsewhere (Khani et al., 2005; Skoric et al., 2000; Ghaffari et al., 2011). Gomez et al. (1999) reported that line and line × tester mean squares were not significant for seed yield in sunflower. In agreement with our results, however, other studies performing line × tester analysis in sunflower have indicated that oil yield is governed by the non-additive gene action (Kadkol et al., 1984; Ghaffari et al., 2011).

3.8 Oil content (%)

Genetic analysis showed that σ^2_A (1.38) was greater than σ^2_D (0.38) (Table 2). The high values obtained for the narrow-sense heritability (60.43) and dominance ratio (0.74) indicate the importance of the additive gene action for the control of oil content. In agreement with our results, Saeidi et al. (2009) reported that additive gene action was more important than the non-additive effects for the genetic control of seed oil content. Contrary to our results, Andarkhor et al. (2013) reported the significant role of dominance gene action for the genetic control of oil yield.

3.9 Heritability of traits

Broad-sense heritability varied between 91.57 (days to maturity) and 56.46 (oil yield) (Table 2). This is while narrow-sense heritability varied between 78.88 (days to maturity) and 19.1 (oil yield) (Table 2). The low-medium values obtained for the narrow-sense heritability demonstrated the low contribution of the additive genetic variance to the total genotypic variance (Kearsey and Pooni, 1996).

3.10 Mean comparison of F_1 hybrids and controls

The mean comparison of the studied traits is presented in Table 3. Earliness is an important trait in most regions of sunflower cultivation in Iran, where sunflower is grown as the second crop following the last irrigation of a main crop or in rotation with cereal crops. Early maturing hybrids are, therefore, appropriate for cultivation in these areas. Also, early maturity enables sunflower genotypes to avoid environmental stresses, especially biotic (diseases and insects) or abiotic stresses (heat and drought) at the ripening stage. In this study, days to maturity was found to range between 93 (Cms14×Rn1-56) and 106.5 (Cms19×Rn1-77) days (Table 3). Depending on the specific genotype used and the environmental conditions, different ranges have been reported for days to maturity in sunflower hybrids (Razi and Assad, 1999; Ghaffari, 2003). In the present study, the Cms14×Rn1-144, Cms14×Rn1-56, Cms522/2×Rn14, Cms522/2×Rn864, and Cms19×Rn1-76 hybrids showed a shorter growth period than did the 'Allstar' hybrid (as the earliest hybrid in Iran) (Table 3). These promising hybrids could, therefore, be applied in breeding programs aimed at producing early maturity genotypes of sunflower. Plant height was found to range from 107 (Cms19×Rn1-77) to 156.3 cm (Hysun-33) in the hybrids (Table 3). Plant height was shorter in all the test hybrids than in the two control ('Haysan-33' and 'Azargol') ones. It may, therefore, be concluded that the hybrids investigated in this study exhibited reduced plant heights as compared to the control genotypes. Razi and Assad (1999) reported that plant height in their study ranged between 124.3 and 222.9 (cm) in sunflower.

Head diameter in the present study ranged between 19.9 cm in Cms19×Rn1-149 and 15.9cm in Cms14×Rn1-56 (Table 3). Based on these results, the hybrids were found superior to the control with respect to head diameter. Stem diameter ranged between 19.6 mm in Cms19×Rn1-60 to 15.9 mm in Cms19×Rn1-76 (Table 3). These results indicate a high variability in the hybrids with respect to stem diameter. Regarding seed weight, the values were observed to range between 75.9 ('Azargol') and 42.6 (Cms522/2×Rn864) (g) (Table 3). Finally, seed yield recorded the highest values in 'Azargol', 'Haysan-33', and 'Allstar' as compared to the other hybrids (Table 3). The highest seed yield (4104.17 Kg/ha) was recorded for Cms19×Rn1-81 (Table 3). However, no other significant differences, were observed between this hybrid and the control genotypes (Table 3). This finding is in agreement with those of Haq et al. (2006), Razi and Assad (1999), Ghaffari (2003), and Arshad et al. (2007). Generally speaking, the hybrid derived from the Cms-19×Rn1-81 cross was found to be the best for seed yield among the hybrids investigated in this study.

Improvement of seed yield and oil content forms a major goal in hybrid production programs. Oil yield is an important sunflower trait which justifies the economical production of specific hybrids since the oil from properly selected and modified genotypes offers a good potential for improving food products while it also has many industrial applications (Seiler, 2007). However, it is not easy to improve these traits due to the low heritability and high sensitivity of the plant to genotypic interactions with the environment (Marinkovic, 1992). The experiments in this study showed that oil yield ranged between 44.7% (Cms19×Rn1-81) and 39.9% (Cms19×Rn1-76) (Table 3). The hybrids of Cms522/2×Rn1-4 and Cms19×Rn1-81 showed to be superior with respect to seed and oil yields (Table 3). Cms19×Rn1-77 was found to be the unsatisfactory hybrid in this study as it recorded the lowest seed and oil yields and the longest growth period. Some hybrids showed early maturity compared to 'Allstar' which is known as an early maturity genotype.

Cluster analysis, as a multivariate analysis, is widely used to describe genetic diversity based on similarities or differences among genotypes (Peeters and Martinelli, 1989). The genotypes investigated in this study were subjected to cluster analysis using the Ward method which yielded a classification of genotypes into four distinct groups (Figure 1), with 6 hybrids assigned to group 1, 6 to group 2, 4 to group 3, and 1 to group 4.

The mean comparison of different traits is presented in Table 4. Significant differences were observed among the groups in all the traits studied, except for stem diameter (Table 4). The differences in days to maturity, plant height, head angle, and head diameter observed among the groups were highly significant (Table 4).

The second group exhibited the highest values of seed yield, oil yield, seed weight, and plant height. The two control hybrids ('Azargol' and 'Haysan-33') were in this group as well. Based on the mean values obtained for all the traits in the hybrids investigated, the hybrids Cms19×Rn1-130, Cms19×Rn1-149, and Cms19×Rn1-81 along with the control 'Azargol' and 'Haysan-33' were found to have the best seed yields. Thus, these hybrids could be recommended for further evaluation from a seed yield improvement viewpoint. The third group was identified as the earliest maturity group. It also exhibited acceptable seed and oil yields. The genotypes in this group could be recommended for cases of limited planting season. The hybrid Cms19×Rn1-77, in group 4, recorded the highest number of days to maturity among the four groups evaluated and ranked the lowest with respect to plant height, head angle, seed weight, and seed yield (Table 4). The highest value for head diameter belonged to this hybrid as well. The hybrids from common parents (i.e., Cms 522/2 and Cms 14) were classified in the same groups, indicating identical effects of parents on the progeny and probably the existence of strong maternal effects in the parents. In contrast, those from the parent Cms-19 were placed in different groups, indicating less of similar parental effects on the progeny.

Generally speaking, the hybrids Cms-19×Rn1-81, Cms19×Rn1-130, and Cms19×Rn1-149 had the best conditions for seed and oil yields. On the other hand, Cms14×Rn1-56, Cms14×Rn1-144, and Cms19×Rn1-76 with suitable seed and oil yields were identified with earliness in growth period. Therefore, depending on the regional conditions, it seems better when selecting the best hybrids to make a tradeoff between yield and growth period. Alba *et al.* (2010) used cluster analysis for categorizing 11 sunflower hybrids based on 8 agronomic characters including oil yield with different sowing dates. The hybrids were classified by cluster analysis with respect to their performance into groups that could be differenced by means and stability.

Table 3: Mean comparison of different studied traits in promising hybrids and control genotypes of sunflower

Code	Genotype	DM	PH (cm)	HA	HD (cm)	SD (mm)	SW (g)	SY (Kg ha^{-1})	OY (Kg ha^{-1})	Oc(%)
1	Cms14×Rn1-144	93.5	122	10.7	17.5	18.2	72.8	3166	1269.5	40.7
2	Cms14×Rn1-56	93	112.7	26.5	15.9	17.9	53.9	3552	1454.7	40.9
3	Cms522/2×Rn14	94	137	44	17.5	18.4	52.6	3447	1493.6	43.4
4	Cms522/2×Rn1-4	102.2	122	39.2	16.5	18.1	45.4	3437	1538.5	44.7
5	Cms522/2×Rn864	93.7	129.25	44.5	16.5	17.7	42. 6	3044.5	1353.6	44. 5
6	Cms522/2×Rn4	97.7	138.5	53	16.5	17.7	44.6	3666.6	1530.2	41.7
7	Cms19×Rn1-28	100.7	149.25	54.7	18.1	16.6	59	3116.6	1326.8	42.6
8	Cms19×Rn1-52	101.2	147. 25	48	16.7	19.1	61.7	3839.5	1684.6	43.9
9	Cms19×Rn1-60	97.2	132.75	42.2	17.6	19.6	56.8	3668.7	1565.8	42.9
10	Cms19×Rn1-76	96.2	114.25	12	17.6	15.9	58. 8	3229.1	1292.4	39.9
11	Cms19×Rn1-130	103.5	149.75	50	17.5	16.3	62.2	3858. 3	1666.4	43.4
12	Cms19×Rn1-49	104	136	34	19.9	17.2	64.1	3924.9	1620.9	41.3
13	Cms19×Rn1-81	100.2	138.5	46.7	19.2	17.4	59.8	4104	1821.6	44.3
14	Cms19×Rn1-77	106.5	107	8	20	17.6	47.5	2287.4	944.4	41.6
15	Allstar	96.7	115.5	20.2	17	18.1	65.9	4358.3	1815.9	41.6
16	Hysun-33	104.7	156.25	42	20	19.2	61.2	4985.4	2035.1	40.8
17	Azargol	102.2	150	57.5	19.5	17.7	75.9	4986. 2	2132.3	42.9
	LSD (P=0.05)	3.19	11.8	22.7	2.31	1.05	6.83	449.3	272.9	2.08

Abbreviations: DM: days to maturity, PH: Plant height, HA: Head angle, HD: Head diameter, SD: Stem diameter, SW: Seed weight, SY: Seed yield, OY: Oil yield, OC: Oil content.

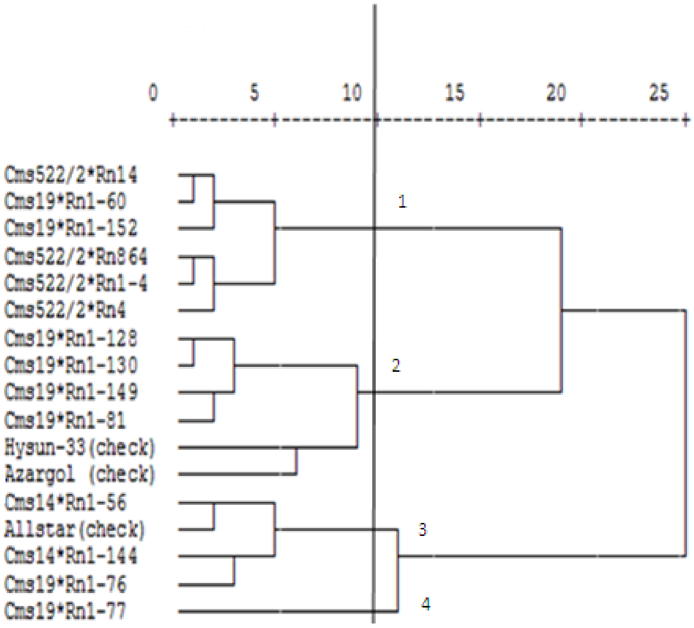

Figure 1: Cluster dendrogram of 17 sunflower genotypes based on Euclidean rescaled distances

The biplots, therefore, provide more useful information for sunflower breeders and PCA can be performed based on agronomic traits data for the determination of real hybrid performances.

Agronomic traits with favorable values of principal components were effectively used to discriminate entries for multivariate selection. Acute angle for seed yield and oil yield indicated a positive relationship between these traits (Figure 2). Seed weight, days to maturity, and head diameter were also closely associated (Figure 2). The associated traits can be, therefore, used for the selection of one of these traits, and this would provide the opportunity to implement a multi-trait selection process in sunflower breeding programs. Oil content was found not to be associated with seed yield or oil yield; rather, oil content exhibited strongly negative associations with oil yield and seed yield because of the obtuse angle of their vectors. Therefore, biplots provide more useful information in this case for sunflower breeders and PCA can be performed based on agronomic traits to determine the real performance of the hybrids. According to Figure 2, Cms19×Rn1-52, Cms19×Rn1-130, and Cms19×Rn1-81 hybrids were the superior ones with respect to plant height, oil content, and stem diameter. The hybrids Cms19×Rn1-76 and Cms19×Rn1-77 showed the least PC values, demonstrating the low breeding value of these hybrids for seed and oil improvement.

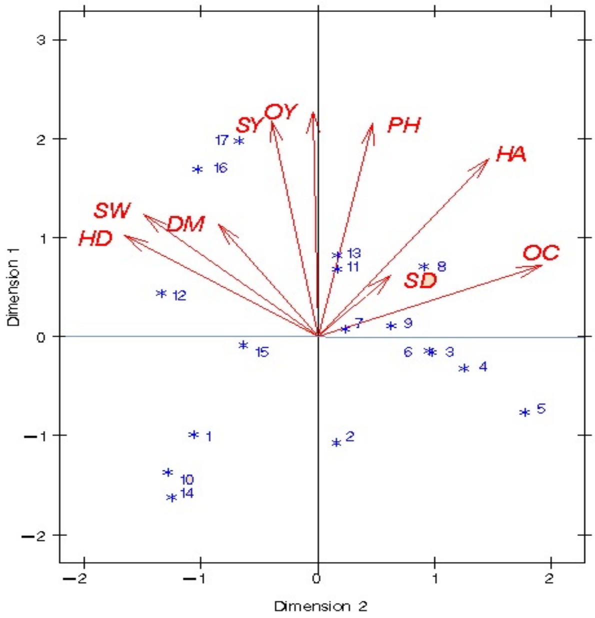

Figure 2: Biplots for the 1st and 2nd principal components used for mean agronomic traits in sunflower

Abbreviations: DM: days to maturity, PH: Plant height, HA: Head angle, HD: Head diameter, SD: Stem diameter, SW: Seed weight, SY: Seed yield, OY: Oil yield, OC: Oil content;

Table 4: Means comparison of groups from cluster analysis based of LSD test for sunflower hybrids

Trait$^{¥}$	Mean squares	Means of groups			
		Group 1	Group 2	Group 3	Group 4
DM	0.33**	97.71b^{c}	102.58^{ab}	94.875^{c}	106.5^{a}
PH (cm)	605.63**	134.46^{a}	146.62^{a}	116.12^{b}	107^{b}
HA	1392.13**	45.17^{a}	48.62^{a}	17.37^{b}	8^{b}
HD (cm)	3.13**	16.89^{b}	19.04^{a}	17^{b}	20^{a}
SD (mm)	2.34^{ns}	18.43^{a}	17.4^{a}	17.49^{a}	17.6^{a}
SW (g)	422.45*	50.62a^{b}	63.69^{a}	62.86^{a}	47.55^{b}
SY (kg/ha)	18831.78*	3517.43^{a}	4162.63^{a}	3576.56^{a}	2287.47^{b}
OY (Kg/ha)	5502*	1527.7^{a}	1767.18^{a}	1458.14^{a}	944.37^{b}
OC (%)	16.05*	43.53^{a}	42.54^{ab}	40.77^{b}	41.36^{ab}

**, *: significant at 1% and 5%, respectively.
¥: Abbreviations: DM: days to maturity, PH: Plant height, HA: Head angle, HD: Head diameter, SD: Stem diameter, SW: Seed weight, SY: Seed yield, OY: Oil yield, OC: Oil content.
Means followed by the same letter in each row are not significantly different at *P* = 0.05.

4 CONCLUSION

This paper exploited the North Carolina Design 1 analysis to investigate the genetic implications regarding seed yield, oil yield, and certain agronomic traits in different new F_1 hybrids of sunflower. Cluster analysis revealed significant differences among all the study groups for all the traits investigated, except for head diameter. The second group with six hybrids showed the highest values for grain yield, yield components, and oil yield. Therefore, the hybrids in this group may be recommended for application in breeding programs. Moreover, the predominance of additive gene action in explaining genetic variations observed in days to maturity, seed weight, and oil content (%) supports the statement that genetic improvement may be suggested through accumulation of favorable alleles from parents and using such proper methods as recurrent selection. The predominance of the dominance gene action in explaining the genetic variation observed in head angle, head diameter, seed oil, and seed yield supports the claim that hybridization breeding methods are required to improve these traits. The importance of both additive and dominance gene actions for the genetic control of plant height and stem diameter supports breeding methods based on both selection and hybridization for improving these traits.

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