Heterosis and Genetic Diversity of Yield and Its Some Components in F1 of Sunflower Inbred Lines

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Abstract

Fall season 2020, six inbred lines of sunflower were crossed by half-diallel crosses to obtain 15 single hybrids. The genotypes (parents and first-generation hybrids -F1) were planted in randomized complete block design (RCBD) with three replications in a field/Babylon Governorate during the spring season 2021. The study aimed to estimate Heterosis of the first generation hybrids from the mean of the parents for the traits; stem diameter, head diameter, number of seeds per head, weight of 100 seeds, seed yield and oil yield per plant. Furthermore, estimation of genetic distance among genotypes using cluster analysis. The results of the analysis of variance showed that there were significant differences at the probability level (0.01) for all the studied traits of the parents and the first generation hybrids. The two hybrids (IxQ) and (QxC) were distinguished a high significant positive heterosis for most of the traits measured. The cluster analysis showed that the two genotypes that include hybrids (QxC) and (QxF) had the highest Euclidean distance (175.92 and 183.66) respectively. This indicated to high degree of genetic diversity between the two hybrids and the rest of the studied hybrids, which it positively reflected on the performance of the hybrids for the studied traits. The results of Principal Component Analysis (PCA) and Dendrogram showed that (Q) genotype was far from the rest of the genotypes and isolated to a single group, whereas the remaining genotypes separated into groups to two separated branches, especially the two genotypes (C and Q). The reason may be due to the distinguish genetic difference of these interested genotypes which have the ability to transfer from parents to its progenies, which resulted from a presence of the clear genetic distance between them, while, other genotypes lacks the of this genetic variation case.

Keywords: Sunflower, Half- diallel, Heterosis, Genetic distance, PCA .

1. Introduction

Sunflower (Helianthus annuus L.) is one of the three most important annual oilseed crops in the world, along with soybeans and rapeseed, which represent (78%) of the world’s vegetable oil production. Globally, sunflower seed oil reached approximately 54.97 million metric tons, Ukraine had the highest sunflower seed oil productivity around 16.5 million metric tons in 2020 [1]. In addition it is considered one of the best nutritional vegetable oils consumed and the percentage of its seed oil ranges from (40-50%), oil with good quality and it is the first oil crop in Iraq [2]. It has been known about cross-pollinated crops that their yield decreases in inbreeding and increases when cross-breeding between genetically distanced parents, and that the main purpose of breeding sunflower crop is need to pure inbreds lines to produce hybrids that will outperform the cultivated commercial varieties in seed yield, oil quantity and the rest of the traits. Therefore, the phenomenon of heterosis and hybrid vigor effectively contributed to increase the yields of many crops in the last five decades [3,4].

The superiority of the plants of the first generation hybrids over the best parents resulting from the cross of two lines or two varieties, named Hybrid vigor, while Heterosis is the superiority of the plants of the first generation hybrids over the average of the parents. Heterosis is also measured by the increase in the first generation hybrids compared to a common commercial variety. However, heterosis is a quantitative traits resulting from a compound syndrome caused by a different gene action of a number of genes. It was concluded that the heterosis rarely appears due to one type of gene action, therefore it mostly results from the participation of three cases of gene action at the same time.

Rathi et al. [5]. Depar et al.[6] and Kumar et al.[7] found positive and significant heterosis for head diameter, 100 seeds weight and seed yield per plant traits. Besides, Lakshman et al. [8] obtained significant positive heterosis for stem diameter, number of seeds per head, seed and oil yield per plant. However, high genetic and environmental interaction reduces the rate of improvement. genetics and affects the accuracy of selection and the use of statistical techniques is necessary to overcome this problem.

Determining the pattern of response to different genotypes is difficult without the aid of graphic display. Therefore, cluster analysis is considered one of the best techniques that plant breeders can rely on to assess the genetic diversity, locate the quantitative traits (QLT) and to preserve genetic resources, which is not necessary to make assumptions about how the data is
distributed [9]. Cluster analysis is called Segmentation or Taxonomye analysis and it searches for identifying similar groups of genotypes for specific traits based on the similarity of their response to surrounding environmental conditions and classifying genotypes according to their genetic affinity or divergence [10]. It depends on the calculation of Euclidean distances, which expresses the amount of Dissimilarity between the rates of quantitative variables and then the production of the Dendogram, which shows the distribution of the studied genotypes into groups according to their performance and genetic origins. This study aimed to estimate the heterosis which depend to the superiority of the plants of the first generation hybrids over the mean of the parents, additionally, finding the genetic diversity between the inbred lines using cluster analysis.

2. Materials and Methods

Six genotypes of sunflower (obtained by seven generation of self-pollination) were planted in a field in Babylon Governorate on 15/7/2020. The genotypes of seeds were from (Zahrat Al-Iraq, Quds, Argensun, EuroFlore, Flamme, Coban), which it provided from Abu Ghraib Research Station and the General Company for Oil Crops Research, Babylon Agriculture Directorate/Agricultural Equipment). The half-diallel crosses [11] were carried out among the parents and according to the method adopted by Al-Jubouri et al. [12]. Six parents and first-generation hybrids (15) were planted on 21/2/2021 in a randomized complete block design (RCBD) with three replications. Three furrows each genotype, the distance between one furrow and another (75 cm), the distance between one plant and another (20 cm), plant population is 66.66 thousands plant per hectare. All crop service operations, including irrigation, fertilization and weeding, were performed according to the recommendations for planting sunflower [13]. Data were recorded on ten plants of each genotype and traits were the stem diameter (mm) was measured from the middle of the stem by using Varnier calipers, head diameter (cm) was measured for the part only containing the seeds [14], number of seeds per head, weight of 100 seeds (g), the seed yield per plant (g) was extracted by weighing the seeds of the ten plants and taking the mean seed weight per plant and oil yield in the plant (g), it was estimated by the following equation (Oil yield g/plant = oil in seeds × seed yield ×100).

The heterosis (%) for the first-generation hybrids was measured depend to the superiority of the plants of the first generation over the mean of the parents according to the following equation:

\[ \text{Heterosis (H)} = \left( \frac{\text{F1} - \text{MP}}{\text{MP}} \right) \times 100 \]

F1 = mean of the trait in the first generation hybrids.

\[ \text{MP} = \text{mean of the adjective for the average of the parents (P1, P2)} \]

Hybrids significant was tested using the standard error (S.E where: \( S.E = \sqrt{\frac{2\text{MS}_{e}}{r}} \)) as mentioned by El-Sahookie [3].

Analysis of variance of studied traits was applied according to the randomized complete block design for results of half diallel crossing by Griffing method [11, 15], the means of the genotypes were compared using the least significant differences test (L.S.D at probability level of 5%) [16]. A cluster analysis was also performed, which consisted of several steps: Creating a matrix for the degree of similarity between the studied genotypes (Proximitie matrix) for the Jaccard Coefficient to draw the cluster analysis scheme [17]. Dendogram formation, which shows the distribution of the studied genotypes into groups according to their performance and genetic origins, calculating the Euclidean distances that express the degree of similarity between the rates of the groups from the Proximitie matrix that was formed in the first stage. All statistical and genetic analysis were carried out using the two programs Excel and SAS.

3. Results and Discussion

Table (1) shows that there are highly significant differences among the genotypes (parents and first generation hybrids) for all the traits under study at a probability level of 0.01%, and other researchers obtained similar results in their studies, including Abbas [18], Lakshman et al. [19], Lakshman et al. [8] and Kadhim and Abbas [20].

| Source of variation | d.f | Steam diameter (mm) | Head diameter (cm) | Number of seed per head | 100 seed weight (g) | Seed yield (g) | Oil yield (g) |
|---------------------|-----|---------------------|-------------------|------------------------|----------------------|----------------|--------------|
| Replications        | 2   | 8.94                | 5.28              | 5936.44                | 0.04                 | 69.64          | 3.07         |
| Genotypes           | 20  | 29.93**            | 26.70**           | 84743.59**            | 3.06**               | 936.27**       | 138.57**     |
| Error               | 40  | 4.43               | 2.73              | 3439.69                | 0.18                 | 41.68          | 4.42         |

**represent significant differences at probability level 1%.

Table (2) shows the mean performance of the six parents and their half diallel crosses without reverse hybrids, the parent (C) was manifested with desirable high values of its traits, it distinguished from the rest of the parents in the characteristics; the number of seeds in the head, the seed yield, plant\(^{-1}\) and the oil yield, plant\(^{-1}\) scored (430, 41.16 g and 21.91 g), respectively. It is followd by parent (F) in traits; stem diameter, head diameter and 100-seed-weight, where they recorded (19.40 mm, 14.74 cm and 6.50 g), respectively. The differences between the parents were reflected on the hybrid resulting of crossing between
them, as the hybrid (Q×C) outperformed by giving the highest significant mean of all studied traits (21.51 mm, 20.53 cm, 1006, 8.35 g, 85.46 g and 32.09 g) respectively. Whereas, some hybrids showed the lowest mean for traits such as hybrid (F×E) for stem diameter (12.31 mm) and head diameter (14.59 cm), hybrid (Q×A) for number of seeds per head (470.67), hybrid (C×E) for 100-seed weight (5.20 g), hybrid (I×A) for seed yield per plant (40.21 g) and oil is in the plant (12.93). It is clearly noted that the parent (C) excelled to the rest of the parents in most of the studied traits, therefore it can be directly efficient in improving the yield of both the seed and oil. Besides, it may be introduced into cross-breeding programs with other varieties, especially with local varieties to transfer the high yield components to their hybrids. For instance the results of hybrid (Q×C), which it revealed a high preformance for all studied traits, thus, it can be benefited as selection index by entering it into selection programs to achieve a new cultivars that is superior in the traits of the yield.

Table 2. Mean values of the parents and first generation hybrids for yield trait and its components.

| Genotypes | Stem diameter (cm) | Head diameter (cm) | Number of seed per head | 100 seed weight (g) | Seed yield (g) | Oil yield (g) |
|-----------|-------------------|--------------------|-------------------------|---------------------|----------------|-------------|
| I         | 10.42             | 11.37              | 290.00                  | 4.94                | 17.05          | 5.73        |
| Q         | 13.26             | 11.47              | 251.00                  | 4.57                | 17.66          | 5.28        |
| F         | 19.40             | 14.47              | 418.67                  | 6.50                | 40.95          | 12.12       |
| C         | 13.38             | 11.53              | 430.00                  | 5.45                | 41.16          | 12.91       |
| E         | 10.37             | 9.20               | 348.33                  | 4.21                | 20.45          | 6.64        |
| A         | 9.84              | 11.30              | 386.67                  | 5.43                | 33.18          | 8.65        |
| I×Q       | 16.72             | 15.69              | 573.33                  | 5.89                | 56.14          | 21.56       |
| I×F       | 15.84             | 15.47              | 590.00                  | 5.75                | 51.91          | 16.35       |
| I×C       | 20.57             | 19.36              | 714.33                  | 7.20                | 71.27          | 27.27       |
| I×E       | 13.30             | 15.18              | 576.67                  | 6.39                | 51.02          | 17.84       |
| I×A       | 17.38             | 18.99              | 498.33                  | 5.74                | 40.21          | 12.93       |
| Q×F       | 16.27             | 15.84              | 673.33                  | 5.90                | 67.39          | 23.31       |
| Q×C       | 21.51             | 20.53              | 1006.00                 | 8.35                | 85.46          | 32.09       |
| Q×E       | 17.74             | 18.70              | 540.67                  | 5.59                | 50.46          | 19.46       |
| Q×A       | 15.07             | 16.57              | 470.67                  | 7.24                | 54.11          | 17.69       |
| F×C       | 14.04             | 15.25              | 573.00                  | 6.68                | 55.74          | 17.49       |
| F×E       | 12.31             | 14.59              | 481.00                  | 6.30                | 48.89          | 17.28       |
| F×A       | 14.64             | 16.65              | 551.67                  | 7.21                | 59.51          | 19.01       |
| C×E       | 16.19             | 17.75              | 563.33                  | 5.20                | 42.86          | 16.72       |
| C×A       | 14.85             | 15.47              | 658.67                  | 7.24                | 69.90          | 21.64       |
| E×A       | 13.91             | 14.74              | 729.00                  | 5.73                | 58.25          | 17.70       |
| Mean      | 15.10             | 3.60               | 539.27                  | 6.07                | 14.09          | 4.59        |
| L.S.D 0.05| 4.59              | 3.60               | 128                     | 0.927               | 14.09          | 4.59        |

From the results below in the table (3) indicated that there is a positive significant heterosis for stem diameter trait, which ranged from (36.1%) to (72.87% ), while seven hybrids gave positive and negative non-significant heterosis. The positive value of heterosis percentage is desirable which means an increase in the thickness of the stem, which leads to an increase in the utilization of nutrients by increasing the vascular bundles of transporting substances to the plant parts, thus the plant stems become strong and more resistant to lodging , these results are consistent with what found by [21,22].

As for the characteristic of the head diameter, Table (3) indicated that there was a positive and significant heterosis for the characteristic of the head diameter (cm) for all crosses except for the two hybrids (I×F) and (F×C). The heterosis percentages of hybrids ranged between (17.33% and 80.97%). However, the hybrid (Q×E) was superior by giving the highest heterosis percentage (80.97%), and it was not significantly different with the two hybrids (Q×C) and (C×E), as they gave a heterosis by (78.65%), and (71.18%), respectively. Increasing the diameter of the head is of great importance because it might lead to an increase in the number of seeds in the head, thus increase the seed yield, and it is clear from the results that the trait may be influenced by of the additional and superior-dominance gene action of the highest parents. These results are compatible with the findings of Encheva et al, [23] and Al-Khafaji [24], who found a significant heterosis for the head diameter.

From the same table, it is observed that the hybrids showed significant positive heterosis for the characteristic of 100-seed weight (g). The heterosis% of the hybrids ranged between (0.52%) and (66.68%). The hybrid (Q×C) exhibited the highest heterosis (66.68%), while the hybrids (C×E), (F×C), (Q×F), (I×F) and (I×A) showed non-significant positive heterosis. However, positive values for the heterosis of the hybrids for 100 seed weight are desirable, because they refer to an increase in the weight of the seed, and it is one of the important components of the yield resulting in an increase in the weight of the seed ,thus an increase in the yield. The reason for the discrepancy in heterosis values of the hybrids is probably due to the additional influence and superior dominance. These results are in accordance with the findings of [16,2,26].

Table (3) demonstrated a significant positive heterosis for the trait of seed yield in the plant, which ranged between (35.67%) and (223.43%). The hybrid (I×Q) outperformed the rest of the hybrids by giving the highest heterosis of (223.43%). While
the two hybrids (F×C) and (C×E) showed non-significant positive heterosis (35.67% and 39.12%), respectively. Positive values of the heterosis are favorite due to an increase in the plant yield of the hybrids compared to its combined parents. These results are in agreement with the findings of Meena [27] and Zia et al. [28].

As for the characteristic of the oil yield per plant (g), it is noted that all the hybrids offered a significant positive heterosis in the desired direction, except for the two hybrids (F×C) and (C×E) which exposed non-significant positive heterosis. Hybrid (Q×C) outperformed the rest of the hybrids by giving it the highest heterosis (291.76%). Whereas, the hybrid (I×A) gave the least significant heterosis (79.92%). The oil yield per plant is directly affected by the seed yield in the plant, however, it is detected that the seed yield has a significant effect on showing the variations among the genotypes in the oil yield. The results, illustrated the effect of the dominance and additional gene action for this trait, this was similar with Lakshman et al. [8].

**Table 3.** Heterosis % based on the superiority of the first generation over the average of the parents for six characteristics in the sunflower.

| Genotypes | Steam diameter (mm) | Head diameter (cm) | Number of seed per head | 100 seed weight (g) | Seed yield (g) | Oil yield (g) |
|-----------|---------------------|--------------------|-------------------------|--------------------|----------------|--------------|
| I×Q       | 41.19               | 37.46              | 111.95                  | 23.71              | 223.43         | 291.76       |
| I×F       | 6.215               | 19.79              | 66.50                   | 0.52               | 78.97          | 83.15        |
| I×C       | 72.87               | 69.08              | 98.42                   | 38.61              | 144.84         | 192.62       |
| I×E       | 27.98               | 47.61              | 80.67                   | 39.64              | 172.12         | 188.64       |
| I×A       | 71.6                | 67.59              | 10.60                   | 60.11              | 79.92          |              |
| Q×F       | -0.86               | 22.16              | 101.09                  | 6.53               | 129.97         | 167.84       |
| Q×C       | 61.46               | 78.56              | 195.44                  | 66.68              | 190.57         | 252.83       |
| Q×E       | 50.15               | 80.97              | 80.42                   | 27.24              | 164.82         | 226.54       |
| Q×A       | 30.48               | 45.59              | 47.62                   | 44.69              | 112.86         | 153.93       |
| F×C       | -14.32              | 17.33              | 35.035                  | 11.83              | 35.76          | 39.71        |
| F×E       | -17.28              | 23.32              | 25.42                   | 17.58              | 59.24          | 84.25        |
| F×A       | 0.105               | 29.21              | 37.00                   | 20.90              | 60.56          | 83.02        |
| C×E       | 36.31               | 71.18              | 44.75                   | 7.55               | 39.12          | 71.08        |
| C×A       | 27.88               | 35.53              | 61.30                   | 33.08              | 88.05          | 100.71       |
| E×A       | 37.68               | 43.8               | 98.36                   | 18.77              | 117.26         | 131.53       |
| S.E       | 28.03               | 21.57              | 41.55                   | 16.99              | 56.18          | 72.49        |

3.1. Genetic diversity values based on the mean of the measured traits

3.1.1. Calculation of the Euclidean distance

The results of table (4) show the Euclidean distances among the study genotypes. The maximum genetic distance between genotype (Q) and genotype (C) was (183.66) and between genotype (Q) and genotype (F) was (175.92), whereas, the lowest Euclidean distance was (28.5) between genotypes (F) and (C).

**Table 4.** Euclidean distance between genotypes depending on the mean of the measured traits.

| G | I | Q | F | C | E | A |
|---|---|---|---|---|---|---|
| I | 0 | 43.95 | 0 | 138.66 | 175.92 | 0 |
| Q | 147.6 | 183.66 | 28.5 | 0 | 60.51 | 98.68 | 83.09 | 89.4 | 0 |
| F | 101.94 | 137.77 | 50.88 | 49.38 | 44.87 | 0 |

3.2. Genetic tree Dendrogram between genotypes based on the mean of measured traits

Figure (1) shows the cluster analysis of six genotypes of the sunflower plant by studying the Euclidean dimension between them based on all the averages of the common measured traits. The genotypes were divided into two main groups (A) and (B) with a Euclidean distance approximately of (132). Group (B) is divided into two subgroups, (B1) and (B2), with a Euclidean distance close to (70). Group (B1) contained genotypes (F) and (C), while group (B2) contained genotypes (E) and (A).
However, the isolation of genotypes from each other in groups or clusters, in addition to the isolation from genotypes (Q) and (I) indicated the genetic divergence in many of the studied traits. This may be due to the resulting of being from different genetic origins. These results are consistent with the findings of [24,29].

3.3. Principal Component Analysis

Figure (2) shows the distribution of genotypes at two axial orthogonal levels, which represent the two highest levels of genetic variance among the studied genotypes. It is clear through the distribution that the aggregates results formed matching the Dendrogram genetic tree that was drawn depending on the average of the measured traits. Also, illustrated that the (Q) genotype was far from the rest of the genotype s. Obviously, its isolation by a group, and the separation of the remaining genotypes in a separate group with two branches.

Figure 1. Dendrogram genetic tree according to the UPGMA method and depending on the average of the measured traits.

Figure 2. Distribution of six genotypes of sunflower on the orthogonal plane according to Principal Co analysis (PCA).

Conclusion

The difference in the genetic origin of the genotypes between the genotype (Q) on the one hand and the two genotypes (C) and (F) on the other hand, which led to the emergence of high hererosis for their hybrids (Q×C) and (Q×F), and the information we obtained confirmed from the results of Principal Component Analysis (PCA) and Dendrogram showed that (Q) genotype was far from the rest of the genotypes and isolated to a single group, whereas the remaining genotypes separated into groups to two different branches, especially the two genotypes (C and Q). Furthermore, their possession of some major genes that can be transferred from parents as a result of the presence of a genetic diversity between them which is missing from the rest of the studied genotype. Hence, it may be provide a remarkable indication to take advantage of these hybrids to improve the characteristics of the sunflower yield and its components.
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