A Study on Heterosis and Combining Ability Through Line X Tester in Some Genotypes of Sunflower (Helianthus Annuus *L*.)

Iqbal. M Ahsan,[1] Asif Ismail[1], Ayesha Nisar[1], Rabia Perveen[1], Zainab Irfan[1], Sohail Ahmad Khan[2]

[1] Department of PBG, University of Agri., Faisalabad (Pakistan)
[2] CABB, University of Agri., Faisalabad (Pakistan)

Abstract

Sunflower (Helianthus annuus L.) is mainly grown for its benefits in oil and protein contents. This research was carried out in the Rajawala Research Station of the University of Agriculture, Faisalabad. During the Autumn of 2022, some sunflower genotypes were sown, four being lines and three as male (testers) to develop twelve cross combinations. During the spring season, of 2023, the parents and their crosses were evaluated using a Randomize Complete Block Design. Data was recorded for different yield parameters including plant height, number of leaves, leaf area, internodal length, stem diameter, head diameter, seed yield/head and 100 seed weight. After that, the data was kept for ANOVA to estimate the significance of the recorded data. Combining ability and heterosis indicated the best combinations among parents and crosses.

Keywords: Heterosis, Combining, Line X Tester, Genotypes, Sunflower

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Introduction

Helianthus annuus L., a member of the Asteraceae family, is a developing oilseed crop that ranks fourth globally. It plays a significant part in Pakistan's economy due to its drought resistance, high yielding, and salt tolerance. Its oil is abundant in polyunsaturated fatty acids, making it a high-quality edible oil that lowers the risk of heart disease (Rani et al., 2017). Heterosis in seed and oil production might result in increased output since it is a cross-pollinated crop. It is utilized as a livestock feed source, for medical and industrial purposes and a great source of fertiliser replacement. (Fernández-Luqueo et al., 2014). The sunflower is said to have originated in America about 3000 BC. Wild sunflowers originated in North America, but it was domesticated in Russia (Heiser,1-1998). It grows annually, with plant heights ranging from 1.5 to 2.5 meters. A temperature of 20-25°C is ideal for its2-development and production. It has 40-60g per 1000 seeds weight and contains 30-50% oil (90% oleic acid and 10% linoleic acid) and 20-30% protein. Hybrid seed accounts for over 90% of output (Arshad et al., 2010). The combining ability and genetic approach for different sunflower agronomic parameters were studied. The GCA and SCA were calculated (Ghaffari et al., 2011). GCA refers to additive variance, while SCA refers to non-additive variance. Heterosis is a method of selecting appropriate combiners from parent lines that are genetically distinct from one another (Kanwal et al., 2015). There is a lot of heterosis among the sunflower genotypes for achene yield and associated parameters (Goksoy et al., 2004). In a strictly statistical sense, the conclusions reached here only apply to the particular sunflower hybrids at issue. Several lines for grain production, days to maturity, 50% flowering, and oil content were investigated in the research. Except for days required to maturity, the research revealed significant findings for GCA and SCA for all characters studied. It was discovered that the epistatic effect had a greater influence on all characteristics than the antagonistic impact of SCA. Along with parental lines, certain well-known lines such as RAI, FT 4, and FT 11 5 have been identified as excellent all-character combiners. GUL and IRA were the top general combiners for yield harvest index among all lines. Early maturity was satisfactory with the FT 334 ARI cross combination (Jan et al., 2005).

Objectives

General combining ability, specific combining ability, and heterosis testing of several inbred lines.

To find potential hybrids for cultivation in general.

Review of Literature

Skoric *et al.* (2000) investigated agronomic parameters such as plant height, achene harvest index, and oil content in 20 female lines, five male lines, and 100 hybrids. The RP-ST-A3, Ha-26A, AHR-N-92, and URS-RF-90 lines demonstrated great practical value.

Sharma *et al.* (2003) investigated the capacity of distinct genotypes under two different environmental situations. A total of twelve lines and five testers were used.Potential combiners were identified as CMS-10A, CMS 43B, LI-IP-324, IL-IP-237, and IL-M-197.

Goksoy *et al.* (2004) investigated the hybrid vigour, GCA, and SCA of several sunflowers. GCA values were high in the CMS 379, CMS 562, CMS 684, AFR-578, and AFR-892 lines. CMS 192 ARF 327 and CMS 192 ARF 298 were recognized as better sunflower-yielding crosses.

Jan *et al.* (2005) investigated several lines for grain production, days to maturity, 50% flowering, and oil content in research. Lines such as RAI, FT 4, and FT 11 have been identified as excellent all-character combiners. GUL and IRA were the top general combiners for yield.

Habib *et al.* (2006) examined 14 sterile cytoplasmic lines and six testers for their capacity to combine all agronomic parameters. The highest yield potential was found in the ORI-4 RL-85 hybrid. Oil reaction was strongest in ORI-7 x RL-30 and ORI48 x RL-70 crosses. Plant height heterosis was greatest in ORI 21 RL-78.

Shankar *et al*. (2007) found that different hybrids and parent lines might combine. R- 272-1 and R-18 were the parents' best achene and oil-yielding lines. One cross, FP-499A P-635 R, was created with the ability to compete with all of the other crosses studied. In these sunflower plant attributes cross, non-additive gene activity was shown to have a significant influence.

Sujatha and Reddy (2009) discovered that sunflower seed yield and seed-related attributes may be combined. The DMCS 35 DSR 15, CMS 8-1A RAH 341, and CMS 8-1A DSR 10 crossings were remarkable achene yield combiners that may be exploited in subsequent breeding programs.

Tan (2010) used Line Tester analysis to determine the capacity of several sunflower lines to combine for oil production, achene yield, days to pubescence, days to flowering, plant height, head width, and the number of leaves. The inbred 0044 CMS, 045 CMS, 0959 CMS, 083 CMS, 004 CMS, 009 Rf, 045 Rf, 052 Rf, and 197 Rf showed significant GCA for most of the characteristics and were considered good combiners.

Kang *et al.* (2013) determined genetic differences, GCA, and SCA of several sunflower lines. To create 36 F1 hybrids, four testers were crossed with nine lines. Lines G94 and G78 exhibited greater significant GCA for all characters. Combiner achenes yield/plant, growth days, and oil content were all high in A5.

Oshundiya *et al.* (2014) evaluated combining ability in twenty inbred lines. Several hybrids exhibited significant combining ability for mentioned traits such as H26-A, RH-18, H48-Ax FT28, PL4-180x HA19-A non-additive gene action observed.

Qamar *et al.* (2015) performed multi-location traits by using a hybrid to produce high-producing parents and yield-related traits in sunflowers. According to trials, GCA variance is greater than SCA variance.

Azad *et al.* (2016) used a Line Tester breeding plan to assess the combining ability and heterosis of four CMS lines and four R-lines. The finest combiners were determined to be HA-03 and HA-54, which had good general combining ability for all characters.

Singh and Kumar (2017) evaluated hybrid vigour for yield-related parameters in sunflowers. To achieve this, four CMS lines and eight different testers were crossed to create 32 crosses. The hybrids DSFH-22, DSFH-19, DSFH-20, DSFH-1, and DSFH-2 performed well in this study.

Iqbal *et al.* (2017) investigated research to study the lines having the best combining ability (GCA and SCA) and heterosis. The line B-SIN-82 and testers RL-54 and RL-51 provided the best results for various traits.

Bhoite et al. (2018) calculated the amount of heterosis, CA, and stability factors in sunflowers. Three CMS lines and 14 testers were mated to produce 42 crosses in a Line Tester breeding strategy. Findings found the predominance of non-additive kinds of gene activation. One line (CMS-17A) and seven testers were assessed for head width and seed yield.

Rezaizad *et al.* (2019) evaluated combining ability by crossing four restorers and eight CMS lines. Hybrids CMS19 R137, CMS19 R217 and CMS1221/1 R137 had high seed yields among all. CMS19 and restorer R864, R137 had the greatest GCA for seed yield CMS 456/2 R217 had the high SCA.

Telangre *et al.* (2019) examined 40 hybrids produced by mating four CMS lines with ten testers utilizing a line x-tester mating scheme. RHA138-2 and EC 601957. PET 2-7-1A x EC 601957, CMS 234A x EC 601924, PET 2-7-1A x R16, and ARM 249A x R 271-1, were shown to increase seed yield per plant.

Materials and Methods

The experiment was carried out at the field of Plant Breeding and Genetics, University of Agriculture, Faisalabad during 2022-23. Seven progenitors were acquired as part of the experimental material. There were four female progenitor lines and three male progenitor lines. In the Line x Tester breeding program of 2022, lines and testers were crossed. Parents and crosses were sowed in 2023, and data was collected. In September 2022, parental lines were planted in the study field during the autumn season. As a test, four female lines (Z_1, Z_2, Z_3, and Z_4) were crossed with three male lines (A_1, A_2, and A_3). Next, the Randomized Complete Block Design with three replications, crossing seed, and parental lines were sown in the field the following growing season. The space between each plant and row was kept at 25 cm and 75 cm, respectively.

Data of the following parameters was recorded, such as; Plant height, Number of leaves/ plant, leaf area (cm), internodal length, stem diameter(cm), head diameter, seed yield/ plant, 100 seed weight(g), biometrical approach (Steel, 2012).

Result and Discussion

The current experiment was carried out at the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. For plant height, the lowest value was observed in Z3xA1 (110.13 cm) while the highest value was observed in Z4xA3 (115.13 cm). Skoric et al. (2000) also investigated plant height in 20 female lines, five male lines, and 100 hybrids. Results showed similar values.

For several leaves, the maximum mean value was observed in Z1×A3 (34.76), followed by Z4×A2 (34.73) and Z2×A3 (34.66), which exhibited high mean performance while Z2×A1 (33.16) showed minimum values among all crosses. Tan (2010) used Line Tester analysis to determine the capacity of several sunflower lines to combine for the number of leaves. These lines showed similar results.

For the leaves area, the highest value was observed in Z1x A2 (144.83 cm2) while the lowest value was observed in Z2 x A2 (130.96 cm2). The lowest value for internodal length was observed in Z1x A1 (10.96 cm) while the highest value was observed in Z1x A2 (13.86 cm). Ahmad et al. (2012) used a Line Tester mating design to assess the leaves area and internodal length for genetic variability. Similar results were obtained about the internodal length and leaves area.

For stem diameter, Z1xA2 (7 cm) exhibited a maximum mean value while Z2 x A2 (4.6) showed minimum values among all crosses. Deshmukh et al. (2016) used fifteen restorers and three lines, as well as conventional checks, to investigate the direction and amount of heterosis. All of the characteristics under investigation showed significant heterosis. Hybrids explained heterosis for the stem width. The same results were found after their experiments.

For head diameter, Z1 x A2 (12.83 cm) and A2 x Z1 (12.76 cm) exhibited maximum mean values while Z3 x A3 (11.23) showed minimum values among all crosses. Shinde et al. (2016) an experiment conducted by crossing five lines and ten testers to evaluate the head diameter, then similar results showed from an experiment.

For 100 seed weights, Z2 x A3 (7.6g) exhibited high mean performance while Z2 x A2 (6.1g) showed minimum values among all crosses. Z4 x A1 (64.83) exhibited high mean performance for seed yield/plant. Jan et al. (2005) investigated several lines for seed production. These lines are identified as excellent seed yielders. GUL and IRA were the top general combiners for yield.

Table 4.11: Specific combination ability effect of crosses

Annexure A

Table 4.16: Mid parent & better parent heterosis for Head Diameter

Annuxure B

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Annexure A

crosses	N.L	L.A	P.H	I.N.L	S.D	H.D	A.W	Y.P
Z1XA1	0.33ns	-2.88**	-1.31**	-0.60ns	-0.76ns	-0.19ns	-0.26**	-2.21ns
Z1XA2	-0.67ns	5.76**	2.62**	1.20**	1.69ns	0.38**	0.51**	6.42**
Z1XA3	0.33ns	-2.88**	-1.31**	-0.60ns	-0.93ns	-0.19ns	-0.26**	-3.21ns
Z2XA1	-0.33ns	2.88**	1.31**	0.60ns	1.51ns	0.19ns	0.26**	3.21ns
Z2XA2	0.67ns	-5.76**	-2.62**	1.20**	-1.68ns	-0.38**	-0.51**	-0.42**
Z2XA3	-0.33ns	2.888*	1.31**	0.60ns	1.17ns	0.19ns	0.26**	3.21ns
Z3XA1	0.33ns	-2.88**	-1.31**	-0.60ns	-1.24ns	-0.19ns	-0.26**	-3.21ns
Z3XA2	0.67ns	5.76**	2.62**	1.20ns	1.65ns	-0.38**	0.51**	6.42**
Z3XA3	0.33ns	-2.88**	-1.31**	-0.60ns	-0.41ns	0.19ns	-0.26**	-3.21ns
Z4XA1	-0.33ns	2.88**	1.31**	0.60ns	0.49ns	0.19ns	0.26**	3.21ns
Z4XA2	0.67ns	-5.76**	2.62**	-1.20**	1.66ns	-0.38**	-0.51**	-6.42**
Z4XA3	0.33ns	2.88**	1.31**	0.60ns	1.18ns	0.19ns	0.26**	3.21ns

Annexure B

Crosses	**Mean**	**Mid Parent**	**Bet Parent**
Z1XA1	11.80	-17.39 **	-22.54 **
Z1XA2	12.37	-19.08 **	-19.35**
Z1XA3	11.80	-23.21 **	-23.87**
Z2XA1	12.37	-10.92 **	-14.32 **
Z2XA2	11.80	-20.72 **	-20.22**
Z2XA3	12.37	-17.37 **	-11.50**
Z3XA1	11.80	-7.09 **	-19.35**
Z3XA2	12.37	-9.73 **	-23.87**
Z3XA3	11.80	-14.39 **	-7.25 ns
Z4XA1	12.37	-2.75 ns	-7.25 ns