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# RESPONSE TO SELECTION FOR SEED YIELD AND ITS COMPONENTS IN $S_2$ FAMILIES OF A SUNFLOWER POPULATION

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**Fifty $S_2$ families from a random mated sunflower population were evaluated in a randomised complete block design with three replications. Significant differences existed among $S_2$ families for the traits evaluated. Three plant traits (achene weight, number of achenes per head and seed yield) indicated greater variation. Their genotypic and phenotypic coefficients of variation were maximum. The estimates of heritability were significant for all the traits studied except head diameter. The traits showing the greater variation also indicated maximum expected genetic advance.**

## INTRODUCTION

Pakistan is deficit in edible oil production and spends a large amount of foreign exchange on the import of edible oils. The Government of Pakistan is striding hard to tackle the problem of oilseed production by increasing area and improving per acre yield of non-conventional oilseed crops like sunflower. Therefore, plant breeders have directed their attention towards the development of sunflower cultivars with improved seed yield and greater percentage of oil. One of the methods to improve the plant population is to use $S_2$ progeny recurrent selection. This includes selected $S_2$ progenies in the breeding nurseries for selection, inbreeding and producing test cross seed. The $S_2$ progenies selected for recombination are the survivors of intensive multiple trait selection in $S_1$ and $S_2$ generation and should have potential in developing new lines.

Much research work on $S_1$ family selection have been carried out in sunflower (Hassan, 1991). The research work on $S_2$ progeny selection is very meagre, only one reference (Cruz, 1986) is available. He crossed $S_2$ lines of sunflower with open pollinated testers and observed significant variation among hybrids. Whereas, Horner *et al.* (1973) reported that the estimates of heritability and expected genetic gain were consistently higher for the $S_2$ progeny method in maize. The present research work is an attempt to estimate the response of seed yield and its components by using $S_2$ family selection.

## MATERIALS AND METHODS

The present study was conducted at the Postgraduate Agricultural Research Station (PARS), University of Agriculture, Faisalabad during spring season 1991. Fifty $S_2$ families derived from a random mated sunflower population were planted in the field by using a modified randomised complete block design with three replications. Each $S_2$ family comprised a single row plot of 3.5 m length by keeping plant to plant and row to row distances of 23 and 75 cm, respectively. In order to reduce the replication size and to increase the precision of the experiment, each replication was grouped into two blocks containing 25 $S_2$ families each. The data of ten randomly selected plants from each $S_2$ family in each replication were recorded for plant height, head diameter, number of achenes per head, 100-achene weight and seed yield.

Analysis of variance of each of the trait was performed separately (Steel and Torrie, 1980). The estimates of broad sense heritability for each trait were calculated on plot mean basis from the analysis of variance table. The standard error of heritability was calculated by using the formula given by Lothrop *et al.* (1985). Response to selection or expected genetic advance (GA) was calculated at 10% selection intensity ($i = 1.755$) by using the following formula:

$$GA = i.\sigma_p.h^2$$

where

$i$ = the selection intensity
$\sigma_p$ = the phenotypic standard deviation, and
$h^2$ = the estimates of broad sense heritability

The expected genetic advance is reported as percentage of mean (relative expected genetic advance) and is the advance expected from one cycle of selection.

## RESULTS AND DISCUSSION

Mean squares (Table 1) indicated highly significant differences among $S_2$ families for plant height, head diameter, number of achenes per head, 100-achene weight and seed yield. The $S_2$ families from the random mated sunflower population exhibited variation for all the plant traits evaluated (Table 2). The phenotypic coefficient of variation for each of the character was greater than its respective genotypic coefficient of variation. However, both genotypic and phenotypic coefficients of variation were maximum for achene weight, number of achenes per head and seed yield. The results indicated greater variation for the plant traits recorded among $S_2$ families and agrees with the findings of Cruz (1986).

Expected genetic advance from selection per cycle in a recurrent selection breeding programme using $S_2$ families with

**Table 1. Mean squares from the analysis of variance of $S_2$ families of sunflower for the five indicated traits**

| Source of variation | df | Plant height (cm) | Head diameter (cm) | Number of achene per head | 100-achene weight (g) | Seed yield (kg acre$^{-1}$) |
|---|---|---|---|---|---|---|
| Blocks | 1 | 57.11 | 6.89 | 29372.01 | 0.70 | 90479.04 |
| Reps/Blocks | 4 | 2581.20 | 9.33 | 89524.82 | 1.86 | 104423.76 |
| $S_2$ families/block | 48 | 949.33** | 8.01** | 43313.21** | 2.77** | 55192.52** |
| Error | 96 | 143.34 | 4.56 | 21888.27 | 0.56 | 31621.38 |

** = Significantly different at 0.01 probability level.

**Table 2.** **Mean range and coefficients of variation for five indicated traits among $S_2$ families of sunflower derived from a random mated population**

| Trait | Mean | Range | Coefficients of variation (%) | |
|---|---|---|---|---|
| | | | Genotypic | Phenotypic |
| Plant height (cm) | 153.4 | 84.0 - 201.2 | 10.69 | 11.60 |
| Head diameter (cm) | 15.3 | 8.33 - 22.4 | 7.02 | 10.69 |
| 100-achene weight (g) | 4.81 | 2.3 - 9.6 | 17.86 | 20.00 |
| No. of achenes head$^{-1}$ | 456.56 | 132 - 920 | 18.51 | 26.32 |
| Seed yield (kg acre$^{-1}$) | 498.76 | 115 - 1280.2 | 17.77 | 27.20 |

**Table 3.** **The estimate of broad sense heritability ($h^2$), expected genetic advance and the relative expected genetic advance among $S_2$ families of sunflower for the five indicated traits**

| Trait | $h^2 \pm$ SE | Expected genetic advance | relative expected genetic advance (%) |
|---|---|---|---|
| Plant height (cm) | 0.849 ± 0.201 | 26.51 | 17.3 |
| Head diameter (cm) | 0.434 ± 0.220 | 1.24 | 8.1 |
| 100-achene weight (g) | 0.798 ± 0.202 | 1.35 | 28.0 |
| No. of achene head$^{-1}$ | 0.495 ± 0.213 | 104.30 | 22.8 |
| Seed yield (kg acre$^{-1}$) | 0.427 ± 0.182 | 101.65 | 20.4 |

SE = Standard error.

broad sense heritability values are listed in Table 3. The estimates of heritability on a $S_2$ progeny-mean basis varied for the plant traits evaluated. These estimates for plant height, achene weight, achenes per head and seed yield differed significantly from zero when tested against their respective standard errors (Table 3). However, the estimate of heritability for head diameter was non-significant. These broad sense heritabilities are the only useful estimates for estimating the expected genetic advance in $S_2$ family selection programmes. The expected genetic advance for achene weight, number of achenes per head and seed yield were quite high (20.4 to 28%) as revealed by the relative expected genetic advance. Horner *et al.* (1973) also observed higher heritability and genetic advance for the $S_2$ families in maize. Based on the broad sense heritability estimates, the results suggest that selection among $S_2$ families for a single trait may result in substantial improvement in seed yield and moderate improvement for head diameter in a recurrent selection breeding programme of sunflower.

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