

# **CORRELATION STUDIES AMONG YIELD RELATED TRAITS FOR SEED YIELD IN SUNFLOWER (*HELIANTHUS ANNUUS L.*) UNDER CHARCOAL ROT STRESS CONDITIONS**

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## **Abstract**

Twenty four different accessions of sunflower evaluated for their resistance to charcoal rot caused by *Macrophomina phaseolina* under artificially field conditions. The accessions were planted according to factorial experiment in randomized complete block design with three treatments within three replications. Mean squares from analysis of variance revealed significant differences among all accessions evaluated for yield related traits and resistance to charcoal rot disease. Genotypic and phenotypic correlation coefficients in each accessions of sunflower derived from random mated sunflower UAF population. The estimates of genetic correlation coefficients were found greater in value than the phenotypic correlation coefficients for all the indicated traits for all accessions of sunflower. Seed yield per plant was positively and significant correlated with all the traits studied i.e. head diameter, number of achenes per head, head weight, 100-seed weight and oil contents at both genetical and phenotypical levels within all three treatments. Hence selection of these characters would contribute for the improvement of the seed yield per plant.

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**Keywords:** Sunflower, Oil Contents, Charcoal rot, Genotypic Correlation, Seed yield

## Introduction

Sunflower (*Helianthus annuus* L.) belongs to the family “Asteraceae” is the world’s fourth largest oilseed crop (Rodriguez *et al.*, 2002). Sunflower reported as non-traditional oil seed crop and is main source of edible oil in Pakistan. 45% oil content and 40% protein contained by the sunflower seed. (Hafizullah *et al.*, 2010). In Pakistan the crop is cultivated on an area of 448000 ha with production of 643000 and 244000 tones of seed and oil, respectively (Anonymous, 2012). It has the ability to meet domestic needs of the country. Charcoal rot among the diseases of sunflower is the serious threat to sunflower growers (Mehdi & Mehdi, 1988; Khan *et al.*, 1999). The *Macrophomina phaseolina* causal agent for charcoal rot distinguished as the most important pathogen on sunflower and more than 500 plants (Purkayastha, *et al.*, 2006). There are monotypic and no physiological races have been reported but it has high genetic variability resulting in a wide host range. Which means that crop rotation is not an effective strategy to overcome the disease (Ijaz *et al.*, 2012). Losses due to charcoal rot exceeds till 60-90% during favorable conditions for infection in sunflower crop (Khan, 2007).

Some sunflower genotypes evaluated to *Macrophomina phaseolina*. The reaction of genotypes was very different to the agent of disease (Dalili *et al.*, 2009). Genotypic and phenotypic correlations were worked out to ascertain the possible effects of accessions and environment on various plant characters and their response to charcoal rot. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for improvement of seed yield (Habibullah *et al.*, 2007). To manage the disease losses caused by charcoal rot, development of resistant varieties is the cheapest source. The one of the most efficient way is considered as use of resistant cultivars (Mahtab *et al.*, 2013). Seed yield is combination of many traits, where polygenic in nature and it is difficult to make direct selection for these traits. There were reported different types of characters associations by sunflower breeders (Punia & Gill, 1994; Patil *et al.*, 1996; Lal *et al.*, 1997; Teklewold *et al.*, 2000; Ashok *et al.*, 2000; Khan, 2001). Since charcoal rot may inflict heavy losses to the crop in the country and the present cultivars are susceptible to this disease (Shahid and Shuaib, 2007). Therefore, this study was initiated to evaluate available sunflower germplasm for identification of resistance sources to breed disease resistance cultivars.

## Material and Methods

Twenty four (24) accessions of sunflower (G-2, A-79, G-30, G-46, A-19, G-3, G-100, G-50, G-40, G-34, G-12, G-61, G-43, G-82, G-54, G-57, HBRS-5, A-50, A-60, HBRS-1, G-16, A-48, G-5 and G-45) developed and

maintained by the Sunflower Research Group, Department of Plant Breeding & Genetics, University of Agriculture, Faisalabad, Pakistan. The casual agent for charcoal rot (*Macrophomina phaseolina*) inoculum was collected from Department of Pathology, University of the Punjab, Lahore, Pakistan. The experiment was conducted during 2008 in the research area of the Department of PB&G, University of Agriculture, Faisalabad, Pakistan. Application of inoculum made before the sunflower heads formation through flooded method when the field was irrigated. Whole preventive measures were taken at the time of inoculation. All the other standard agronomic practices were applied to sunflower crop, needed for the crop establishment e.g. land preparation, seed rate, number of irrigations and dose of fertilizer. Accordingly factorial experiment in Randomized Complete Block Design (RCBD), experiment was laid out having 3 replications with plant to plant and row to row distances of 25 cm and 75 cm, respectively.

**Treatment-1:** Applied inoculum of fungal isolate (*Macrophomina phaseolina*) to crop along with use of fungicide

**Treatment-2:** Applied inoculum with fungal isolate (*Macrophomina phaseolina*) to crop with none use of any fungicide

**Treatment-3:** Normal/Control (No fungal inoculum/ fungicides applied)

Identical cultural and agronomic practices were applied to all the experimental units.

The data recorded on ten randomly selected plants of each entry from each replication for head diameter, number of achenes per head, head weight, 100-achene weight and seed yield. Oil contents were determined by Soxhlet Extraction Method in Sunflower Lab in Department of PB&G, University of Agriculture, Faisalabad, Pakistan. Charcoal rot disease reaction was recorded by carefully examining the external disease symptoms on stem of the inoculated plants. A six point 0-5 (0= 0% immune; 1= 1-9% resistant; 2= 10-24% moderate resistant; 3= 25-49% moderate susceptible; 4= 50-74% susceptible and 5= 75% & above highly susceptible) disease severity rating scale for charcoal rot of sunflower caused by *Macrophomina phaseolina* was used according to the description of James (1971). The collected data for above mentioned parameters was statistically analyzed for variance by the method given by Steel *et al*, (1997). Genotypic and phenotypic correlation coefficients among the characters under study were estimated according to the statistical techniques outlined by Kown and Torrie (1964). This kind of model mostly used by sunflower's research scientists e.g. Marinkovic, 1992; Lakshimanrao *et al.*, 1985; Punia & Gill, 1994 and Ivanov & Stoyanova, 1980. Seed yield was kept as resultant variable and other characters as casual variables.

## Results & Discussion

Analysis of results expressed (Table 1) that head diameter, seed yield per plant, number of achenes per plant and disease incidence are significant ( $P < 0.05$ ) for all the accessions while 100-seed weight, head weight and oil contents are highly significant. In other hand interaction of Accessions x treatments expressed as significant ( $P < 0.05$ ) for oil contents only. Seed yield and 100-seed weight are significant ( $P < 0.01$ ) and no significant difference found in seed yield and 100-seed weight at 5 percent seed infection of *Macrophomina phaseolina* (Bhutta *et al.* 1998). Sunflower had significantly higher oil content than others yield attributes (Owen, 1983). Under Charcoal rot stress condition there was reduction in grain yield (14.4%), head diameter (20.3%), 1000-grain weight (15.7%), oil content (15.7%) and plant height (16.9%) in susceptible genotypes (Abdul and Shabeer, 2001).

**Table-1: Analysis of variance for yield related traits**

| Source of Variance | Reps.    | Treatments(Tr.) | Accessions (Acc.) | Tr. x Acc. | Error      |
|--------------------|----------|-----------------|-------------------|------------|------------|
| <b>DF</b>          | <b>2</b> | <b>2</b>        | <b>23</b>         | <b>46</b>  | <b>142</b> |
| <b>HD</b>          | 3.26*    | 116.85**        | 8.51*             | 0.1        | 0.94       |
| <b>SY/P</b>        | 3.27*    | 11.30*          | 10.27*            | 0.061      | 55.74      |
| <b>100-SW</b>      | 5.94*    | 76.75**         | 19.61**           | 0.38       | 0.31       |
| <b>Ach/P</b>       | 4.80*    | 3.29*           | 6.43*             | 0.86       | 1331.63    |
| <b>HW</b>          | 0.73     | 9104.42**       | 1815.51**         | 0.01       | 2.76       |
| <b>OC</b>          | 4.03*    | 1511.88**       | 446.92**          | 9.98*      | 0.73       |

\*Significant at 5% level of probability

**HD** = Head diameter, **SY/P** = Seed yield per plan, **100-SW** = 100-Seed weight, **Ach/P** = Achenes per plant, **HW** = Head weight, **OC** = Oil contents

The correlation analyses expressed in Table-2,3&4 that seed yield per plant was positively and significant correlated with all the traits studied i.e. head diameter, number of achenes per head, head weight, 100-seed weight and oil contents at both genetical and phenotypical levels within all three treatments. These results are in conformity with results those of Habibullah, 2007 whose reported correlation between seed yield and other traits is positive and significant both genetically and phenotypically. Talat and Mehdi (2003) also reported seed yield positively and significant correlated with all the traits studied at both phenotypic and genetic levels except oil contents which were positive but non-significant at genetic levels and head diameter was found negatively correlated at phenotypic and genetic levels. 100-achene's weight displayed positive and significant genotypic correlated with number of seeds per head and seed yield (Habibullah, 2007). These results are in agreement with the findings of Vanisree *et al.* (1988), Lal *et al.* (1997) and Teklewold *et al.* (2000). Seed yield showed highly significant and

positive correlation with plant height, seeds per head, oil content and seed weight (Hakim, 2007).

Oil Contents found positively and significant genotypic correlated with 100-seed weight and head weight with in all treatments and phenotypically positive and non-significant correlated within treatment 2 and 3 while 100-seed weight is significant and head weight non-significant within treatment 1 at phenotypical level. There is negative and non-significant correlation between oil contents and head diameter within all treatments at genetic and phenotypic levels. It is estimated that head weight both genetically and phenotypically is positive and significant correlated with head diameter and number of achenes per plant in all three treatments while with 100-seed weight in treatment-1 only. Head weight is positive and significant at genetical level but non-significant at phenotypical level with 100-seed weight within treatments 2&3.

Head diameter is observed positive and non-significantly correlated with 100-seed weight while significantly correlated with number of achenes per plant both genetically and phenotypically within all treatments. these findings not related to the results of Anandhan *et al*, (2010), Sasikala (2000) and Moorthy (2004) which were recorded that head diameter exerted significant positive correlation with 100-seed weight. Number of achenes per plant expressed positive and significantly correlated with 100-seed weight at genetical level within all treatments while positive and non-significant correlated at phenotypic level within treatments 1 & 3 while phenotypically significant correlation within treatment 2.

**Table-2: Estimation of genotypic and phenotypic correlations among yield related traits of treatment 1**

|               |                      | <b>SY/P</b> | <b>HD</b>          | <b>Ac/H</b>        | <b>OC</b>           | <b>HW</b>          |
|---------------|----------------------|-------------|--------------------|--------------------|---------------------|--------------------|
| <b>100-SW</b> | <b>r<sub>G</sub></b> | 1.32*       | 0.16 <sup>ns</sup> | 0.25*              | 0.35*               | 0.30*              |
|               | <b>r<sub>P</sub></b> | 0.98**      | 0.15 <sup>ns</sup> | 0.22 <sup>ns</sup> | 0.31**              | 0.25*              |
| <b>SY/P</b>   | <b>r<sub>G</sub></b> | 1           | 0.38*              | 0.44*              | 0.33*               | 0.44*              |
|               | <b>r<sub>P</sub></b> | 1           | 0.28*              | 0.40**             | 0.28*               | 0.38**             |
| <b>HD</b>     | <b>r<sub>G</sub></b> |             | 1                  | 0.91*              | -0.11 <sup>ns</sup> | 1.09*              |
|               | <b>r<sub>P</sub></b> |             | 1                  | 0.66**             | -0.10 <sup>ns</sup> | 0.88**             |
| <b>Ac/H</b>   | <b>r<sub>G</sub></b> |             |                    | 1                  | -0.06 <sup>ns</sup> | 0.79*              |
|               | <b>r<sub>P</sub></b> |             |                    | 1                  | -0.06 <sup>ns</sup> | 0.66**             |
| <b>OC</b>     | <b>r<sub>G</sub></b> |             |                    |                    | 1                   | 0.06*              |
|               | <b>r<sub>P</sub></b> |             |                    |                    | 1                   | 0.06 <sup>ns</sup> |

**Table-3: Estimation of Genotypic and phenotypic correlations among yield related traits of treatment 2**

|               |                      | <b>SY/P</b> | <b>HD</b>          | <b>Ac/H</b> | <b>OC</b>          | <b>HW</b>          |
|---------------|----------------------|-------------|--------------------|-------------|--------------------|--------------------|
| <b>100-SW</b> | <b>r<sub>G</sub></b> | 1.11*       | 0.08 <sup>ns</sup> | 0.47*       | 0.23*              | 0.22*              |
|               | <b>r<sub>P</sub></b> | 0.95**      | 0.13 <sup>ns</sup> | 0.29*       | 0.22 <sup>ns</sup> | 0.21 <sup>ns</sup> |
| <b>SY/P</b>   | <b>r<sub>G</sub></b> | 1           | 0.35*              | 0.68*       | 0.36*              | 0.42*              |
|               | <b>r<sub>P</sub></b> | 1           | 0.27*              | 0.53**      | 0.32**             | 0.37**             |

|             |                      |  |   |        |                     |                    |
|-------------|----------------------|--|---|--------|---------------------|--------------------|
| <b>HD</b>   | <b>r<sub>G</sub></b> |  | 1 | 0.89*  | -0.13 <sup>ns</sup> | 1.19*              |
|             | <b>r<sub>P</sub></b> |  | 1 | 0.61** | -0.10 <sup>ns</sup> | 0.88**             |
| <b>Ac/H</b> | <b>r<sub>G</sub></b> |  |   | 1      | 0.35*               | 0.80*              |
|             | <b>r<sub>P</sub></b> |  |   | 1      | 0.25*               | 0.61**             |
| <b>OC</b>   | <b>r<sub>G</sub></b> |  |   |        | 1                   | 0.08*              |
|             | <b>r<sub>P</sub></b> |  |   |        | 1                   | 0.08 <sup>ns</sup> |

**Table-4: Estimation of Genotypic and phenotypic correlations among yield related traits of treatment 3**

|               |                      | <b>SY/P</b> | <b>HD</b>          | <b>Ac/H</b>        | <b>OC</b>           | <b>HW</b>          |
|---------------|----------------------|-------------|--------------------|--------------------|---------------------|--------------------|
| <b>100-SW</b> | <b>r<sub>G</sub></b> | 1.24*       | 0.19 <sup>ns</sup> | 0.25*              | 0.24*               | 0.15*              |
|               | <b>r<sub>P</sub></b> | 0.90**      | 0.13 <sup>ns</sup> | 0.17 <sup>ns</sup> | 0.23 <sup>ns</sup>  | 0.14 <sup>ns</sup> |
| <b>SY/P</b>   | <b>r<sub>G</sub></b> | 1           | 0.43*              | 0.50*              | 0.39*               | 0.51*              |
|               | <b>r<sub>P</sub></b> | 1           | 0.33**             | 0.41**             | 0.30**              | 0.40**             |
| <b>HD</b>     | <b>r<sub>G</sub></b> |             | 1                  | 1.11*              | -0.05 <sup>ns</sup> | 1.01*              |
|               | <b>r<sub>P</sub></b> |             | 1                  | 0.73**             | -0.05 <sup>ns</sup> | 0.86**             |
| <b>Ac/H</b>   | <b>r<sub>G</sub></b> |             |                    | 1                  | -0.33 <sup>ns</sup> | 0.87*              |
|               | <b>r<sub>P</sub></b> |             |                    | 1                  | -0.25*              | 0.66**             |
| <b>OC</b>     | <b>r<sub>G</sub></b> |             |                    |                    | 1                   | 0.10*              |
|               | <b>r<sub>P</sub></b> |             |                    |                    | 1                   | 0.10 <sup>ns</sup> |

**r<sub>G</sub>**= genotypic correlation; **r<sub>P</sub>**= phenotypic correlation; **100-SW**= 100-seed Weight; **SY/P** = seed yield per plant; **HD**= head diameter; **Ac/H**= number of Achenes per head; **OC**= oil contents; **HW**= head weight

## Conclusion

The conclusion revealed through present study that seed yield per plant has positive and significant association with head diameter, number of achenes per head, head weight, 100-seed weight and oil contents at both genotypically and phenotypically. The selection of these yield related traits would be more effective to bring about simultaneous improvement for yield in sunflower.

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