

## GENETICS AND ASSOCIATION OF YIELD CONTRIBUTING CHARACTERS FOR ACHENE YIELD IN SUNFLOWER (*Helianthus annuus* L.)

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### ABSTRACT

Seed yield in sunflower is a quantitatively inherited character highly affected by environmental factors. These factors are related among themselves and with yield either favorably or unfavorably. In this study, data collected from eight (8) sunflower hybrids *i.e.* W-001, W-002, W-003, W-004, W-005, W-006, Hissun-33 and SF-187 were analyzed for correlations between yield and yield contributing factors. Majority of characters showed significantly positive correlations either both at genotypic or phenotypic level, however stem girth showed positive non-significant correlation with seed yield. While number of rows per head, number of achenes per head, head diameter and 100 achene weight considered as variables significantly influencing seed yield in sunflower. Overall, this study identified the potential traits whose genetic improvement could lead to the genetic improvement in overall yield in Sunflower.

**Keywords:** *Helianthus annuus*, genotypic and phenotypic traits, correlation

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### INTRODUCTION

Sunflower is one of the significant edible oilseeds crops grown all over the world next to soybean and groundnut. Sunflower oil is a major source of linoleic acid (64 %) and oleic acid (25-30%). Sunflower (*Helianthus annuus* L.) belongs to the family "Asteraceae" is the world's fourth major oilseed crop (Divya et al. 2019). It is classified as third among major oil producing crops (cotton, brassica and sunflower) in Pakistan. Area of sunflower during 2018-19 was 0.264 million acres having oil production of 54000 tons (Economic Survey of Pakistan 2018-19). Sunflower seeds contain 50% Fat and 20% protein. Its oil is one of the best quality oils because of improved percentages of unsaturated fatty acids, light color, less quantity of linolenic acid, mix flavor. Oleic and linoleic acid are primary fatty acids (approximately 90% unsaturated fatty acids) in sunflower oil, however other are palmitic and stearic saturated fatty acids (Arshad et al. 2019).

Understanding the association of yield with its contributing components is inevitable to reveal inter-relationships of economic characters. Higher the seed yield in sunflower, higher will be the vegetable oil production by it. Seed yield in sunflower is a quantitatively inherited character which is highly correlated with environmental factors. It is a complex and multigenic character and is a function of several component characters and their interaction with environment. Seed yield also depend on genetic potential of hybrids and varieties. It also depends on positive effects of other yield contributing factors on seed yield in sunflower such as head diameter, 100 achene weight, plant height, number of rows per head, number of achenes per row etc. Sunflower breeders emphasize to exploit the highest grain yield potential through selection of varieties and expression of heterosis in hybrids. Sunflower yield is greatly affected by abiotic factors, therefore, seed yield changes dramatically year to year depending on climatic conditions (Kaya 2003). It is observed that inter-relationship between economic factors and yield contributing characters needs to be understand so that a selection criterion could be outlined for yield improvement. Evaluation of correlated responses of yield contributing characters is of prime importance for the selection of elite genotypes (Ali et al. 2009; Riaz et al. 2019). Path analysis partitions the correlations coefficients into direct and indirect effects of yield contributing characters on the seed yield per head.

Majority of sunflower hybrids in Pakistan are imported and due to difference in agro climatic conditions of the development, evolution and production, the full potential of yield is not exploited in our agro climatic conditions. Moreover, there is always chance for potential danger and threat of new insect pests and diseases. This scenario urges

necessitates the need for development of locally, well-adapted, high yielding sunflower genotypes under local agro climatic conditions. Keeping in view the above-mentioned facts, the present work was carried out to develop selection criterion for achieving high achene yield in sunflower.

## MATERIALS AND METHODS

The experimental material comprised of eight high performing elite hybrids i.e. W-001, W-002, W-003, W-004, W-005, W-006, Hisun-33 and SF-187. The design used for the experiment was randomized complete block design with three replications. The experiment was repeated twice at Warble farms of Bahaudin Zakaria University, Multan in year 2009 (year 1) and 2010 (year 2) to minimize environmental errors. Seeds were sown in the field at the depth of 3 cm, keeping within rows and between rows distances of 25 cm and 70 cm, respectively. Standard agronomic practices were followed time to time during the growing season of the crop for both years. Nitrogen in the form of Urea and  $P_2O_5$  in the form of Triple Super Phosphate (TSP) were applied at the rate of 90 and 50 kg/ ha, respectively. Half of the Nitrogen was applied at the time of seedbed preparation, while the other half with first irrigation.

At maturity, ten plants from each entry were selected at random from each replication and data was recorded following characters including; Plant Height (PH), number of leaves (NOL), leaf length (LL), leaf width (LW), internodal length (INL), stem girth (SG), head diameter (HD), number of rows per head (NRPH), number of achenes per rows (NAPH), 100 achenes weight (100AW), leaf area (LA) and total head weight (THW) for both year 1 and year 2. Data was analyzed for variations using ANOVA. Heritability ( $h^2$ ) in broad sense, genotypic (GCV) and Phenotypic (PCV) coefficients of variability were estimated as described by Singh et al. (1993). Genetic advance (GA) was estimated in accordance to Falconer (1989) and Johnson et al. (1955).

**Statistical Analysis:** Genotypic and phenotypic correlation coefficients were estimated by following the method of Kwon and Torrie (1964). Distribution of correlation coefficients into direct and indirect components was done as described earlier (Dewey and Lu 1959).

## RESULTS AND DISCUSSION

Analysis of variance, genotypic (GCV) and phenotypic (PCV) coefficient of variance, heritability (broad sense) and genetic advance (GA) for both experimental years are estimated as showed in Table 2. Our results showed that mean square values for all the characters (except 100AW) were highly significant ( $P < 0.01$ ) while significant ( $P < 0.05$ ) for 100 achenes weight. These results indicated that enough potential of variability available so that effective selection can be made to develop highly promising lines from the material used in experiment. Similar results were reported earlier by Mudassar et al. (2009). Genotypic (GCV) and phenotypic coefficient of variation (PCV) were observed to be highest for THW followed by LA and INL for both experimental years, thus confirming maximum amount of variability to be subjected to selection for these characters. The minimum PCV & GCV values were observed for NRPH & SG (Table 2) revealed the fact that selection was of limited scope for these characters due to minimum variability. Very minimum differences observed between PCV and GCV values clearly indicated that there was a very little impact of Genotype  $\times$  Environment added to the repeated experiment. GCV values are not enough to determine the genetic variability. This could be done with the help of heritability and genetic advance estimates to assess the heritable portion of total variation thus providing a tool to determine genetic gain for selection. Heritability is the ratio of variance due to hereditary differences and genotypic variance to the total phenotypic variance (Mudassar et al. 2009). Broad sense heritability includes total genetic variance. Heritability estimates are reliable along with high values of genetic advance. Heritability along with genetic advance (GA) proved to be an authentic tool for selection in any crop for improvement as it emphasized that selected variability would be transmitted and could be observed in next generations. Higher values of heritability along with higher values of genetic advance for both years provided strong evidence that these characters can be improved through selection in early generations. It also confirmed the presence of enough genetic and additive effects in inheritance of this character. High values of heritability confirmed that these traits are mainly expressed by genetic factors and influence of environmental factors is low which indicates that selection is reliable in early generations. Similar results were also reported by Mudassar et al. (2009). Following LA, PH and THW showed high heritability values along with moderate values of GA for both years, advocating that selection can be proved helpful for these traits. Shrinivasa (1982) reported moderate values of heritability for THW. Moderate values of heritability along with lower values of genetic advance for SG indicates the involvement of non-additive genetic effects in inheritance of these characters thus forcing selection in later generations for this character. GCV along with heritability and GA are considered as good estimate of genetic gain to be expected from selection on phenotypic character (Mahmood et al. 2003). A trait having high heritability and high genetic advance is considered under control of additive genes, which highlights the usefulness of plant selection based on phenotypic performance (Mondal et al. 2000).

Table 1: Genetic correlation analysis between yield and yield contributing traits in sunflower

NOL (Number of Leaves), LL (Leaf Length): LW (Leaf Width): INL (Inter nodal Length) SG (Stem Girth): HD (Head Diameter): NRPH (Number

		PH	NOL	LL	LW	INL	SG	HD	NRPH	NAPH	100AW	LA
NOL	Rg	0.279										
	Rp	0.269										
LL	Rg	0.582**	0.035									
	Rp	0.577**	0.041									
LW	Rg	0.337	0.525	0.861**								
	Rp	0.332	0.486	0.834**								
INL	Rg	0.906**	0.001	0.650**	0.449*							
	Rp	0.877**	-0.019	0.630**	0.455*							
SG	Rg	-0.057	-0.629**	0.586**	0.850**	0.189						
	Rp	-0.053	-0.569*	0.536**	0.748**	0.201						
HD	Rg	0.130	0.094	0.781**	0.781**	0.141	0.693*					
	Rp	0.123	0.107	0.750**	0.746**	0.122	0.538					
NRPH	Rg	0.116	-0.274	0.430*	0.553*	0.201	0.647**	0.698**				
	Rp	0.117	-0.271	0.419*	0.536*	0.196	0.594*	0.667**				
NAPH	Rg	0.198	0.329	0.509*	0.445	0.228	0.354	0.818**	0.750**			
	Rp	0.184	0.273	0.464*	0.397	0.188	0.286	0.739**	0.709**			
100AW	Rg	0.641*	0.170	-0.760*	0.830**	0.239	0.514*	0.910**	0.304	0.510*		
	Rp	0.440	0.122	-0.703*	0.637*	0.203	0.374	0.683*	0.232	0.393		
LA	Rg	0.562*	0.265	0.957**	0.974**	0.558*	0.755**	0.833**	0.545*	0.524*	0.925**	
	Rp	0.559	0.257	0.948**	0.955**	0.540*	0.686*	0.804**	0.541	0.501	0.693*	
THW	Rg	0.361	0.238	0.870**	0.702**	0.359	0.537*	0.947**	0.650**	0.782**	0.907**	0.825**

of Rows per Head): NAPH (Number of Achene per Head): 100AW (100 Achene Weight): LA (Leaf Area) and THW (Total Head weight)

Correlation coefficient analysis is used to determine the mutual relationship between various plant traits and it is a useful tool in determining the component characters on which selection is based for the improvement of seed yield. It is a measure of interrelationship between a pair of characters (Ali et al. 2009). Knowledge of correlation is required to obtain the expected response of other characters when selection is applied to the character of interest in a breeding program. Correlation coefficients of PH have been presented in Table 1. PH was found to show positive and significant correlations to NOL, LL, LW, INL, LA and THW at genotypic level (Table 1). Moreover, PH was found to be highly significant to all mentioned characters for both experimental years but at phenotypic level. Similar results were reported earlier by Chikkadevaiah et al. (2002), Kaya et al. (2007), Mudassar et al. (2009), Kaya et al. (2009) and Yasin and Singh (2010). This study showed negative relation of PH to HD, NRPH and NAPH whereas Khokhar et al. (2006) and Kaya et al. (2008) have also reported negative relation of PH with HD. On contrary, Arshad et al. (2007) have reported contradicted findings in this regard. Pertaining to results in Table 1, pH showed positive but non-significant relation to 100 achenes weight.

Positive but non-significant relation of NOL is found to LL, INL and HD. But its negative, non-significant relation to NRPH, NAPH, 100AW and LA is found in both experimental years. However, Mudassar et al. (2009) and Yasin and Singh (2010) have reported positive relation between NOL and LA. Pertaining to results in Table 1, it is revealed that NOL have positive and significant correlation to LW, SG and THW. These results were found to be in accordance with Chikkadevaiah et al. (2002) and Yasin and Singh (2010).

Positive and highly significant relation of LL to LW and LA at both genotypic and phenotypic levels determined for both experimental years. Moreover, LL, LW and LA all have presented positive and significant or highly significant relation to all studied characters (Table 1). The almost similar results were reported by Mudassar et al. (2009) and Yasin and Singh (2010). Genotypic correlation values tend to remain higher than phenotypic values for most of the characters, which confirm the authenticity of results.

Stem girth (SG) was found to be negative and non-significant to head diameter and plant height (Table 1). Its positive and significant relationship was found with NRPH, NAPH, THW and LA. These results were in closely related with the results of Habib et al. (2007). A negative correlation was reported by Mudassar et al. (2009) between PH and SG. Khokhar et al. (2006) has reported that THW is positive and significantly related to SG. Table 1 provides authenticity to these reported facts. Moreover, very small but non-significant, correlation was found between SG and

100AW. Internodal length (INL) was positively significant to pH at genotypic while highly significant at phenotypic level. It also showed negative correlation with HD, NRPH, NAPH and 100AW. Positive and significant relation was found between INL and PH at both genotypic and phenotypic levels. However, its positive non-significant relation to plant height has been earlier reported by Khokhar et al. (2006).

**Table 2:** Genetic variability parameters for yield and yield contributing traits in sunflower

Parameters	h <sup>2</sup> (bs)	GA as % of mean	PCV	GCV
Plant Height	0.68	7.01	13.90	13.68
Number of Leaves	0.72	5.29	8.06	7.67
Leaf Length	0.87	7.84	13.34	13.10
Leaf Width	0.86	6.38	10.81	10.20
Inter Nodal Length	0.73	6.90	12.93	12.48
Stem Girth	0.62	4.74	7.79	7.07
Head Diameter	0.53	6.63	11.91	11.21
Number of Rows Per Head	0.78	5.25	6.92	6.67
Number of Achene Per Head	0.72	5.34	7.91	7.60
100 Achene Weight	0.45	3.31	8.21	6.15
Leaf Area	0.71	9.44	21.01	20.05
Total Head Weight	0.69	6.38	25.45	25.04

Where h<sup>2</sup>(bs) = Broad sense heritability, GA as % of mean = Genetic Advance as percent of mean, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation

Head diameter (HD) was found to be positively significant and highly significant to NRPH, NAPH, LA, THW & 100AW at genotypic and phenotypic levels respectively. These findings are in closely related with (Habib et al. 2007). HD presented non-significant correlation to PH. This was also reported by (Khokhar et al. 2006). But Kaya et al. (2003) has proved contradictions. Similarly, HD is negatively correlated to SG. This result was not in agreement with that of Mudassar et al. (2009) and but confirmed the results reported by Khokhar et al. (2006).

100 Achene Weight (100 AW) displayed positive significant relation to LL, LW, HD and THW at genotypic and phenotypic level (Table 2). It also presented positive significant relation to NAPH at genotypic level. Moreover, 100 AW displayed positive significant correlation to HD (rg & rp). A weak negative non-significant relation was also observed between INL and 100 AW. These all findings are exactly similar with findings of Khokhar et al. (2006) and Habib et al. (2007).

Number of achenes per row (NAPR) and number of rows per head (NRPH) showed positive significant correlation to THW, SG and HD. These were also reported by Ashok et al. (2000) and Mudassar et al. (2009). NAPH was found to be positively significant to THW. These results were also in close agreements with findings of Farhatullah and Khalil (2006) and Habib et al. (2007).

Total head weight (THW) showed positive and highly significant correlation values among all the characters studied, either at genotypic or at phenotypic level, but have non-significant correlation with SG. Positive non-significant relation with SG has been reported earlier by Khokhar et al. (2006). Inter-relation of THW on significant characters provided a great potential to be exploited by breeders for improvement of total seed yield in sunflower. Dagustu (2002), Farhatullah and Khalil (2006) and Yasin and Singh (2010) also concluded the same results earlier.

**Conclusion:** Correlation values give a better insight into the cause and effect relationship between the different pairs of characters. Pertaining to results presented in Table 1, it was found that PH, SG, HD, NRPH, NAPH, LA and 100 AW had positive effect while NOL, LL, LW and INL showed negative effect on yield (THW) in sunflower. The highest positive effect through PH was imparted by NOL and LA while LL and INL showed the highest negative effect through PH (Table 1). Thus, either LL or INL minimizing the positive effect of PH on yield (THW). Positive indirect effect of PH and NRPH masked the direct negative effect of NOL on THW in Sunflower. Meanwhile, LW and SG enhanced its negative direct effect.

**Contribution of Authors:** The experiment was designed and executed by MMA and SBH. MMA collected and analyzed the data. Manuscript was written by MMA and MWA. Manuscript critically reviewed and suggestions were provided for improvement by MHNT, MJA, AAK and AA. MHNT and AA also contributed in final Editing.

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