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Gene Action in the Expression of Achene Yield and Oil Content in Sunflower (*Helianthus annuus* L.)

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Abstract: A study on a 8x8 diallel fashion in sunflower was conducted at NWFP Agricultural University Peshawar Pakistan. The genetic analysis showed that additive and non-additive effects were significant for achene yield (kg ha^{-1}). The maternal and non-maternal reciprocal effects were also controlling the inheritance of the trait. The non-additive effect was more pronounced from $H_1 > D$. The W_r/V_r did not give a slope so the mean degree of dominance $(H_1/D)^{1/2}$ better reflected the overdominance effect for the trait. In case of oil content, the Hayman complete analysis suggested the involvement of additive and non-additive components of variation. Dominance genetic variances H_1 and H_2 were also significant indicated that genetic variances for oil content was under control of both additive and non-additive effects. The W_r/V_r graph indicated that overdominance is controlling oil content in these genetic materials. The heritability estimates in broad sense were from moderate to high while heritability estimates in narrow sense were low to moderate for both the traits.

Key words: Sunflower, gene action additive, non-additive, heritability

INTRODUCTION

Research on breeding of high yielding sunflower varieties is essential for increasing yield per unit area. The genetic variability plays a distinct role in breeding and assessment of germplasm.

Plant breeders must have a good knowledge of inheritance of economic traits for improvements of crop plants. The diallel analysis as outlined by Hayman^[1] and Mather and Jinks^[2] attempts to partition phenotypic variation into genotypic and environmental components and are to further subdivide genotypic variation into its additive and dominance components.

The diallel analysis techniques developed by Hayman^[3] provide a fairly reliable mechanism to properly understand the genetic system and gene action involved in the expression of important plant attributes. The diallel crossing procedure provides a statistical approach of genetic study which is widely used by breeders for analyzing metric characters in different species. It furnishes logical information about the genetic architecture of the plant, and heredity behaviour of the parameters under study in early generation like F_1 and F_2 . It also describes how to measure additive and dominance variation and the relative dominance properties of the parental lines.

The studies on genetic analysis of sunflower would help the breeder to formulate appropriate selection

procedure for screening of these inbred lines and evaluation of their progenies for various purposes. It provides heritability estimates of the character, which helps to predict progress through selection. The character showing high heritability could be improved through direct phenotypic selection. On the other hand, in case of progenies involving a greater non-additive genetic variance including dominance, overdominance, epistasis and linkage, selection of desirable genotypes is not a straightforward procedure. There are number of biometrical approaches available to estimate genetic components of variations^[4,5] have been very few attempts to apply them to the phenomenon of genetic analysis of sunflower.

In the present study the Hayman^[1] approach has been applied with the objective to ascertain the type of gene action involved in the expression of yield and oil content of sunflower and secondly to help assess the gene action and components of variations.

MATERIALS AND METHODS

A complete set of diallel cross experiment, involving eight sunflower (*Helianthus annuus* L.) TF-lines and hybrid cultivars, was conducted for three consecutive years i.e., year 2002-03 to 2004-05 at Malakandher farm NWFP Agricultural University Peshawar, Pakistan. Inbred lines were developed from these TF-series and hybrid

cultivars by continuous selfing and selections for four consecutive seasons and were named as TF-1, TF-4, TF-7, TF-11, TF-335, GUL, ARI and PESH.

These inbred lines were crossed in 8x8 diallel fashion. These crosses were repeated for two consecutive years to get good enough F_0 seed for my experiment. Hybrid seeds (F_1) of 56 crosses along with their eight parents were tested in an experiment in a Randomized Complete Block Design with three replications. Each row was 4 m long. Plant to plant and row-to-row distance was kept 25 and 60 cm, respectively. Normal cultural practices and plant protection measures were adopted during the crop season. The data on the following two parameters were recorded.

Achene yield (kg ha^{-1}): The achene weight m^{-2} was recorded and converted to kg ha^{-1} by multiplying with 1000.

Oil-content (g kg^{-1} achene) : The achene per plant were collected from parental lines and crosses. These achenes were bulked separately for each treatment. Five random samples (50 g) each of eight parental lines and 56 crosses were collected for oil content. The oil analysis was made by Soxhlet method at Nuclear Institute for Food and Agriculture Tarnab, Peshawar. The grains of each sample were grinded, put on filter paper and then placed in a clean-dried thimble. Forty mlli liter petroleum ether was taken in a receiving flask connected with extraction unit. Heater and water were turned on and extraction was continued for about 5-6 h. The oil collecting cups were kept in an oven at 105°C until a constant weight was obtained. The cups were cooled in desiccators for 30 min and then weighed. Crude fat in each sample was calculated as follows:

$$\%CF(\text{g kg}^{-1}) = \frac{\text{Weight of oil} \times 1000}{\text{Weight of sample}}$$

The data on the above parameters was subjected to Hayman analysis^[1]. Before subjecting data to the diallel analysis technique, an ordinary analysis of variance^[6] was performed to determine whether significant genotypic differences are present for the characters under study in F_1 data independently. Only significant genotypic differences for the characters validate analysis of the data using Jinks and Hayman^[3] approaches. In the first phase, formal analysis of variance of the diallel table partitions the family mean effects into additive (a) and dominance (b) components. It also detects maternal (c) and reciprocal (d) effects. The dominance (b) component is further partitioned into directional dominance effects (b_1 , the

mean deviation of the crosses from the mid-parent values); effects due to unequal contribution of the dominant alleles by parents (b_2) and specific gene interaction (b_3), which is termed as specific combining ability and refers to those cases in which certain parental combinations perform relatively superior or inferior than expectation based on the average potential of the genotypes involved.

The second step of the analysis is the computation of the variance of the components of each array (V_r), the covariance of all the offspring included in each parental array with the non-recurrent parents (W_r) and the variance of the parental means (V_oL_o) is computed. In addition, the means of array variance (V_iL_i), the variance of mean of array (V_oL_i) and the means of the array covariance (W_oL_o) were also computed. These statistics are involved in the estimation of genetic components, D, an estimate of additive effect, H_1 , H_2 , variation due to dominance effects of genes, F provides an estimate of the relative frequency of dominant to recessive alleles in the parental lines and the variations in dominance over loci. Thus F will be positive whenever the dominant alleles are more frequent than the recessive alleles, irrespective of the dominant alleles have increasing or decreasing effects.

RESULTS AND DISCUSSION

Achene yield (kg ha^{-1}): All the effects like additive a, directional dominance b_1 , dominance due to unequal distribution of dominant alleles in the parents b_2 , residual dominance effect b_3 , overall dominance b, maternal effects c and reciprocal differences not ascribable to c, d were significant (Table 1a). The c and d items were highly significant against their block interactions, therefore, the item a and b along with its components were retested against c and d mean squares, respectively. The retesting resulted non-significance of all the components. However the significance of these components tested against their own block interaction is still valid. The inferences suggested that genetic variation was contributed by additive and dominance variances. A significant role of maternal and non-maternal reciprocal differences was also observed.

The contribution of all the items like environmental component E, additive genetic variance D and dominance variances H_1 and H_2 were non-significant (Table 1b). The non-additive effects as pronounced by larger value of H_1 than D ($H_1 > D$) whereas the direction of dominance was nebulous however the evidence showed it towards the parents because the value of h^2 was positive though it was non-significant. The positive F statistic exhibited that dominant alleles were more frequent than recessive alleles

Table 1a: Analysis of variance for achene yield (kg h⁻¹) in Sunflower (*Helianthus annuus* L.)

F ₁ generation				
Item	df	MS	F-ratio	F-ratio
a	7	92998.09	11544.49**	1.04ns
b ₁	1	65847.88	171172.26**	0.91ns
b ₂	7	24407.71	15076.93**	0.33ns
b ₃	20	68977.21	12505.86**	0.95ns
b	28	57723.07	13244.81**	0.80ns
c	7	89188.89	20188.02**	
d	21	71984.92	16937.90**	
Total	91			
a x block	14			
b ₁ x block	2			
b ₂ x block	14			
b ₃ x block	40			
b x block	56			
c x block	14			
d x block	42			
Total x block	182			

**Significant at 1% level of probability. ns Non-significant

Table 1b: Estimates of genetic components of variation for achene yield (kg ha⁻¹) in sunflower (*Helianthus annuus* L.)

Components	Value	SE
E	6.04ns	3314.87
D	6611.64ns	9944.60
F	4960.70ns	23498.18
H ₁	44567.37ns	22861.17
H ₂	38469.97ns	19889.21
h ²	9600.17ns	13338.54
(H ₁ /D) ^{1/2}	2.60	
H ₂ /4H ₁	0.216	
(v4DH ₁ + F)	1.34	
(v4DH ₁ - F)		
Heritability (ns)	0.16	
Heritability (bs)	0.54	

* = Value is significant when it exceeds 1.96 when it is divided by SE, ns = Non-significant

in the parents. The value of H₁ is greater than H₂ at all the loci and H₂/4H₁ value was less than 0.25 which indicated the presence of unequal gene frequencies in the parents.

The additive and dominance genetic variance were significant, which exhibited that both additive and non-additive components were contributing to the variations in F₁ generation. The gene frequency was reflected by ratio that was more than one of dominant to recessive alleles [(4DH₁)^{1/2} + F/(4DH₁)^{1/2} - F], which showed the prevalence of dominant genes.

These results showed that additive and non-additive effects were significant for achene yield (kg ha⁻¹). The maternal and non-maternal reciprocal effects were also controlling the inheritance of the trait. The non-additive effect was more pronounced from H₁>D. The Wr/Vr did not give a slope so the mean degree of dominance (H₁/D)^{1/2} better reflected the overdominance effect for the trait. The non-additive effect for achene yield in sunflower has also been reported by Merinkovic^[7] and Bajaj *et al.*^[8]. The regression of Wr on Vr for achene yield (kg ha⁻¹)

Table 2a: Analysis of variance for oil contents (g kg⁻¹) in sunflower (*Helianthus annuus* L.)

F ₁ generation				
Item	df	MS	F-ratio	F-ratio
a	7	26.38	6.10**	0.52ns
b ₁	1	38.49	7.65**	0.84ns
b ₂	7	63.02	10.10**	1.38ns
b ₃	20	29.76	4.03**	0.65ns
b	28	38.39	5.47**	0.84ns
c	7	50.50	3.09**	
d	21	45.70	9.37**	
Total	91			
a x block	14	4.33		
b ₁ x block	2	5.03		
b ₂ x block	14	6.24		
b ₃ x block	40	7.39		
b x block	56	7.02		
c x block	14	16.34		
d x block	42	4.88		
Total x block	182			

** Significant at 1% level of probability, ns Non-significant

Table 2b: Estimates of genetic components of variation for oil content (g kg⁻¹) in Sunflower (*Helianthus annuus* L.)

Components	Value	SE
E	2.401ns	1.50
D	10.69**	4.49
F	23.05**	10.62
H ₁	34.74**	10.33
H ₂	20.79**	8.99
h ²	4.56ns	6.03
(H ₁ /D) ^{1/2}	1.80	
H ₂ /4H ₁	0.150	
(v4DH ₁ + F)	3.98	
(v4DH ₁ - F)		
Heritability (ns)	0.06	
Heritability (bs)	0.43	

* = Value is significant when it exceeds 1.96 when it is divided by SE, ns = Non-significant

presented in Fig. 1 shows that the regression line intercepted Wr-axis above the origin, but the regression line was not a unit slope and resulted dominance type of gene action in F₁ generation. The array points were scattered around the regression line. However inbred lines ARI, GUL and TF-7 were relatively closer to the origin, and tended to dominant gene effects. Inbred lines TF-4, TF-335 and TF-1 were away from the origin indicating no dominance for the achene yield. While TF-11 and PESH, being farthest from the origin, showing recessive gene effects.

Oil content (g kg⁻¹): The Table 2a presented effect 'b' maternal 'c' and non maternal reciprocal differences 'd' offered significant endowment in F₁ generation. The c and d were highly significant against their block interactions, therefore, the item a and b along with its components were retested against c and d mean squares, respectively. The retesting resulted non-significance of all the components suggested the involvement of both

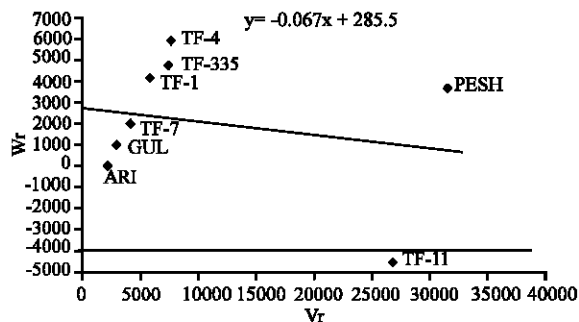


Fig. 1: Wr/Vr graph of achene yield (kg ha^{-1}) in 8x8 diallel of sunflower

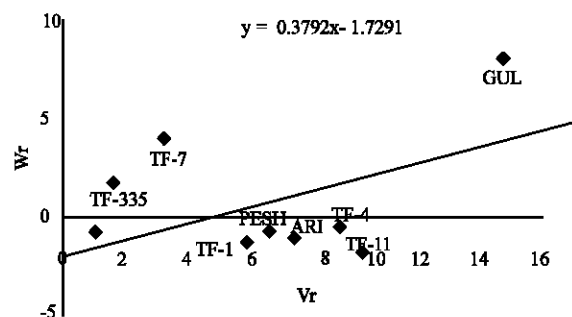


Fig. 2: Wr/Vr graph of oil content of 8x8 diallel in sunflower

additive and non-additive component of variation for oil content in F_1 generation. Table 2b demonstrated the value of E was non-significant. However the effect of additive D and dominance genetic variances H_1 and H_2 were significant. Therefore, it is suggested that oil content was controlled by both additive and non-additive components with more pronounced non-additive effect as $H_1 > D$. The component F was positive and significant which suggested that dominant alleles were more frequent for oil content. The component h^2 was positive but non-significant in F_1 generation. The mean degree of dominance determined by the ratio of $(H_1/D)^{1/2}$ for F_1 , showed over dominance for oil content in sunflower. The estimates for heritability in narrow sense were moderate 34% while an estimate for heritability in broad sense was 65% indicating important through selection.

The regression line intercepted W_r -axis below the origin giving negative ordinate values (Fig. 2). The W_r/V_r graph elucidated that over dominance type of gene action was operating. The position of array points along the regression line showed three distinct classes. The inbred

lines TF-335 and TF-7 were being close to the origin indicating dominant gene effects, while TF-1, PESH, ARI, TF-4 and TF-11 were displaying their position below the origin showed over dominance type of gene action. Inbred line GUL showed its position, farthest from the origin exhibited recessive gene effects for the oil content in sunflower.

In case of oil content, the Hayman complete analysis suggested the involvement of additive and non-additive components of variation. Dominance genetic variances H_1 and H_2 were also significant indicating that genetic variances for oil content was under control of both additive and non-additive effects. The W_r/V_r graph indicated that overdominance is controlling oil content in these genetic materials. These inferences are in agreement with that of Pathak *et al.*^[9] who found non-additive gene action for oil content with other parameters. Similarly Rather *et al.*^[10] found overall dominance effect highly significant for various characters in sunflower including oil content.

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