

COMBINING ABILITY AND GENETIC COMPONENTS FOR SEED YIELD IN SUNFLOWER (*HELIANTHUS ANNUUS* L.)

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ABSTRACT

Being one of the most important oil crops in the world main goals in sunflower breeding are increased seed and oil yield per hectare. Bearing in mind breeding direction and global importance of this oil crop objective of this study was to evaluate general combining ability (GCA) of six sunflower genotypes and specific combining ability (SCA) of their crosses as well as to estimate components of genetic variability for seed yield/plant. Genotypes were crossed according to incomplete diallel method (without reciprocals) and fifteen F1 progenies were derived. Both, additive and non-additive, genetic components were significant in seed yield expression but according to GCA/SCA ratio additive component was more important. The highest GCA value was recorded in G1 genotype, while the highest SCA value was recorded in combination G2xG3, for seed yield. Analysis of components of genetic variability revealed that dominant gene effects (H1) were more important than additive (D) and frequency of dominant genes was greater than recessive ones. Dominant and recessive genes were not equally distributed among parents as presented by the $H_2/4H_1$ ratio which was different than 0.25 (0.17). According to average degree of dominance (1.14) superdominance was the case in seed yield expression.

Key words: seed yield, combining ability, dominant and recessive genes

INTRODUCTION

Sunflower (*Helianthus annuus* L.) is one of the most important oilseed crops in the World and main crop for production of edible oil in Serbia. Consequently, main goals in sunflower breeding are increased seed yield and thus oil yield per hectare. Sunflower seed yield, as a complex trait, requires the most effort in breeding process because all other goals in breeding through improving individual properties are in a function of increasing seed yield and thus oil yield. The success in creating new, superior, genotypes largely depends on the possession of adequate genetic variability in the parental material because the greater are the chances for obtaining superior F1 plants. Furthermore, for successful breeding it is necessary to dispose information about mode of inheritance and combining ability. Obtained information helps in breeding process through selection of perspective parental lines with the aim of creating genotypes that will improve production. There are many papers that deal with this topic which differ in the results. Previous results have found that both, additive and non-additive, components are important in the inheritance of seed yield (Škorić et al., 2007). Some authors emphasize the larger importance of additive component of genetic variance for seed yield (Putt, 1966; Sindagi et al., 1979; Petakov, 1992 and Karasu et al., 2010). Contrary to them, larger role of non-additive component on the inheritance of seed yield was determined in previous research by many authors (Marinković, 1984; Mihaljčević, 1989; Joksimović, 1992; Lande et al., 1997; Rather et al., 1998; Goksoy et al., 2000; Cecconi et al., 2000; Jocić, 2002, 2012; Sakthivel, 2003; Farrokhi et al., 2008; Gvozdenović et al., 2008 and Hladni et al., 2010). Combining abilities are divided into general (GCA), which represent the value of the parent used in crosses, and specific (SCA), representing the value of certain crossing. The most reliable method for testing combining abilities of genotypes is diallel (Živanović et al., 2006). Diallel crossing was proposed by the zoologist-geneticist Dr. Schmidt (1919) and firstly applied in plants by Sprague and Tatum (1942). Masood et al. (2005) used 8x8 diallel to test combining ability in sunflower and

found greater importance of non-additive effects in controlling seed yield. Vice versa Mijić et al. (2008) in 6x6 diallel of sunflower inbred lines found greater significance of additive component. Investigating the GCA/SCA ratio in inbred lines of sunflower using the method line x tester Andarkhor et al. (2013) have found greater importance of non-additive genetic components in controlling seed yield, considering that GCA/SCA ratio was less than 1 (<1).

Objective of this study was to evaluate combining abilities of sunflower genotypes through their crossings and to obtain information about components of genetic variance.

MATERIAL AND METHODS

Six sunflower genotypes were crossed according to incomplete diallel (without reciprocals). F1 progeny and parents were sown in three replicates in a randomized block design at Rimski šančevi experimental field of the Institute of Field and Vegetable Crops from Novi Sad. Experimental plot size was 10 m² with four, 3.6 m long rows and 70x30 cm plant spacing. The data were recorded on 10 plants in each replicate from middle rows. Harvest was done at the stage of physiological maturity and seed yield/plant was recorded in laboratory on a technical scale with an accuracy of 0.01 g. General combining abilities (GCA) of parents and specific combining abilities (SCA) of F1 were tested according to diallel method 2 by Griffing (1956). The assumption of this method is that there are no differences in reciprocal crosses.

Mathematical model for analysis of combining abilities as follows:

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + 1/bc \sum \sum e_{ijkl}$$

Analysis of components of genetic variance was performed according to the method suggested by Mather and Jinks (1971).

RESULTS AND DISCUSSION

Analysis of variance of combining ability for seed yield/plant showed statistically highly significant differences in the general (GCA) and specific (SCA) combining abilities between parents used in this experiment (Tab. 1). As GCA and SCA provide information for additive and non-additive gene actions considering that GCA/SCA ratio was higher than 1 it can be concluded that additive gene action played greater importance in the inheritance of seed yield/plant. In earlier studies Putt (1966) and Sindagi et al. (1979) found that general combining ability for seed yield in sunflower is more important than specific combining ability, indicating that additive component is more important than non-additive. In contrast, a significant impact of non-additive component of genetic variance in the inheritance of seed yield/plant in sunflower was observed by many authors (Marinković, 1993; Bajaj et al., 1997; Kumar et al., 1998; Chandra et al., 2011 and Andarkhor et al., 2012). The highest and statistically significant and positive GCA value was calculated for the G1 genotype so it can be concluded that this genotype represents the best general combiner for improving this trait (Tab. 2). Parental genotypes G4 and G5 also demonstrated positive GCA values but without statistical significance. In other parent genotypes were established negative GCA effects. Significant and positive value of SCA effect was recorded only in crossing combination G2xG3. In other crossing combinations SCA values were not statistically significant, while in five crossings were found negative SCA values.

Table 1. Analysis of variance of combining abilities for seed yield/plant in sunflower.

Source	Df	SS	MS	F-value
GCA	5	2718.59	543.72	11.31**
SCA	15	2664.86	177.66	3.70**
Error	40	1922.97	48.07	

Table 2. GCA (diagonal) and SCA (above diagonal) effects for seed yield/plant in sunflower

Genotypes	G1	G2	G3	G4	G5	G6
G1	13.62**	-21.39	-0.04	-1.83	-9.65	10.48
G2		-5.83	17.59*	-10.48	3.22	1.92
G3			-3.78	13.45	11.96	1.26
G4				3.81	14.29	-14.33
G5					1.61	5.52
G6						-9.43

LSD_{0.05} GCA= 7.00LSD_{0.05} SCA= 17.16LSD_{0.01} GCA= 9.37LSD_{0.01} SCA= 22.96

The analysis of components of genetic variance revealed that the dominant component (H₁) was greater than the additive (D), which shows that most of the genetic variation in the inheritance of seed yield/plant makes the non-additive component (Tab. 3). According to the calculated F value dominant genes prevailed in relation to recessive ones, as confirmed by the calculated frequency of dominant (u) and recessive (v) genes. Furthermore, calculated value of the H₂/4H₁ ratio indicated the unequal representation of dominant and recessive genes in parents. From the K_D/K_R ratio, which is greater than one, is also evident that the dominant genes prevailed in respect to the recessive ones, in the inheritance of seed yield/plant. Average degree of dominance $\sqrt{H_1/D}$ (1.14) indicated that superdominance was the case in expression of seed yield/plant, considering all crossings.

Table 3. Components of genetic variance for seed yield in sunflower.

Components	Value
D	535.98
H ₁	698.17
H ₂	473.63
F	544.60
E	48.07
u	0.78
v	0.22
H ₂ /4H ₁	0.17
$\sqrt{H_1/D}$	1.14
K _D /K _R	2.60

CONCLUSIONS

Main objective in breeding programme is development of superior synthetics or hybrids. To achieve this aim it requires estimation of gene action in various traits in order to design an efficient breeding plan for further genetic improvement of the initial material. Sunflower seed yield is one of the most important traits considering this crop and information about combining abilities and components of genetic variance are necessary for improving this valuable trait. In this research we found that both, additive and non-additive, genetic components were important in expression of seed yield/plant but additive genetic component prevailed. According to GCA value genotype G1 is the best general combiner for improving this trait and that genotype will be used in further hybrid combinations in order to obtain highly productive hybrids of sunflower. Crossing combination G2xG3 had the highest and significant SCA value and that combination will be tested with other

perspective hybrid combinations. Analysis of components of genetic variance revealed that dominant genes were prevalent in expression of seed yield/plant, as confirmed by the frequency of dominant genes. Dominant and recessive genes were not equally distributed among parents as presented by the $H_2/4H_1$ ratio which was different than 0.25 (0.17). According to average degree of dominance (1.14) superdominance was the case in seed yield expression.

ACKNOWLEDGEMENTS

This research is part of project TR-31025, funded by the Ministry of Science and Technological Development of the Republic of Serbia.

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