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ASSESSMENT OF COMPONENTS OF GENETIC VARIANCE OF MASS 1000 SEEDS IN SUNFLOWER (*HELIANTHUS ANNUUS* L.)

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Ten F_1 hybrids obtained by crossing five sunflower inbred lines were used to analyze the impact of genes with additive and dominant effects and their interactions on the inheritance of mass 1000 seeds. The linkage among the expected progeny means was tested using the scaling tests method (MATHER, 1949), while the estimates of gene effects and mode of inheritance were made by generation mean analysis (MATHER and JINKS, 1982). The additive-dominant model was not proved adequate for all crosses in both years of study. It was adequate in crosses C_1, C_2, C_3 and C_5 in the first year and in crosses C_3, C_8, C_9 and C_{10} in the second year of study. Besides the main gene effects (additive and dominant), epistatic gene effects were also of large importance in the inheritance of this trait. Duplicate epistasis between dominant decreasers was found in C_1, C_4, C_5, C_6 and C_8 in the first year and in crosses C_4, C_9 and C_{10} in the second year of study. Complementary epistasis between dominant decreasers was found in cross C_{10} in the first year and duplicate epistasis between dominant increasers in cross C_5 in the second year of study.

Key words: scaling tests method, additive-dominant model, inheritance, duplicate epistasis, complementary epistasis

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INTRODUCTION

After the number of plants per unit area and the number of seeds per plant, the mass of 1000 seeds is the third most important yield component. This is a highly variable trait, which is affected by both genetic and environmental factors. Variability of the trait is characteristic for a group of genotypes grown in a single location as well as for a single genotype grown in several locations (MARINKOVIĆ *et al*., 1994). The mass of 1000 seeds is a varietal characteristic that reflects the success of seed filling. Seeds possessing large mass are desirable in seed production. Their mass indicates that such seeds have sufficient nutrient reserves and well-developed embryo. Seedlings developing from such seeds grow rapidly even under unfavorable climatic and edaphic conditions.

To be able to foresee the results of breeding for a certain trait, it is necessary to be able to determine the values of genetic variance, environmental variance and their interaction within the total phenotypic variance. Genetic variance reflects the sum action of all genes controlling the expression of a quantitative trait and it comprises three components: variance due to the action of additive genes, variance due to the action of dominant genes and the variance due to interactions among these genes.

To establish the presence and the role of genetic factors in the forming of a quantitative trait, appropriate methods must be applied to obtain information on the effect of individual genes, interactions among genes from a single locus and interactions among genes from different loci. It is also necessary to provide information on the effects of environment (nongenetic parameters) and information on interactions between genotype and the environment.

To make inbred lines that possess high values of a certain trait, whose crosses exhibit heterosis in the inheritance of this trait, it is necessary to have initial breeding material with high genetic variability and to use an appropriate breeding method. Choice of breeding method depends on the available knowledge of the mode of inheritance and the nature and size of gene action for that particular trait.

In view of the above, generation mean analysis of MATHER and JINKS (1982) was used in this study. The analysis provides estimates of not only the additive and dominant gene effects but also of the portions of the three types of digenous epistasis, additive x additive, additive x dominant and dominant x dominant (GANGAPPA *et al*., 1997).

The objective of this study was to check the adequacy of the additive - dominant model for the inheritance of the mass of 1000 seeds in crosses of several sunflower inbred lines.

MATERIAL AND METHOD

Adequacy of the additive - dominant model was tested in ten diallel crosses between five sunflower inbred lines: C_1 (NS-MR-1 x NS-MR-2), C_2 (NS-MR-1 x NS-MR-3), C_3 (NS-MR-1 x NS-MR-4), C_4 (NS-MR-1 x NS-MR-5), C_5 (NS-MR-2 x NS-MR-3), C_6 (NS-MR-2 x NS-MR-4), C_7 (NS-MR-2 x NS-MR-5),

C_8 (NS-MR-3 x NS-MR-4), C_9 (NS-MR-3 x NS-MR-5) and C_{10} (NS-MR-4 x NS-MR-5). The diallel set included the F_1 generation, backcrosses with both parents (BC_1 and BC_2) and the F_2 generation. The female plants of the inbred lines and the F_1 generation had been emasculated manually to prevent selfing. The emasculation was done in early morning hours.

Field experiments, established in the system of random blocks in three replications, were conducted at Rimski Šančevi experiment field of Institute of Field and Vegetable Crops in Novi Sad in 2001 and 2002. Seeds (several seeds per hill) were planted manually in carefully prepared plots at optimum time. The rows were 70 cm apart, with plants in the row 30 cm apart. Thinning to final stand was performed at the stage of 2-3 pairs of permanent leaves. The parent lines and F_1 hybrids were each planted in four rows, the F_2 generation and backcrosses in eight rows. Between-row cultivation and hoeing were performed in the course of the growing season to control weeds. Herbicides were not used in the experiments.

The mass of 1000 seeds was determined in laboratory after husking of individual heads. Sample size was 20 plants per replication or 60 plants per experiment in the case of the parent lines and F_1 hybrids and 60 plants per replication or 180 plants per experiment in the case of the F_2 generation and the backcrosses. The samples excluded the end plants in the inner rows and the entire border rows.

Scaling tests and estimates of the effects of additive, dominant and epistatic genes were done according to models of MATHER (1949) and MATHER and JINKS (1982).

RESULTS AND DISCUSSION

Highly significant values of separate or all scaling tests (Table 1) of A, B and C showed that the additive-dominant model proved inadequate for the crosses C_4, C_6, C_7, C_8, C_9 and C_{10} in the first year and for the crosses C_1, C_2, C_4, C_5, C_6 and C_7 in the second year of study. This indicated that in these crosses other parameters played a role in the inheritance of the studied trait. The additive-dominant model was adequate for the cross C_3 and inadequate for the crosses C_4, C_6 and C_7 in both years of study. In the remaining crosses (C_1, C_2, C_8, C_9 and C_{10}), the model was adequate in one year and inadequate in another. In these crosses, the expression of the trait was affected not only by the additive and dominant genes but also by the interaction of the nonallelic genes as well as by other factors.

The additive gene effect predominated in the crosses C_7, C_8 and C_9 in the first year and in the crosses C_1, C_3, C_6, C_7, C_8 and C_9 in the second year of study. Conversely, the dominant gene effect predominated in the crosses C_1, C_5 and C_6 in the first year and in the cross C_5 in the second year of study. In the crosses C_4 and C_{10}, the effects of both additive and dominant genes were significant in both years.

Predominance of the additive gene effect in the inheritance of the mass of 1000 seeds was reported by RAO and SINGH (1977), SINDAGI *et al*. (1979), MARINKOVIĆ (1984) and JOCIĆ (2002). On thj eother hand, KOVAČIK and ŠKALOUD (1972), EL-HITY (1992) and JOKSIMOVIĆ *et al*. (2004) reported the predominance of the dominant gene efect.

The epistatic gene effects (i, j and l) were not equally important in the inheritance of the studied trait in the two years of study (Table 2). Besides the major gene effects, the epistatic effects additive x additive and dominant x dominant were important in the crosses C_1, C_6 and C_8 in th efirst year and in the crosses C_4, C_5 and C_{10} in the second year of study. All three epistatic gene effects were important only in the cross C_8 in the first year and in the cross C_5 in the second year of study.

Type of epistasis could not be determined in the crosses C_2, C_3, C_7 and C_9 in the first year and in the crosses C_1, C_2, C_3, C_6, C_7 and C_8 in the second year of study because neither the dominant nor the epistatic gene effects dominantan x dominantan were significant. The other crosses from the first year exhibited two types of epistasis. The cross C10 showed complementary epistasis between dominant decreasers, while the remaining crosses (C1, C4, C5, C6 and C8) showed duplicate epistasis between dominant decreasers.

In the second year of study, the crosses C4, C9 and C10 showed duplicate epistasis between dominant decreasers. In the fourth cross in which epistasis type could be determined, C5, we found duplicate epistasis between dominant increasers.

EL-HITY (1992) and JOCIĆ (2002) mentioned the presence of duplicate epistasis between dominant increasers. However, in an analysis of 10 sunflower crosses, JOCIĆ observed negative duplicate epistasis between dominant genes and even negative complementary epistasis betwen dominant genes. Conversely to JOCIĆ, GANGAPPA *et al*. (1997) established the presence of positive complementary epistasis between dominant increasers.

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OCENA KOMPONENATA GENETIČKE VARIJANSE MASE 1000 SEMENA KOD SUNCOKRETA (*HELIANTHUS ANNUUS* L.)

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Izvod

Kod deset F_1 hibrida nastalih ukrštanjem između pet inbred linija suncokreta po dialelnoj šemi analiziran je uticaj gena sa aditivnim i dominantnim efektima kao i njihovih interakcija u nasleđivanju mase 1000 semena. Povezanost između očekivanih srednjih vrednosti potomstava proverena je primenom metode scaling testova (MATHER, 1949), a procena genskih efekata i način nasleđivanja urađeni su po metodi Generation Mean Analysis (MATHER and JINKS, 1982). Aditivno-dominantan model nije bio adekvatan kod svih ukrštanja u obe godine ispitivanja. Bio je adekvatan kod ukrštanja C_1, C_2, C_3 i C_5, u prvoj i kod ukrštanja C_3, C_8, C_9 i C_{10} u drugoj godini ispitivanja. Pored glavnih genskih efekata, aditivan i dominantan, u nasleđivanju ovog svojstva veliki značaj imali su i epistatični genski efekti. Duplikatni tip epistatze između dominantnih gena sa negativnim predznakom nađen je kod ukrštanja C_1, C_4, C_5, C_6 i C_8 u prvoj i kod ukrštanja C_4, C_9 i C_{10} u drugoj godini ispitivanja. Komplementarna epistaza između dominantnih gena sa negativnim predznakom nađena je kod ukrštanja C_{10} u prvoj, a duplikatna epistaza između dominantnih gena sa pozitivnim predznakom je nađena u ukrštanju C_5 u drugoj godini ispitivanja.

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