

EVALUATION OF GENETIC VARIANCE COMPONENTS FOR SOME QUANTITATIVE TRAITS IN RAPESEED (*Brassica napus* L.)

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Three hybrid combinations obtained by crossing six winter rapeseed cultivars were analyzed for the impact of genes with additive and dominant effects and their interactions with inheritance of plant height and first lateral branch height. The linkage among the expected progeny means was checked using the scaling test method (Mather, 1949), while the estimates of genetic effects and mode of inheritance was made by the Generation Mean Analysis (Mather and Jinks, 1982). The additive dominant model did not prove adequate for plant height in all three crosses, and for first lateral branch height in the second and third cross. The inadequacy of the model showed epistatic gene effects were also of large importance in the inheritance of these traits.

Duplicate epistasis for plant height inheritance was found in all three cross combinations and for inheritance of height of the first lateral branch in second and third cross combination. However, it should be emphasized that duplicate epistasis among dominant positive genes occurred on plant height inheritance in C1 and C3, and on inheritance of first lateral branch height in C3. Duplicate epistasis among dominant negative genes occurred in C2 on the mode of inheritance of both traits.

Key words: additive and dominant effect, epistasis, height of the first lateral branch, plant height

INTRODUCTION

High adaptability to environmental conditions found in rapeseed resulted in its worldwide dispersion. Rapeseed is considered to be among the four most significant oil crops. It can serve as the alternative plant to sunflower in securing oil production increase. The increase

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in productivity is of major importance to further enlargement of the field area cultivated by rapeseed in growing regions and its expanding in non-growing regions. Evaluation of genetic variance, which reflects the overall action of genes controlling the quantitative traits expression, is essential in predicting the results of breeding for specific traits in a population. To establish the presence and role of genetic factors in forming quantitative traits requires appropriate methods which provide data about gene effects, interaction in the same locus and between the loci. Environmental effects data is necessary i.e. the non-genetic parameters representing genotype and environment interaction.

Most commercially significant plant traits are the quantitative ones. With the purpose of characterization these traits are measured in population individuals, and their average values, variance and other statistical data are calculated. During the interpretation of calculated statistical indicators, genetic and non-genetic factors which cause quantitative traits variability must be included. Methods used for obtaining data on the average effect of genes and interaction among the loci should be applied in order to determine the presence and role of some genetic factors in quantitative traits formation. Information about the environmental effects i.e. the non-genetic parameters and interaction between genotype and environment is necessary.

First attempts to analyze the structure of statistical indicators (research of two pure lines crossing progeny) were made by FISHER *et al.* (1932), and developed by MATHER (1949), HAYMAN and MATHER (1959), HAYMAN (1958) etc. during their research.

Changeability of parental lines and in the F_1 generation results from the effect of environmental factors (non-hereditary), while in the F_2 and other generations with divisions, it also depends on the differences in both homozygotes, in terms of average values in each pair of allele genes with divisions, hereditary and non-hereditary components included. All the variance components are estimated using the parameters of para-additive, dominant, allele and locus interaction, and environmental effects (DABINA and KATANSKAJA, 1973).

The correctness of the hypothesis stating that the average values in progenies depend exclusively on additive and dominant genes can be tested in several ways, one being the Scaling test described by MATHER (1949). The estimate of epistatic effects of genes is necessary in case the additive-dominant model proves inadequate (MATHER and JINKS, 1982).

The objective of this study was to acquire information on gene action, above all the epistatic effects on specified traits, as well as manner of inheritance and heterosis effect on plant height and height of the first lateral branch.

MATERIALS AND METHODS

Three cross combinations between six winter rapeseed cultivars were selected in order to determine the adequacy of additive/dominance model: C_1 (Casino x Kata), C_2 (Carola x Isabela), C_3 (Banačanka x Slavica). Besides the F_1 generation, backcrosses with both parents (BC_1 and BC_2) and F_2 generation were included. To avoid self-pollination, anthers of female plant cultivars were removed by hand during early morning hours.

Trials including parents (P_1 and P_2), F_1 and F_2 generation and backcrosses (BC_1 and BC_2), were planted at the Experimental Fields of the Institute of Field and Vegetable Crops – Novi Sad in Rimski Šančevi. The material was planted mechanically in prepared soil during the optimal period, in the system of random blocks in three replications with five rows per replication.

Trial including cultivars, F₁ hybrid combinations, F₂ generations, and backcrosses was planted at the Experimental Fields of the Institute of Field and Vegetable Crops – Novi Sad in Rimski Šančevi during crop season 2006/2007. It was planted in the system of random blocks in three replications. The material was planted mechanically in well prepared soil in the optimal period. Row-to-row distance was 25 cm, with 5-6 cm between the rows. The studied traits (plant height and first lateral branch height) were established before the blossom fall. Sample size was 20 in cultivars, 30 in the F₁ generation, 50 in BC₁ and BC₂ hybrid combinations, and 80 per replication in F₂ generation, or 60, 90, 150 and 240 plants per trial.

In this study we analyzed the effect of genes on the mode of inheritance of plant height and first lateral branch height. The linkage among the expected progeny means was checked using the scaling test method (MATHER, 1949), while generation mean analysis was used to estimate the genetic effects and mode of inheritance (MATHER and JINKS, 1982).

RESULTS AND DISCUSSION

In Casino x Kata (C₁) cross, the studied traits varied significantly, with higher values found in cultivar Carola. Compared to the better parent, mode of inheritance of both traits in F₁ generation was characterized by heterosis - at plant height of 18.28%, and at first lateral branch height of 123.29%. Expected value of heterosis for the estimated gene effect values was 26.06% and 23.29%. Based on the calculated values of backcrosses, we can confirm the existence of other non-genetic factors (maternal effect, interaction, etc.) in the expression of both studied traits. Expected mean value of backcrosses was lower than the average of mean values of the first parent and F₁ generation. Cultivar Carola had a larger number of dominant genes than cultivar Kata (Table 1).

Applying the additive/dominance model, plant height was affected by dominant genes and equal effect of additive and dominant genes was observed on first lateral branch height (Table 2). Besides additive and dominant genes, epistatic gene effects were observed as highly significant in studying both traits: additive x additive (*i*) and additive x dominant (*j*). Epistatic gene effects (*l*) were not significant on first lateral branch height (Table 2).

Opposite marks in the estimated values of effects (*h*) and (*l*) indicated duplicate epistasis occurrence in both traits between the dominant decreaseers which is not favorable since it decreases the value of dominant genes effect.

In Carola x Izabela (C₂) cross, significant differences were observed between cultivars, i.e. higher value of both studied traits in cultivar Carola compared to cultivar Izabela. Phenotypic variances of backcrosses with the first parent were lower than mean cross values, meaning that Carola had a larger number of dominant genes than Izabela. Heterosis effect occurred in the inheritance of both traits – at plant height of 11.83%, and at first lateral branch height of 15.20%. The expected value of heterosis in the estimated values of gene effects was 9.56% i.e. 10.15%. The effects which are not solely connected to the action of additive and dominant genes were observed in the additive/dominance model, i.e. non-allele interaction (epistasis). This process was indicated by coherence between tests A, B and C.

Significance of additive genes effect was confirmed in both studied traits. Estimated values of gene effects in the model with 6 parameters confirmed significance of the dominant effects in the mode of inheritance of both traits, but with different values – positive in plant height and negative in first lateral branch height. Interaction effects with the largest contribution

to genetic variance are dominant x dominant for first lateral branch height, and additive x additive for plant height.

Table 1. Mean values of the tested traits, and values of tests A, B and C for three rapeseed hybrids

| Generation | Crosses | | | | | |
|-----------------|-----------------------|--------------------------------|----------------------|-----------------------------|----------------------|-----------------------------|
| | C 1 | | C 2 | | C 3 | |
| | Trait | | Trait | | Trait | |
| | Plant height | First lateral branch height | Plant height | First lateral branch height | Plant height | First lateral branch height |
| P ₁ | 162.79 | 52.48 | 142.47 | 50.03 | 142.43 | 48.48 |
| BC ₁ | 151.21 | 55.19 | 118.22 | 27.78 | 131.67 | 42.38 |
| F ₁ | 168.64 | 50.73 | 148.48 | 45.47 | 147.30 | 51.13 |
| F ₂ | 135.38 | 45.17 | 154.04 | 61.26 | 132.67 | 24.67 |
| BC ₂ | 155.23 | 43.56 | 141.87 | 46.92 | 162.79 | 54.48 |
| P ₂ | 122.38 | 29.81 | 123.09 | 21.78 | 132.00 | 43.55 |
| A | -29.01±7.56** | 7.16±7.70^{ns} | -54.50±22.91 | -39.95±9.14** | -26.40±3.44** | -14.85±4.21* |
| B | 19.45±12.25 | 6.59±4.76^{ns} | 12.18±9.06 | 26.58±7.23* | 46.27±2.51** | 14.29±8.22 |
| C | -80.91±10.51** | -3.09±6.93^{ns} | 53.63±12.19** | 82.28±6.33** | -38.37±6.57** | -95.63±9.06** |

In Banačanka x Slavica (C₃) cross, significant differences were observed between the two cultivars, similar to the previous two crosses. Higher values in both tested traits were observed in cultivar Banačanka. Average values of the F₁ generation were higher than in the better parent indicating the occurrence of heterosis in the inheritance of both traits at plant height of 7.35%, and first lateral branch height of 11.13%. The expected value of heterosis was 10.08% and 5.12%. Calculated values of back crosses between the first parents of the F₁ generation were lower than the averages of F₁ generation, which means that cultivar Slavica has a larger number of dominant genes. Similar to the previous two crosses, additive/dominance model did not prove adequate for plant height, due to high significance shown in all three tests. The model was also not adequate for the first lateral branch height due to significance or high significance found in tests A and C. Therefore, zero hypothesis stating that average values of generations depend solely on the effects of additive and dominant genes has to be rejected (Table 2).

Additive and dominant gene effects proved to be of large importance in the inheritance of both traits, with the prevailing role of positive dominant genes. Additive gene effect was not significant at first lateral branch height.

However, in the inheritance of both traits, as shown in Carola x Isabela crosses, all three interaction effects were highly significant (*i, j, l*).

Positive sign was found in values of dominant effect of genes in both traits, and negative in the interaction (*l*) effect of genes, confirming duplicate epistasis between the dominant increasers in the inheritance of these traits.

Table 2. Results of joint scaling test for the studied traits in hybrids $L_1 \times L_5$ and $L_2 \times L_3$

| Gene effects | Crosses | | | | | |
|--------------|--------------|-----------------------------|--------------|-----------------------------|--------------|-----------------------------|
| | C 1 | | C 2 | | C 3 | |
| | Trait | | Trait | | Trait | |
| | Plant height | First lateral branch height | Plant height | First lateral branch height | Plant height | First lateral branch height |
| $m \pm se$ | 136.69±2.04 | 40.46±1.58 | 134.31±1.47 | 51.00±1.53 | 141.47±1.01 | 32.62±1.80 |
| $ d \pm se$ | 25.37±2.06 | 10.33±1.90 | 9.66±1.51 | 24.70±1.67 | -12.55±0.97 | 1.46±1.94 |
| $ h \pm se$ | 24.89±3.07 | 10.27±2.85 | 17.07±2.50 | 14.01±2.90 | 8.74±1.53 | 17.56±2.06 |
| $X^2_{(3)}$ | 81.34 | 6.05 | 27.00 | 294.86 | 526.11 | 130.36 |
| P | | | | | | |

| Trait | Crosses | Gene effect | | | | | | Type of epistasis |
|-----------------------------|---------|-------------|----------|-----------|----------|----------|----------|-------------------|
| | | <i>m</i> | <i>d</i> | <i>h</i> | <i>i</i> | <i>j</i> | <i>l</i> | |
| Plant height | C 1 | 71.23** | 20.20** | 159.21** | 71.35** | -48.46** | -61.80 | Duplicate |
| | C 2 | 228.73** | 9.69** | -218.52* | -95.95* | -66.68* | 138.27* | Duplicate |
| | C 3 | 78.98** | 5.21* | 146.43** | 58.24** | -72.67** | -78.12** | Duplicate |
| First lateral branch height | C 1 | 24.31** | 11.34* | 57.00* | 16.83 | 0.57 | -30.58 | Duplicate |
| | C 2 | 131.55** | 14.12** | -195.08** | -95.64** | -66.53** | 109.00** | Duplicate |
| | C 3 | -49.05** | 2.47 | 194.69** | 95.07** | -29.13* | -94.51** | Duplicate |

++ Complementary epistasis between dominant increasers

-- Complementary epistasis between dominant decreaseers

+ - Duplicate epistasis between dominant increasers

-+ Duplicate epistasis between dominant decreaseers

CONCLUSIONS

The majority of used cultivars showed significant or highly significant differences between the studied traits.

In the mode of inheritance of both traits, F_1 generation was highly significant in all three crosses compared to the better parent, thus confirming the occurrence of heterosis.

Additive x additive interaction (*i*) was highly significant in all three crosses, additive x dominant (*j*) highly significant in C_1 and C_3 , and significant in C_2 , and dominant x dominant (*l*) was insignificant in C_1 , significant in C_2 , and highly significant in C_3 .

Additive/dominance model was not adequate for plant height in any of the crosses, and for first lateral branch height in C_1 and C_3 .

Duplicate epistasis between dominant decreaseers was expressed in the inheritance of studied traits of F_1 generation in C_1 and C_3 , and duplicate epistasis between dominant decreaseers with the second.

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OCENA KOMPONENATA GENETSKE VARIJANSE ZA NEKA KVANTITATIVNA SVOJSTVA KOD ULJANE REPICE (*BRASSICA NAPUS* L.)

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Izvod

Kod tri hibridne kombinacije nastale ukrštanjem 6 sorti ozime uljane repice analiziran je uticaj gena sa aditivnim i dominantnim efektima, kao i njihovih interakcija u nasleđivanju visine biljke i visine do prve bočne grane. Povezanost između očekivanih srednjih vrednosti potomstava proverena je primenom metode scaling testova (Mather, 1949), a procena genetskih efekata i načina nasleđivanja urađeni su po metodi Generation Mean Analysis (MATHER and JINKS, 1982). Aditivno dominantan model nije bio adekvatan za visinu biljaka kod sva tri ukrštanja, a za visinu do prve bočne grane kod drugog i trećeg ukrštanja. Neadekvatnost modela ukazala je da su u nasleđivanju navedenih svojstava u tim ukrštanjima veliki značaj imali i epistatični genski efekti.

U nasleđivanju visine biljke kod sva tri ukrštanja i visine do prve bočne grane kod drugog i trećeg ukrštanja ispoljila se duplikatna epistaza. Međutim, treba napomenuti da se u nasleđivanju visine biljke kod prvog i trećeg ukrštanja i u nasleđivanju visine do prve bočne grane kod trećeg ukrštanja ispoljila duplikatna epistaza između dominantnih gena sa pozitivnim predznakom. Na drugoj strani kod drugog ukrštanja u nasleđivanju oba svojstva ispoljila se duplikatna epistaza između dominantnih gena sa negativnim predznakom.

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