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# GENETIC ANALYSIS OF PRODUCTIVITY COMPONENTS IN MALTING BARLEY (*HORDEUM VULGARE*, L.) HYBRID PROGENIES

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## Abstract

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The investigation was conducted on the experimental field of the Agricultural University of Plovdiv, during the period 2011–2014. Coefficients of heritability and selection, the number of genes, transgressions and heterosis in relation to main-traits, determining productivity in malting barley crosses were studied. For this purpose biometrical data of $P_1$, $P_2$, $F_1$ and $F_2$ populations of four hybrid combinations were used. Hybridological analysis data of studied barley populations showed that the inheritance of some traits as plant height, productive tilling, main spike lenght, number of spiklets and grains, grains weight on spike and 1000-grain weight is mainly overdominant in direction of the higher trait values. Parental genotypes Kaskadior, 96105046, 96105023, Emon, 96105027 and 96105024 differ in a small number of genes affecting expression of productive tillering and grains weight on the spike. Based on the conducted analysis it was found that the mass selection by phenotype for main spike lenght, number of spiklets and grains and 1000-grains weight would be more effective in earlier hybrid generations ($F_2$-$F_3$).

*Key words:* productivity components, hybridological analysis, inheritance, malting barley, barley breeding

## Introduction

One of the main tendencies in two-row barley breeding is to improve productive potential traits (Spunar et al., 2008; Momčilović and Pržulj, 2008). Knowing the genetic control of these traits allows us to select and implement effective breeding procedures in malting barley hybrid progeny. Genetic analysis was used by a number of authors to establish the inheritance of the main yield components (Ganusheva et al., 2004). In this case studying the way of trait inheritance forming production is mainly based on biometric analysis of parents and hybrid combinations with subsequent statistical processing (Mersinkov and Zapryanov, 1994). Data reveals the type of inheritance and its genetic conditioning, which indicates the selection effectiveness in different stage of barley breeding (Mersinkov, 1982; Valchanov, 1990; Mersinkov and Valcheva, 2003). Therefore, the parameters which give us an indication of genetic distance's impact on the phenotype are established, as well as the number of genes for which parental forms, selected for hybridization differ (Ganusheva and Dimova, 1996; Dimova and Marinkov, 1999).

The aim of current research is to determine nature of genetic effects in relation to inheritance of economically valuable traits and to predict the effect of selection in consecutive hybrid generations in order to increase the efficiency of breeding process.

## Materials and Methods

The investigation was carried out at the experimental field of the Agricultural University of Plovdiv, during the period 2011–2014. The present research involves biometric analysis of $P_1$, $P_2$, $F_1$ and $F_2$ populations of four barley crosses: (96105023 x Kaskadior); (Emon x 96105046); (96105027 x

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96105023) and (96105024 x 96105046). Subject to biometric measurement are main yield traits such as: plant height, productive tillering, main spike lenght, spiklets and grains number, grains weight in spike and 1000 grains weight.

The arithmetic mean ($\bar{x}$), index of accuracy (S$\bar{x}$%), coefficient of variation (S%), degree of dominance (d/a) according to Mather's formula, heterosis effect (HP) in reference to the parental form with higher trait values; transgression indicator (Tn), number of genes differentiating the parental forms (N), dominance (D), epistasis (E), heredity coefficient ($H^2$), and selection efficiency coefficient (Pp) were calculated for all of studied traits. Genetic analysis of parental and hybrid genotypes by elements of productivity was carried out according Sobolev (1976).

## Results and Discussion

Plant height was inherited incompletely dominant (d/a 0.28) only in Emon x 96105046 combination (Table 1). The values of d/a index revealed nature of inheritance of quantitative traits. Positive values of D index (D 12.1, 1.59, 12.79, 15.83) revealed that inheritance of higher stem was determined by dominant alleles (Table 2). There wasn't any significant heterosis effect (HP) observed among $F_1$ hybrid progeny. The values of transgression (Tn) were relatively low. Differences between gene numbers that distinguished the parental forms in relation to plant height varied over a wide range (of 7 to 20). Values of the coefficients Pp indicated that the selection of plants with shorter stem would be more effective in the later hybrid generations ($F_5$–$F_6$) or by applying multiple individual selection.

Tillering is an important yield component and also as a foundation in terms of the crop uniformity and plant density, directly affecting the crop structure and degree of barley lodging resistance. The productive tillering in all crosses was inherited overdominantly (d/a > 1) (Table 3). There were dominant alleles determining more productive tillers per plant. Investigated transgression indicators were positive in all combinations as higher values characterized 96105023 x Kaskadior (2.48) (Table 4). Relatively low values of heredity coefficient ($H^2$) and selection efficiency coefficient (Pp) defined productive tillering, as a trait highly influenced by environment and the mass selection for it would be more effective if initiated as early as in $F_5$–$F_6$ hybrid generations.

Biometric data for main spike length showed that three of hybrid combinations exhibited overdominant heredity (d/a>1) in which heterosis effect was established (Table 5). Positive transgressions (Tn) were observed in all combinations (Table 6). Number of genes by which parental forms differ (N) in relation to main spike lenght varies in wide range, from 1 to 20. Current research revealed relatively hight values of coefficient of inheritance ($H^2$ from 0.05 to 0.35). Phenotype expression of studied trait was rather due to genotype than the environmental conditions. Type of the gene interaction as well as relatively high values of the coefficient of selection efficiency Pp (from 0.52 to 0.66) indicated a probalitily to choose a homozigous genotypes by their phenotypic expression. Mass selection would be more effective and could be started even in earlier hybrid generations.

The values for degree of dominance of spiklets number in main spike showed that the inheritance was incom-

**Table 1**

**Plant height in consecutive generations, d/a values and heterosis**

| Parameters | $P_1$ | | $P_2$ | | $F_1$ | | $F_2$ | | d/a | HP |
|---|---|---|---|---|---|---|---|---|---|---|
| Crosses | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | | |
| 96105023 x Kaskadior | 87 | 0.21 | 78.1 | 0.73 | 89.19 | 0.08 | 71.1 | 1.77 | 1.49 | 102.52 |
| Emon x 96105046 | 100 | 0.20 | 78 | 0.32 | 92.13 | 0.41 | 95.14 | 0.48 | 0.28 | 92.13 |
| 96105027 x 96105023 | 85 | 0.07 | 87 | 0.21 | 76.91 | 0.10 | 86.4 | 0.14 | 9.09 | 84.40 |
| 96105024 x 96105046 | 81.7 | 0.16 | 78 | 0.32 | 82.03 | 0.24 | 87.84 | 0.40 | 1.17 | 100.39 |

**Table 2**

**Values of the genetic parameters characterizing plant height**

| Parameters<br>Crosses | Tn | N | D | E | $H^2$ | Pp |
|---|---|---|---|---|---|---|
| 96105023 x Kaskadior | -0.1 | 7 | 12.1 | 13.59 | 0.8 | -1.59 |
| Emon x 96105046 | -0.05 | 20 | 1.59 | -1.31 | 0.38 | 0.52 |
| 96105027 x 96105023 | 1.84 | 20 | 12.79 | -23.66 | 0.07 | 0.51 |
| 96105024 x 96105046 | 0.02 | 12 | 15.83 | -14.67 | 0.42 | -3.19 |

pletely dominant for 96105023 x Kaskadior (d/a –0.66) and 96105027 x 96105023 (d/a –0.34), while for the other crosses overdominant inheritance was observed (Table 7). There wasn't any heterosis effect (HP) in case of incomplete dominance. According to the positive values of D, dominant alleles determined greater number of spiklets (Table 8). Relatively high values for coefficient of inheritance ($H^2$–0.29 to 0.38) and efficiency of selection (Pp) indicated insignificant environmental variability and the spiklets number appeared to be highly inheritable. Manifestation can be easily predicted and faster stabilization could be obtained ($F_2$–$F_3$).

The grains number in main spike of crosses Emon x 96105046 (d/a 1.55) and 96105024 x 96105046 (d/a 2.53) were inherited overdominantly, while in combinations 96105023 x Kaskadior (d/a -0.60) and 96105027 x 96105023 (d/a –0.27)– incompletely dominantly (Table 9). Alleles of genotypes with a larger number of grains in the main spike dominate – respectively Kaskadior, Emon and line 96105024. In crosses with the exception of 96105023

**Table 3**

**Productive tillering in consecutive generations, d/a values and heterosis**

| Parameters<br>Crosses | $P_1$ | | $P_2$ | | $F_1$ | | $F_2$ | | *d/a* | *HP* |
|---|---|---|---|---|---|---|---|---|---|---|
| | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | | |
| 96105023 x Kaskadior | 5.64 | 2.13 | 5.2 | 2.26 | 7.18 | 1.18 | 8.1 | 3.18 | 8.00 | 127.30 |
| Emon x 96105046 | 5.43 | 0.90 | 4.7 | 2.16 | 5.87 | 1.18 | 5.59 | 1.37 | 2.21 | 108.10 |
| 96105027 x 96105023 | 3.6 | 1.37 | 5.64 | 2.13 | 6.04 | 1.01 | 5.75 | 1.59 | 1.39 | 107.09 |
| 96105024 x 96105046 | 5.14 | 1.54 | 4.7 | 2.16 | 5.38 | 0.79 | 5.76 | 0.87 | 2.07 | 104.61 |

**Table 4**

**Values of the genetic parameters characterizing productive tillering**

| Parameters<br>Crosses | **Tn** | *N* | *D* | *E* | $H^2$ | *Pp* |
|---|---|---|---|---|---|---|
| 96105023 x Kaskadior | 2.48 | 1 | 3.32 | -2.67 | 0.38 | 0.03 |
| Emon x 96105046 | 0.59 | 1 | 1.35 | -0.51 | 0.05 | 0.23 |
| 96105027 x 96105023 | 1.76 | 1 | 4.19 | -2.70 | 0.06 | -0.3 |
| 96105024 x 96105046 | 0.77 | 1 | 5.24 | 4.41 | 0.04 | -0.31 |

**Table 5**

**Main spike lenghtin consecutive generations, d/a values and heterosis**

| Parameters<br>Crosses | $P_1$ | | $P_2$ | | $F_1$ | | $F_2$ | | *d/a* | *HP* |
|---|---|---|---|---|---|---|---|---|---|---|
| | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | | |
| 96105023 x Kaskadior | 5.91 | 0.76 | 8.63 | 0.80 | 8.91 | 0.90 | 7.7 | 1.32 | -1.21 | 103.24 |
| Emon x 96105046 | 7.86 | 0.33 | 7.7 | 0.44 | 9.37 | 0.99 | 8.47 | 0.84 | 19.88 | 119.21 |
| 96105027 x 96105023 | 11.4 | 0.71 | 5.91 | 0.76 | 8.71 | 0.46 | 9.13 | 0.49 | 0.02 | 76.40 |
| 96105024 x 96105046 | 7.71 | 1.58 | 7.7 | 0.44 | 8.64 | 0.86 | 7.42 | 1.27 | 187.6 | 112.21 |

**Table 6**

**Values of the genetic parameters characterizing main spike lenght**

| Parameters<br>Crosses | *Tn* | *N* | *D* | *E* | $H^2$ | *Pp* |
|---|---|---|---|---|---|---|
| 96105023 x Kaskadior | 4.18 | 1 | 0.03 | 0.55 | 0.35 | 0.6 |
| Emon x 96105046 | 2.12 | 1 | 0.53 | 0.19 | 0.34 | 0.52 |
| 96105027 x 96105023 | 0.5 | 20 | 0.67 | -0.67 | 0.05 | 0.66 |
| 96105024 x 96105046 | 2.15 | 1 | 0.96 | 1.40 | 0.29 | 0.59 |

x Kaskadior and 96105027 x 96105023 heterosis was determined for. The variation of studied quantitative traits was due to the fact that parental varieties used for hybridization contained alleles of different genes from the polygenic set. Values of genetic parameters characterizing grains number in main spike in Table 10 showed that the number of genes (N) for which differ parential forms range from 1 to 20. The highest value of transgression coefficient (Tn) was found in 96105023 x Kaskadior (6.06%). Mostly negative values for epistatic interactions (E) indicated potential for lower phenotypic expression of the trait in subsequent generations. Data from the genetic analysis revealed that the selection by phenotype for grains number would be more effective in later hybrid generations ($F_5$–$F_6$).

Final grain yield is summarizing components, one of the most consistent of which is average grain weight. Barley grain size determined mainly by the plants genetics i.e. the variety, the nutrition and length of the grain filling period.

**Table 7**

**Spiklets number in consecutive generations, d/a values and heterosis**

| Parameters<br>Crosses | $P_1$ | | $P_2$ | | $F_1$ | | $F_2$ | | *d/a* | *HP* |
|---|---|---|---|---|---|---|---|---|---|---|
| | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | | |
| 96105023 x Kaskadior | 19.73 | 0.66 | 27.3 | 1.06 | 26 | 0.50 | 30.9 | 1.1 | -0.7 | 95.24 |
| Emon x 96105046 | 30.57 | 0.98 | 18.8 | 0.75 | 31.94 | 0.41 | 33.25 | 0.50 | 1.23 | 104.48 |
| 96105027 x 96105023 | 33.4 | 0.45 | 19.7 | 0.66 | 24.21 | 0.40 | 29.51 | 0.78 | -0.3 | 72.49 |
| 96105024 x 96105046 | 22.43 | 1.40 | 18.8 | 0.75 | 24.42 | 0.50 | 22.33 | 1.32 | 2.10 | 108.87 |

**Table 8**

**Values of the genetic parameters characterizing spiklets number in main spike**

| Parameters<br>Crosses | *Tn* | *N* | *D* | *E* | $H^2$ | *Pp* |
|---|---|---|---|---|---|---|
| 96105023 x Kaskadior | 6.68 | 10 | 9.65 | -8.76 | 0.29 | 1.5 |
| Emon x 96105046 | -6.1 | 1 | 12.2 | 9.76 | 0.34 | 6.63 |
| 96105027 x 96105023 | -0.12 | 20 | 2.10 | -2.5 | 0.35 | 0.52 |
| 96105024 x 96105046 | 0.83 | 1 | 1.15 | 0.28 | 0.38 | 0.31 |

**Table 9**

**Grains number in main spike in consecutive generations, d/a values and heterosis**

| Parameters<br>Crosses | $P_1$ | | $P_2$ | | $F_1$ | | $F_2$ | | *d/a* | *HP* |
|---|---|---|---|---|---|---|---|---|---|---|
| | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | $\bar{x}$ | ±S$\bar{x}$% | | |
| 96105023 x Kaskadior | 19.36 | 0.73 | 26.4 | 1.37 | 25 | 0.44 | 29.40 | 1.2 | -0.6 | 94.70 |
| Emon x 96105046 | 29.71 | 0.89 | 18.0 | 0.94 | 32.94 | 0.31 | 31.31 | 0.52 | 1.55 | 110.87 |
| 96105027 x 96105023 | 30 | 0.77 | 19.4 | 0.73 | 23.25 | 0.37 | 27.95 | 0.87 | -0.3 | 77.50 |
| 96105024 x 96105046 | 20.57 | 1.80 | 18 | 0.94 | 22.54 | 0.78 | 20.42 | 1.68 | 2.53 | 109.58 |

**Table 10**

**Values of the genetic parameters characterizing grains number in main spike**

| Parameters<br>Crosses | *Tn* | *N* | *D* | *E* | $H^2$ | *Pp* |
|---|---|---|---|---|---|---|
| 96105023 x Kaskadior | 6.06 | 8 | 9.43 | -8.59 | 0.27 | 1.42 |
| Emon x 96105046 | -0.9 | 20 | 3.55 | -1.99 | 0.23 | 0.26 |
| 96105027 x 96105023 | 0.10 | 16 | 2.68 | -2.94 | 0.30 | 0.36 |
| 96105024 x 96105046 | 1.90 | 1 | 0.40 | 0.62 | 0.36 | 0.55 |

Incomplete dominance of grains weight in main spike was found only in 96105027 x 96105023 (d/a –0.89) cross. There were high positive values of heterosis (HP) in case of overdominant trait inheritance, strongly expressed in 96105024 x 96105046, 68.91 % (Table 11), respectively.

Relatively high values of Tn coefficient were found as well (Table 12). Parental forms used as an initial material for hybridization differed in one gene (N) which alleles had overdominant interaction towards higher weight of the grains. Negative epistasis interactions were found between alleles and reducing the extent of trait phenotypic expression was assumed. Based on the values of gene interactions (E) and the coefficients of heritability ($H^2$), we could predict that the selection of plants in relation to studied trait would be more effective in later hybrid generations ($F_5$–$F_6$).

Inheritance of the 1000 grains weight was overdominant in all crosses (d/a > 1) (Table 13). The highest heterosis effect (HP) was found in 96105023 x Kaskadior (31%). The

**Table 11**

**Grains weight in main spike in consecutive generations, d/a values and heterosis**

| Parameters<br>Crosses | $P_1$ | | $P_2$ | | $F_1$ | | $F_2$ | | *d/a* | *HP* |
|---|---|---|---|---|---|---|---|---|---|---|
| | $\bar{x}$ | $\pm S\bar{x}\%$ | $\bar{x}$ | $\pm S\bar{x}\%$ | $\bar{x}$ | $\pm S\bar{x}\%$ | $\bar{x}$ | $\pm S\bar{x}\%$ | | |
| 96105023 x Kaskadior | 0.99 | 1.03 | 1.43 | 1.67 | 1.77 | 1.86 | 1.51 | 2.19 | 2.55 | 122.92 |
| Emon x 96105046 | 1.53 | 1.50 | 0.79 | 1.45 | 1.56 | 0.50 | 1.79 | 0.63 | 1.08 | 101.96 |
| 96105027 x 96105023 | 1.54 | 1.55 | 0.99 | 1.03 | 1.02 | 1.54 | 1.64 | 1.89 | -0.89 | 66.23 |
| 96105024 x 96105046 | 1.19 | 1.85 | 0.79 | 1.45 | 2.01 | 1.40 | 1.80 | 1.74 | 5.10 | 168.91 |

**Table 12**

**Values of the genetic parameters characterizing grains weight in main spike**

| Parameters<br>Crosses | Tn | N | *D* | *E* | $H^2$ | *Pp* |
|---|---|---|---|---|---|---|
| 96105023 x Kaskadior | 3.56 | 1 | 0.19 | -0.02 | 0.28 | 0 |
| Emon x 96105046 | 1.2 | 1 | 3.72 | -3.02 | 0.08 | 0 |
| 96105027 x 96105023 | 2.72 | 1 | 0.58 | -0.66 | 0.32 | 0 |
| 96105024 x 96105046 | 1.64 | 1 | 1.19 | -0.64 | 0.16 | 0 |

**Table 13**

**1000 grains weight in consecutive generations, d/a values and heterosis**

| Parameters<br>Crosses | $P_1$ | | $P_2$ | | $F_1$ | | $F_2$ | | *d/a* | *HP* |
|---|---|---|---|---|---|---|---|---|---|---|
| | $\bar{x}$ | $\pm S\bar{x}\%$ | $\bar{x}$ | $\pm S\bar{x}\%$ | $\bar{x}$ | $\pm S\bar{x}\%$ | $\bar{x}$ | $\pm S\bar{x}\%$ | | |
| 96105023 x Kaskadior | 51.09 | 0.52 | 54 | 0.54 | 70.88 | 0.91 | 53.85 | 0.9 | 12.65 | 131.26 |
| Emon x 96105046 | 51.16 | 0.73 | 43.8 | 0.83 | 53.57 | 0.34 | 54.45 | 0.62 | 1.65 | 104.71 |
| 96105027 x 96105023 | 51.16 | 0.76 | 51.1 | 0.52 | 51.03 | 0.56 | 54.9 | 0.34 | 2.71 | 99.75 |
| 96105024 x 96105046 | 57.62 | 0.41 | 43.7 | 0.83 | 60.33 | 0.37 | 57.68 | 0.40 | 1.39 | 104.70 |

**Table 14**

**Values of the genetic parameters characterizing 1000 grains weight**

| Parameters<br>Crosses | *Tn* | *N* | *D* | *E* | $H^2$ | *Pp* |
|---|---|---|---|---|---|---|
| 96105023 x Kaskadior | 2.6 | 4 | 11.4 | 27.34 | 0.25 | 0.13 |
| Emon x 96105046 | 0.05 | 20 | 5.91 | -4.26 | 0.54 | 0.85 |
| 96105027 x 96105023 | 0.03 | 1 | 23.95 | -23.44 | 0.05 | 55.23 |
| 96105024 x 96105046 | 7.14 | 1 | 86.9 | 41.16 | 0.26 | 30.89 |

values of Tn showed that in the $F_2$ populations resulting from the crosses Kaskadior x 96105023 and 96105024 x 96105046, plants who have a significantly higher weight of grains as compared to the parental forms can be successfully selected (Table 14). Gene interactions (E) had a positive value in the combinations 96105023 x Kaskadior and 96105024 x 96105024. Coefficients of heritability ($H^2$) were relatively higher (except for the 96105027 x 96105023 cross) and it can be assumed that the genetic share in phenotypic expression was larger. The values of the Pp suggest that the selection of plants with larger grain will be effective in earlier generations ($F_2$–$F_3$).

A method by Sobolev was suggested for analysis of polygenic characters based on comparing the hybrid generation‘s arithmetical mean components with genotypic dispersion. Conducted hybridological analysis revealed the type and value of the gene interaction. Overdominance effects prevailed in current research and to alesser extent – incomplete dominance of elements of productivity in malting barley. Dominant alleles determined higher values of traits in all studied genotypes. The variation of studied quantitive traits was found to be due to the fact that parental varieties used in the hybridization schemes contained different alleles of genes from the polygenic set. The method allowed us to determinethe number of genes by which parental forms differed, as well. Heterosis effect only in case of overdominant traits inheritance was observed. The data presented revealed possibilities for prediction and utilization of selection efficiencyin the use of malting barley breeding programs.

## Conclusions

Genetic analysis of quantitative traits among studied malting barley crosses 96105023 x Kaskadior; Emon x 96105046; 96105027 x 96105023; 96105023 x 96105046 reveals that the inheritance of plant height, productive tillering, main spike lenght, spiklets number, grains number and weight in spike, and 1000 grains weight is inherited overdominantly, and always dominate parents with higher values of the investigated traits.

The number of genes for which initial parental forms Kaskadior, 96105046, 96105023, Emon, 96105027 and 96105024 differ in relation to plant height, main spike lenght, spiklets number, grains number and 1000 grains weight is much bigger than the number of genes that determine productive tillering and grains weight in spike.

Transgressions are established in 96105023 x Kaskadiorfor most of the quantitative traits such as studied yield`s components.

Data from the genetic analysis performed according Sobolev reveals that the selection by phenotype in later hybrid generations ($F_5$–$F_6$) will be more effective for plant height, productive tillering and grains weight on spike.

Values of studied indexes shows that the selection of plants with longer main spike, higher number of spikelets, grains and 1000 grains weight will be more effective in early stages of breeding process ($F_2$-$F_3$ generation).

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