

REGRESSION ANALYSIS OF HEAD MASS AND MASS OF USEFUL PART OF HEAD IN CABBAGE (*Brassica oleracea* var. *capitata* L.)

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ABSTRACT: The objective of this paper was to determine the genetic mode of inheritance of quantitative traits in cabbage via regression analysis in complete diallel crossing. The regression analysis of head mass traits showed that the regression line was distant from the limiting parabola, indicating nonadditive gene action in head mass inheritance. The expected line of regression intersected the Wr axis below the coordinate origin, confirming the presence of superdominance in this inheritance. As useful head part mass comprises the bulk of total head mass, the regression analysis results were similar. The regression line was also far from the limiting parabola, indicating nonadditive gene action in this trait's inheritance. Similarly, the regression line intersected the Wr axis below the origin, suggesting we had a case of superdominance in the inheritance of this trait as well.

Key words: cabbage, regression analysis, head

INTRODUCTION

The main problem in cabbage production is a lack of uniformity with respect to more or less all traits. This problem is resolved by replacing the existing cultivars with hybrids, which are characterized by high uniformity. The first step in this process is to choose the right parents from which self-incompatible lines will be bred to be used as components of hybrids (Riggs, 1988).

In parallel with its line development program, the Vegetables Department of the Institute of Field and Vegetable Crops in Novi Sad is testing the combining abilities of seven cultivars that will be used to obtain the lines mentioned above in the next cycle of selection.

Across the world, heterosis of plants of the genus *Brassica* is used on a massive scale. The basic procedure for obtaining hybrid seed is based on the self-incompatibility or self-sterility of plants obtained by cloning.

As cultivars used in our crosses are divergent with respect to the traits studied, it was realistic to expect that heterosis would occur in the F_1 generation relative to the better parent. This assumption was confirmed in our study, mostly because superdominance is usually the most common mode of inheritance of the traits involved.

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MATERIALS AND METHODS

Seven divergent cabbage genotypes with differing head mass and useful part of head, were chosen based on previous studies. These cultivars all have different origin, which represents a potential source of desirable gene combinations to be used in future breeding work. Used in the study were the following cultivars: Futoški, SM-10, Ditmar, Kopenhaški, Prva Žetva, Pourovo Červene, Kboce.

The experimental part of the study was carried out in the greenhouse and in the field at the Experiment Field of the Vegetables Department of the Institute of Field and Vegetable Crops in Novi Sad. In the greenhouse, the cultivars (each cultivar was represented with six plants) were crossed using the complete diallel cross method. After the fruit bearing and seed setting, a field trial was established. A randomized block design with five replications was used. Each combination was represented by 30 samples and head mass and useful part of head, were measured.

The genetic system of quantitative traits inheritance in diallel crosses was determined by regression analysis according to Mather and Jinks. (1982). The coefficient of regression was tested according to Steel and Torrie. (1960) via regression coefficient (b) and standard regression error (Sb) using the formula:

$$t = \frac{b - 1}{sb}$$

Degrees of freedom: (n - 2)

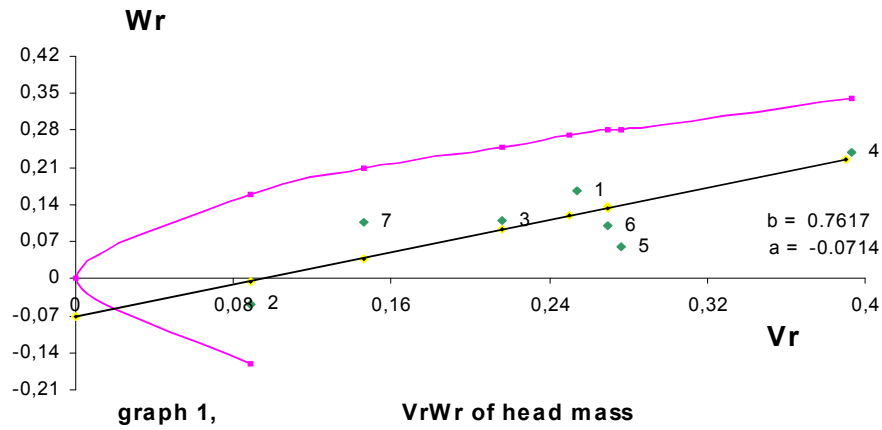
Regression analysis of cabbage head mass

The regression line was far from the limiting parabola, indicating the predominance of nonadditive gene action in the inheritance of head mass in the F₁ generation. This was in agreement with the calculated value of $\sqrt{H1/D}$, which was above the value of one in genetic variance components analysis (1.66). Further supporting the above conclusion was the point of intersection of the expected regression line and the Wr axis. The expected line of regression intersected the Wr axis below the start of the coordinate system, indicating superdominance in the inheritance of head mass (Graph 1).

Neither of the parents were located at the intersection of the parabola and the regression line, so neither had all of the dominant or all of the recessive alleles. Instead, one of the parents had more dominant and less recessive genes for head mass, while with the other it was vice versa.

Point distribution in the dispersion diagram along the expected line of regression was indicative of the parents' genetic divergence. The cultivars Futoški, SM-10, and P. Červene had more dominant and less recessive genes for head mass, since dispersion diagram points were the closest to the start of the coordinate system. The other cultivars, which were farther from the coordinate system start, had a larger number of recessive and a smaller number of dominant genes for head mass (Graph 1).

As the calculated value of b = 0.753 was smaller than the critical tabular value of t_{0.05} = 4.032, the hypothesis is accepted, which suggests an absence of interallelic interaction (Sb = 0.240, Se = 0.058, t = 1.028)

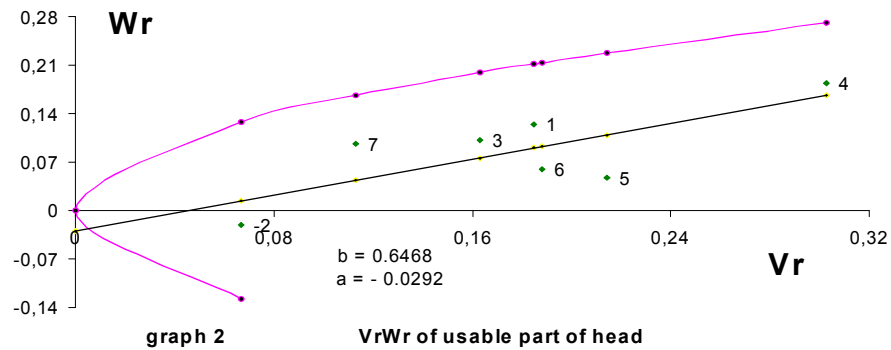


Regression analysis of the useful part of the head

The useful part of the head is a trait comprising most of the head mass trait, so the regression analyses of the two traits are similar. In this case as well, the regression line was remote from the limiting parabola, which means that here too nonadditive gene action predominated in the inheritance of the trait in the F_1 generation. This was confirmed by the value of $\sqrt{H1/D}$, which was larger than one (1.583), (Graph 2).

The regression line intersected the W_r axis below the start of the coordinate system, indicating the presence of superdominance in the inheritance of the useful part of the head. With this trait too, neither of the parents was situated at the point of intersection of the parabola and the line of regression. The distribution of points in the dispersion diagram along the expected regression line was the same as with head mass. The cultivars Futoški, SM-10, and P. Červene were the closest to the coordinate start, so they had more dominant genes controlling the inheritance of this trait (Graph 2).

The tabular value of $t_{0.05} = 4.032$ was higher than the calculated value of $b=0.644$, indicating an absence of interallelic interaction in this case as well ($S_b = 0.253$, $S_e = 0.047$, $t = 1.405$).



DISCUSSION

The results of regression analysis showed that the highest concentration of dominant genes was found in Futoški (6 traits), SM-10 (5 traits), and Kopenhaški (4 traits). By contrast, only two of the cultivars (Kbose and Ditmar) had recessive genes for all traits. The cultivars Pourovo Červene and Prva Žetva had more recessive than dominant genes for the traits studied (for 4 traits in total). Futoški had more recessive genes for only one trait (outer stem length). The cultivar SM-10 had more recessive genes for two traits (inner stem length and outer stem length). Interallelic interaction was found to be present for the yield trait. The results of our regression analysis are in agreement with those of Hansen (1989).

CONCLUSION

The regression analysis of the cultivars showed that 21 of the 49 cabbage combinations studied had inheritance of traits with dominant genes, while the other 28 had inheritance of traits with recessive genes.

Interallelic interaction was found for yield. Contributing to this were three cultivars: Kbose, Ditmar and Prva Žetva.

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