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# REGRESSION ANALYSIS OF THE INHERITANCE OF LEAF SIZE IN F1 AND F2 PROGENIES IN VARIOUS TOBACCO GENOTYPES

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## ABSTRACT

*Investigations were made on the inheritance of length, width and middle belt leaf area in progenies of six F1 and six F2 diallel crosses from four parental varieties (oriental Prilep P12-2/1, Pobeda P-2 and Yaka YV 125/3 and semi-oriental Forchheimer Ogrodowny - FO). Crossing was made in 2004 and 2005, and the trial with parents and hybrids was set up in 2006, in the field of Tobacco Institute-Prilep, at randomized block system with four replications.*

*The aim of the investigations was to present a comprehensive picture on the genetic system of leaf size, through regression analysis.*

*Values of the major genetic components required for graphic presentation were calculated from the average values of the investigated characters.*

*The regression analysis reveals partially dominant mode of inheritance of leaf size and lack of interallelic interaction. According to the position of points along the regression line, there is higher number of dominant genes in P 12-2/1 and of recessive genes in P-2 for inheritance of leaf size in both generations. In YV 125/3 higher frequency of dominant genes was observed in F1 and of recessive genes in F2 for inheritance of leaf length; of recessive genes in F1 and dominant genes in F2 for leaf width; of dominant genes in F1 and equal number of dominant and recessive genes in F2 for inheritance of middle belt leaf area. In FO, higher frequency of dominant genes for inheritance of leaf length was observed in both generations, of recessive genes in F1 and dominant genes in F2 for leaf width and equal number of dominant and recessive genes in F1 and of recessive in F2 for inheritance of middle belt leaf area.*

**Keywords:** tobacco (*Nicotiana tabacum* L.), inheritance, leaf size, regression analysis

## Introduction

Inheritance of measurable genetic characters of living organisms is studied by quantitative genetics. It applies large number of methods and models to get knowledge which can be used in selection activities.

Subject of investigations in this paper is the regression analysis, based on the methods applied to create and interprete regression graphs. In fact, genetic interpretation is based on the position of dispersion points along the regression line in the limiting parabola.

Many authors used the regression analysis in their genetic investigations of various crops. Ibrahim and Avratovscukova (5) in a diallel of five flue-cured tobacco varieties and ten F1 crosses showed partial dominant type of inheritance for stalk height, over dominant type for leaf length, partial dominance for leaf width and overdominance for green mass yield. Jung & co. (6) in six oriental varieties and fifteen F1 crosses revealed non-allelic gene interaction for leaf number, partial dominance for stalk height and over dominance for inheritance of yield. Lee & Chung (8), in Korean local and oriental varieties and 28 F1 hybrids showed partial dominance for leaf number and leaf size. Dobhal (3) revealed over dominant type of inheritance for leaf size and green/dry leaf mass yield in a diallel of ten parental genotypes of Nicotiana rustica. During the 4-years investigation of four Burley varieties and six F1 crosses, Butorac & co. (2)

revealed partial dominance in1992/1993 and total dominance in 1994/1995 for leaf number and over dominance for inheritance of yield. In the analysis of three oriental and one semi-oriental variety and their six F1 and F2 crosses, Korubin-Aleksoska (7) showed partial dominance in the inheritance of stalk height, leaf number and green/dry mass yield per stalk, and absence of interallelic interaction.The aim of investigation was to give a comprehensive vision of the complete genetic system for the inheritance of leaf size from parents to F1 and F2 generations. Results obtained will be used in selection, for creation of new tobacco varieties

## Materials and Methods

By previous investigations of the assortment of Tobacco Institute-Prilep, four varieties were selected, of which three oriental (P 12-2/1, P-2 and YV 125/3) and one semi-oriental (Forchheimer Ogrodowny FO). They were used for diallel crossing and the obtained crosses, along with their parents, were subject of investigation in this paper.

In 2004, during the flowering stage, seed from six diallel combinations for F1 generation was obtained by hand castration and pollination. In 2005, in a trial with selected homozygous parental genotypes and their F1 progeny, the seed for F2 generation was selected and new diallel crossings were made to obtain seed for F1 generation. In 2006, randomized trial with four replications was set up in the field of Tobacco Institute-Prilep, including parents, six F1 and six F2 diallel crosses: P 12-2/1 x P-2, P 12-2/1 x YV 125/3, P 12-2/1 x FO, P-2 x YV 125/3, P-2 x FO and YV 125/3 x FO.

Parents and their crosses were sawn in seedbeds under polyethylene on 10.04.2006 and seedlings were transplanted on 4.06.2006, on diluvial-colluvial type of soil. Space between rows was 45 cm, leaving a protective raw at the beginning and end of each replication. Space in the row differred depending on parent/cross type. Thus, for oriental parents it was 15 cm, for FO 25 cm, for combinations which included only oriental varieties 15 cm and for those which included FO - 20 cm.

The area of each replication was about 235 m$^2$. The total useful area was 940 m$^2$, and together with paths it approximated 1100 m$^2$.

All suitable cultural practices were applied during the growing period of tobacco.

Knowing that environmental factors affect the manifestation of characters, we should inform that meanmonthly air temperature in this period (May-September) was 19.44$^0$C, and total amount of precipitations was 164.1mm.

Investigation was made on the characters length, width and area of the middle belt leaf. Length and width were measured during the tobacco flower stage (end July - August). In parental genotypes and F1 generation 100 leaves were measured from each replication, i.e. 400 leaves in total, and in F2 200 leaves were measured from each replication, i.e. 800 leaves from middle primings in the whole trial.

Leaf area was calculated by multiplication of length and width, with the coefficient k=0.6354 (relative area).

Variational statistical analysis was made on the data obtained for each character by combinations, for F1 and F2 generation.

**Type of inheritance** was estimated according to test-significance of the mean value of F1 and F2 in relation to the parental average (1).

**Genetic components** needed to compose the graphs for F1 were estimated by the methods of Hayman (4), and for F2 by the methods of Mather and Jinks (10).

**Regression analysis** was made by the methods of Mather and Jinks (9). It is based on interpretation of $\overline{V_R}$ $\overline{W_R}$ -graphs, where $\overline{V_R}$ is the variance of all progenies from all parents, and $\overline{W_R}$ is covariance of the parental progeny.

## Results and Discussion

The average values for middle belt leaf size (**Table 1**) reveal significant differences among parental genotypes and presence of all possible types of inheritance of the characters, with predominance of the intermediate inheritance. Positive heterosis in F1 was revealed in P 12-2/1 x P-2 and in P-2 x YV 125/3.

Values presented in **Table 1** are starting units for further biometric methods, until composition of the regression graph, which will allow us to have a complete picture of the genetic system in inheritance of investigated characters.

The graph of regression ($V_R$, $W_R$) for middle belt **leaf length** in F1 and F2 almost equals to 1 and differs significantly from 0, which indicates absence of interallelic interaction. The expected regression line is close to the limiting parabola (especially for F2 generation), which indicates predominance of additive genes in inheritance of this character. Cross-section of the expected regression line with Wr-ordinate is on the origin, which is an indication of partial dominant type of inheritance. Position of dispersion points on the diagram confirms the divergence of parental genotypes for the investigated character.

**TABLE 1**

Type of inheritance of middle belt leaf size in F1 and F2 generations

| Parents and F1 hybrids | Leaf length (cm) | | Leaf width (cm) | | Leaf area (cm²) | |
|---|---|---|---|---|---|---|
| | F1 | F2 | F1 | F2 | F1 | F2 |
| 1. P 12-2/1 | 27 | 27 | 13 | 13 | 221 | 221 |
| 2. P-2 | 20 | 20 | 11 | 11 | 132 | 132 |
| 3. YV125/3 | 22 | 22 | 12 | 12 | 169 | 169 |
| 4. FO | 39 | 39 | 24 | 24 | 597 | 597 |
| 1 x 2 | **28+h** | 24pd | **15+h** | 11pd | **274+h** | 177 i |
| 1 x 3 | 25 i | 23pd | 12 i | 11-h | 195 i | 167-d |
| 1 x 4 | 33 i | 31 i | 18 i | 17pd | 387 i | 331pd |
| 2 x 3 | **25+h** | 22+d | **15+h** | 12+d | **234+h** | 168+d |
| 2 x 4 | 33pd | 31.5i | 21pd | 18.2i | 440pd | 364 i |
| 3 x 4 | 31 i | 31.9i | 17 i | 17.3i | 347 i | 352 i |

The position of FO, P 12-2/1 and YV 125/3 in the coordinate system shows significantly higher number of dominant than recessive genes in F1 generation. Their points are closest to the cross section of the parabola and the regression line on the side of the origin, according to which they possess mostly dominant genes in inheritance of this character. P-2 is positioned on the opposite side of the origin, which indicates predominance of additive gene effect (**Fig. 1**).

From the analysis of F2 generation (**Fig. 2**), the position of FO and P 12-2/1 shows that dominant genes prevail, whereas in YV 125/3 and P-2 additive genes prevail in inheritance of the character.

The coefficient of regression graphs for the caharacter **leaf width** in both generations almost equals to 1, and the position of regression line is very close to the limiting parabola (especially that of F2 generation). It denotes absence of interallelic interaction and dominance of the additive gene effect, which is specificity in inheritance of quantitative characters. The expected regression line intersects the Wr-ordinate above the origin, which shows partial dominance in inheritance of this character.

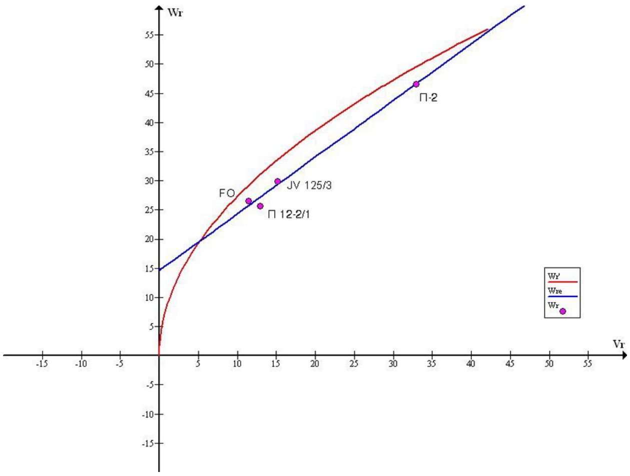

**Fig 1.** Graphic presentation of the inheritance of leaf length in F1 generation

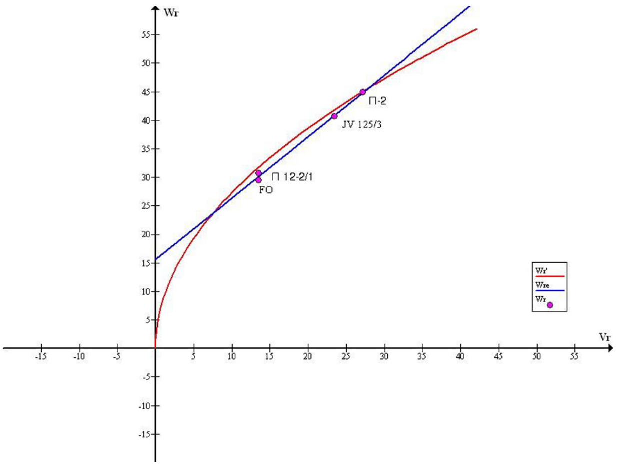

**Fig. 2**. Graphic presentation of the inheritance of leaf length in F2 generation

Distribution of points along the expected regression line for F2 (**Fig. 3**) shows the distance of parents in relation to this character. The sequence of varieties is not identical to that of F1. YV 125/3, P 12-2/1 and FO are closer to the point of intersection of the parabola and the regression line on the side of ordinate, which denotes that dominant gene effect prevails in inheritance of this character. In P-2 variety recessive genes are prevailing, as can be seen from its position on the regression line.

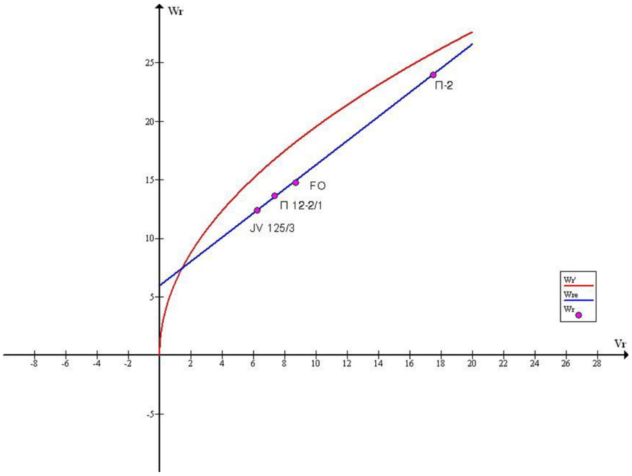

**Fig. 3.** Graphic presentation of the inheritance of leaf width in F1 generation

Distribution of points for F1 generation (**Fig. 4**) shows that P 12-2/1 is closest to the point where parabola intersects the regression line on the side of ordinate. Accordingly, in this variety dominant genes prevail over the neglectable number of recessive genes in inheritance of width. YV 125/3, as well as P-2 and FO are positioned on the opposite side, which reveals that the additive gene effect prevails over the dominant.

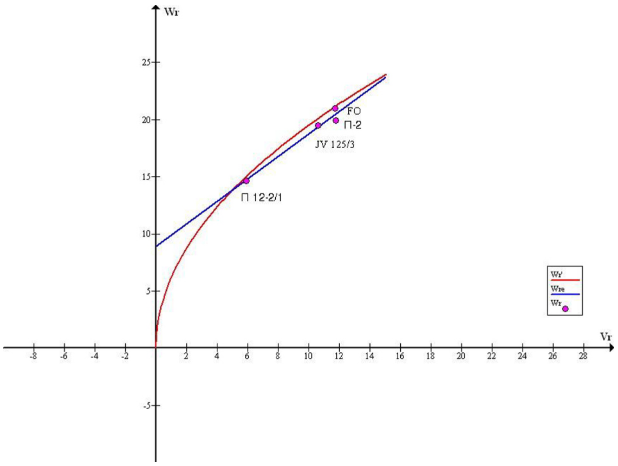

**Fig. 4.** Graphic presentation of the inheritance of leaf width in F2 generation

The coefficient of the regression graph for **leaf area** in F1 and F2 almost equals to 1 and significantly differs from 0, which indicates an absence of interallelic interaction. The expected regression line is close to the limiting parabola (especially the one for F2 generation) and it denotes that additive genes have the leading role in inheritance of this character. The expected regression line intersects the Wr-ordinate above the origin, which points to partial dominant type of inheritance. Distribution of points in the diagram gives genetic picture of parental genotypes for the character investigated.

The position of YV 125/3 and P12-2/1 in the coordinate system for F1 generation shows the significantly larger number of dominant genes over the recessive. Their points are closest to the cross-section of the parabola and regression line on the side of the origin, which shows that dominant gene effect prevails in inheritance of this character. The location of FO denotes approximately equal number of dominant and recessive genes, and the location of P-2 on the opposite side of origin shows dominance of the additive genes. Regression analysis for this character is presented in **Fig. 5**.

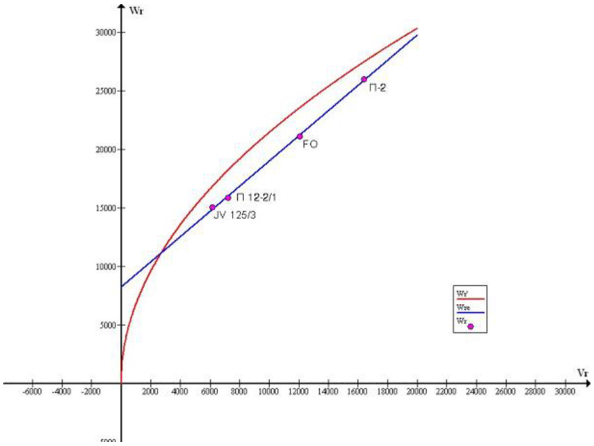

**Fig. 5.** Graphic presentation of the inheritance of leaf area in F1 generation

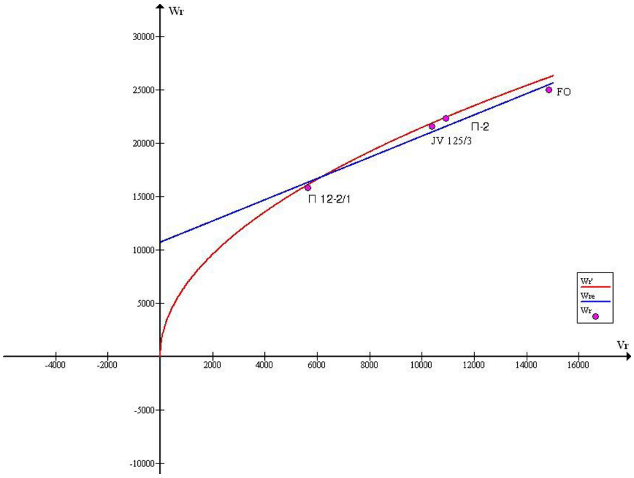

**Fig. 6.** Graphic presentation of the inheritance of leaf area in F2 generation

The analysis of F2 generation (**Fig. 6**) shows that in P 12-2/1dominant gene effect prevails, in YV 125/3 and P-2 the number of dominant and recessive genes is almost identical and in FO additive genes prevail in inheritance of this character.

Values for **Figures 1, 2, 3, 4, 5** and **6** are presented in **Table 2**.

**TABLE 2**

Cell growth parameters on ‘Rider’ media, supplemented with 20 g $L^{-1}$ lactose, and induction of β-galactosidase activity

| **No.** | **Strain denotation** | **$\mu^{max}$ [$h^{-1}$]** | **$Y_S$** | **$q_S$ [$h^{-1}$]** | **Residual lactose [g $L^{-1}$]** | **β-galactosidase [U $mg^{-1}$]** |
|---|---|---|---|---|---|---|
| **1.** | $t_1$ | 0.26 ± 0.09 | 0.29 ± 0.03 | 0.14 ± 0.01 | 12.11 ± 1.40 | 280.3 ± 23.4 |
| **2.** | **$t_3$** | **0.29 ± 0.03** | **0.38 ± 0.05** | **0.25 ± 0.03** | **0.35 ± 1.82** | **480.0 ± 11.3** |
| **3.** | $90_1$ | 0.28 ± 0.03 | 0.36 ± 0.01 | 0.28 ± 0.01 | 0.17 ± 0.95 | 412.4 ± 25.8 |
| **4.** | $90_2$ | 0.30 ± 0.04 | 0.38 ± 0.08 | 0.24 ± 0.02 | 0.07 ± 1.21 | 435.1 ± 10.4 |
| **5.** | $90_3$ | 0.30 ± 0.06 | 0.38 ± 0.09 | 0.25 ± 0.02 | 0.21 ± 1.41 | 420.0 ± 15.8 |
| **6.** | **$90_4$** | **0.33 ± 0.02** | **0.44 ± 0.08** | **0.32 ± 0.04** | **0.70 ± 1.40** | **500.0 ± 22.4** |
| **7.** | $90_5$ | 0.31 ± 0.01 | 0.40 ± 0.02 | 0.32 ± 0.03 | 0.24 ± 0.90 | 450.5 ± 22.4 |
| **8.** | $90_6$ | 0.30 ± 0.01 | 0.42 ± 0.02 | 0.31 ± 0.03 | 1.87 ± 1.35 | 450.4 ± 18.8 |
| **9.** | $90_7$ | 0.30 ± 0.08 | 0.40 ± 0.03 | 0.32 ± 0.01 | 1.29 ± 1.87 | 420.5 ± 16.2 |
| **10.** | $90_8$ | 0.30 ± 0.07 | 0.38 ± 0.04 | 0.25 ± 0.02 | 0.22 ± 2.10 | 395.5 ± 13.5 |
| **11.** | $90_9$ | 0.24 ± 0.09 | 0.31 ± 0.05 | 0.24 ± 0.03 | 0.37 ± 1.46 | 320.0 ± 11.4 |
| **12.** | $90_{10}$ | 0.13 ± 0.02 | 0.15 ± 0.05 | 0.20 ± 0.02 | 16.52 ± 1.55 | 120.2 ± 11.6 |
| **13.** | $90_{11}$ | 0.23 ± 0.01 | 0.28 ± 0.07 | 0.11 ± 0.02 | 6.51 ± 1.80 | 410.4 ± 10.2 |
| **14.** | $90_{12}$ | 0.10 ± 0.02 | 0.15 ± 0.04 | 0.19 ± 0.01 | 16.04 ± 2.10 | 210.1 ± 9.8 |
| **15.** | $90_{13}$ | - | - | - | 21.12 ± 2.34 | 10.0 ± 3.2 |
| **16.** | $90_{14}$ | - | - | - | 20.42 ± 2.10 | 10.2 ± 2.4 |
| **17.** | $90_{15}$ | 0.26 ± 0.02 | 0.33 ± 0.08 | 0.27 ± 0.04 | 0.42 ± 1.10 | 385.1 ± 21.5 |
| **18.** | **$90_{16}$** | **0.26 ± 0.05** | **0.33 ± 0.08** | **0.28 ± 0.01** | **0.21 ± 0.80** | **492.0 ± 23.4** |
| **19.** | $90_{17}$ | 0.24 ± 0.08 | 0.28 ± 0.09 | 0.25 ± 0.02 | 2.69 ± 1.40 | 300.5 ± 18.6 |
| **20.** | $90_{18}$ | 0.13 ± 0.01 | 0.16 ± 0.03 | 0.10 ± 0.02 | 14.87 ± 1.40 | 212.0 ± 18.1 |
| **21.** | $90_{19}$ | - | - | - | 18.00 ± 2.00 | 50.2 ± 5.4 |
| **22.** | $90_{20}$ | - | - | - | 18.40 ± 1.35 | 62.8 ± 3.2 |
| **23.** | $90_{21}$ | - | - | - | 20.00 ± 2.25 | 62.4 ± 4.4 |
| **24.** | $90_{22}$ | 0.09 ± 0.02 | 0.12 ± 0.01 | 0.05 ± 0.01 | 17.70 ± 1.41 | 70.1 ± 4.4 |
| **25.** | $90_{23}$ | - | - | - | 19.20 ± 1.85 | 75.9 ± 3.6 |

## Conclusions

**a)** Parental genotypes are homogenous, with significant differences among them;

**b)** The inheritance of length, width and area of the middle belt leaf in F1 and F2 differs, but the most represented type is intermediate inheritance. Positive heterosis in F1 progeny was observed in P 12-2/1 x P-2 and in P-2 x YV 125/3;

**c)** Distribution points on the regression graph are located on the interior side of limiting parabola. The expected regression line intersects the Wr (y) - axis above the origin, which indicates partial dominant type of inheritance. The regression lines differs significantly from 1, which denotes an absence of interallelic interaction. The patterns of distribution points along the regrssion line of the diagram reveal prevalence of dominant gene effect in P 12-2/1 and of recessive gene effect in P-2. In YV 125/3 both dominant and additive gene effects are significant, with small prevalence of one over the other depending on character and generation, whereas the semi-oriental FO is governed mostly by dominant genes.

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