ISSN 0494-3244

Тутун/Tobacco, Vol.63, N^{0}1-6,8-19, 2013 UDC: 633.71-152.75:575.1(497.775)”2006/2007”

Original Scientific paper

GRAPHIC ANALYSIS OF THE INHERITANCE OF LEAF SIZE IN SOME TOBACCO VARIETIES AND THEIR DIALLEL F1 AND F2 HYBRIDS

Ana Korubin-Aleksoska[1], Jane Aleksoski
[1]*Scientific Tobacco Institute – Prilep, Republic of Macedonia*
e-mail: anakorubin@yahoo.com

ABSTRACT

The paper presents investigations on the inheritance of length, width and area of middle belt leaf in oriental tobacco varieties Prilep (P0 10-3/2), Djebel (Pobeda P-2) and Yaka (YK 48), and the semi-oriental Forchheimer Ogrodowny - FO, including their six F1 and six F2 hybrids. Investigations and crosses were made in 2006 and 2007, and the final trial with parents and hybrids was set up in 2008, in the field of Scientific Tobacco Institute-Prilep, in randomized block system with four replications.

The aim of investigations was to present a comprehensive picture on the genetic system of inheritance of these characters by the use of graphic analysis.

Values of the major genetic components required for graphic presentation were calculated from the average values of the investigated characters, using the methods of Mather and Jinks (1974).

The regression graphs reveal partially dominant type of inheritance of the characters and absence of interallelic interaction. The position of points along the regression line reveals higher number of dominant genes in P 10-3/2 for inheritance of length, width and area of the middle belt leaves. P-2 variety has higher number of recessive genes. In YK 48 both dominant and additive genes are present, with small prevalence of ones over the others. In FO variety dominant genes prevail for inheritance of leaf length and width, and recssive genes for inheritance of middle belt leaf area.

Key words: tobacco (*Nicotiana tabacum L.*), inheritance, quantitative characters, graphic analysis

ГРАФИЧКА АНАЛИЗА ЗА НАСЛЕДУВАЊЕТО НА ДИМЕНЗИИТЕ НА ЛИСТОВИТЕ КАЈ ТУТУНСКИ СОРТИ И НИВНИТЕ ДИЈАЛЕЛНИ F1 И F2 КРСТОСКИ

Трудот опфаќа истражувања за наследување на должината, ширината и површината на листовите од средниот појас, кај сорти од ориенталските генотипови: прилеп (П 10-3/2), џебел (Победа П-2) и јака (ЈК-48), и Forchheimer Ogrodowny – FO од полуориенталски тип, како и нивните шест F1 и шест F2 крстоски. Вкрстувањата беа направени во 2006 и 2007 година, а финалниот опит со родителите и крстоските беше поставен во 2008 година на опитното поле во Научниот институт за тутун – Прилеп по случаен блок – систем во четири повторувања.

Целта на нашите истражувања е преку графичката анализа да се даде комплетна слика на генетскиот систем за наследување на наведените својства.

Вредностите на главните генетски компоненти потребни за графиконите беа добиени врз база на просечните вредности од мерењата на својствата, со примена на методите на Mather и Jinks (1974).

Од графиконите на регресија се открива парцијално доминантен начин на наследување на својствата и непостоење на интералелна интеракција. Од позицијата на точките на дисперзија по должината на линијата на регресија дознаваме дека сортата П 10-3/2 има повеќе доминантни гени за наследување на должината, ширината и површината на листовите од средниот појас. Сортата П-2 има повеќе рецесивни гени. ЈК 48 поседува доминантни и адитивни гени, со мали предности на едните или на другите. FO има претежно доминантни гени за наследување на должината и ширината на листовите, а рецесивни за наследување на нивната површина.

Клучни зборови: тутун (*Nicotiana tabacum L.*), наследување, квантитативни својства, графичка анализа.

INTRODUCTION AND AIM OF INVESTIGATIONS

Plant selection is a creative process of obtaining new and superior genotypes. For improvement of the genetic potential of wanted traits it is necessary to get a good knowledge on the mode of their inheritance, genetic regulations and selection methods. By application of the method of graphical analysis, a complete picture of the quantitative traits inheritance system can be obtained.

Many authors used the graphical analysis in their genetic investigations. Ibrahim and Avratovscukova (1982) in a diallel of five flue-cured tobacco varieties and ten F1 crosses showed overdominant type of inheritance for leaf length and partial dominant type for leaf width. Jung & co. (1982) in six oriental varieties and fifteen diallel F1 crosses revealed non-allelic gene interaction for leaf number, partial dominance for stalk height and overdominance for inheritance of yield. Lee & Chang (1984), in Korean local and oriental varieties and 28 F1 hybrids showed partial dominance for leaf number and leaf size. Dobhal (1988) revealed overdominant 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. (1999) revealed partial dominance in1992/1993 and total dominance in 1994/1995 for leaf number and overdominance for inheritance of yield.

The aim of our investigations was to present and interpret the regression graphs for inheritance of middle belt leaf size in tobacco varieties of different genotypes and their diallel F1 and F2 progenies. The methods of creation and interpretation of graphs can be used in genetic investigations of quantitative traits in many other crops.

MATERIALS AND METHODS

Based on previous investigations of the varieties available in Scientific Tobacco Institute-Prilep, four varieties were selected, of which three oriental (P 10-3/2, P-2 and YK 48) and one semi-oriental (Forchheimer Ogrodowny FO). After two-years diallel crossing and measurin, six F1 and six F2 crosses were obtained, and they served as a basic material for this paper. By application of genetic analyses, we developed a scheme applicable to any other diallel.

In 2006, in flowering stage, a seed of six diallel combinations for F1 generation was obtained by manual castration and pollination. In 2007, in a trial with selected homozygous parental genotypes and their F1 progeny, a seed for F2 generation was collected and additional diallel crossings were made to obtain seed for F1 generation. In 2008, a randomized trial was set up with four replications in the experimental field of Scientific Tobacco Institute-Prilep. Beside parents, it included six diallel F1 and six F2 crosses: P 10-3/2 x P-2, P 10-3/2 x JK 48, P 10-3/2 x FO, P-2 x JK 48, P-2 x FO and YK 48 x FO.

Parents and their crosses were sown in polyethylene covered seedbeds on 11.04.2008 and seedlings were transplanted on 2.06.2008. The trial was set up on diluvial-colluvial soil.

Space between rows was 45 cm, with protective raw at the beginning and end of each replication. Space within the row differed depending on the type of the parent, i.e. cross. For oriental parents it was 15 cm, for FO 25 cm, for combinations with only oriental varieties 15 cm and for those which included FO it was 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.

Manifestation of quantitative characters greatly depends on the effect of environmental factors. Thus, in 2008, during tobacco growth in field (May - September), the mean monthly temperature was 19.91^{0}C and the total amount of precipitation 235.44 mm.

The following morphological characters were subject of analyses: length, width and area of the middle belt leaf. The 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 from middle primings, and in F2 200 leaves were measured from each replication, i.e. 800 leaves in the whole trial.

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

Data obtained for each character by combinations for F1 and F2 generations were subject of variational-statistical analysis.

Type of inheritance was estimated according to the test-significance of the mean values of F1 and F2 in relation to the parental average (Borojevic , 1981).

Genetic components needed to compose the graphs for F1 were estimated by the methods of Jinks(1954) and Hayman (1963), and for F2 by the methods of MatherandJinks (1977).

Graphical analysis (regression analysis) was made by the methods of Mather and Jinks (1974). 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. Here, cross-section of the regression line with Wr-ordinate is very important, as well as the position of dispersion points on the diagram along the regression line. Points of the dispersion diagram are always within the limiting parabola ($\overline{W_R}^2 = \overline{V_R} \cdot Vp$), and the interallelic interaction depends on the quadrant in which they are placed. In case of absence of interallelic interaction, the regression line always equals to 1 (b=1). The cases where the regression coefficient "b" is significantly different from 1 and insignificantly different from 0, indicate the presence of interallelic interaction or epistatsis.

Cross-section of the expected regression line with Wr-ordinate in the origin is marked with "a" in the equation which denotes the direction of the line (y = a + bx) and it is an indication of the level of dominance. When D is higher than H1, and "a" has a positive value, the expected regression line intersects the Wr-ordinate above the origin, which denotes partial dominance. If D and H1 have an equal value, "a" equals 0 and the expected regression line cuts the origin, it is an indication of full dominance. When D is lower than H1, "a" has negative value and the expected regression line intersects the

WR-ordinate below the origin, it denotes a presence of overdominance.

Dispersion points on the diagram along the regression line shows the distribution of dominant and recessive genes in the parents. Points that are closer to the origin present the parents with a higher number of dominant genes and vice-versa, points on the opposite side of the origin present the parents with higher number of recessive genes. The completely dominant parents are positioned on the lowest part of the expected regression line, closest to the origin where it intersects the lower part of the limiting parabola. Parents in which recessive genes are predominant are positioned on the upper part of the expected regression line, where it intersects the limiting parabola at the most distant point from the origin.

Estimation of the regression coefficient $\beta = 1$ is made through the regression coefficient (b) and the standard error (Sb), according to Stell and Torrie (1960).

RESULTS AND DISCUSSIONS

Measuring of the characters and estimations of their average values in quantitative genetics are the basic ground for investigations of their inheritance.

Average values obtained for the characters length, width and area of the middle belt leaves and the mode of their inheritance are presented in Table 1. There are significant differences among parental genotypes. The smallest leaves were recorded in P-2 and the largest in FO. All modes of inheritance are present, but the intermediate is prevailing. Positive heterotic effect in F1 was recorded in P 10-3/2 x P-2 and P-2 x JK 48.

In further genetic invetigations, data presented in Table 1 will give innitial material for realization of biometrical methods and creation of regression graphs from which a more complete picture in the genetic system of inheritance will be obtained.

Table 1. Type of inheritance of leaf size in F1 and F2 generations

Parents and hybrids	Middle belt leaf length (cm)		Middle belt leaf width (cm)		Middle belt leaf area (cm²)	
	F1	F2	F1	F2	F1	F2
P 10-3/2	26,5	26,5	12,7	12,7	213,84	213,84
P-2	19,5	19,5	11,0	11,0	136,29	136,29
YK 48	21,8	21,8	11,9	11,9	164,83	164,83
FO	38,3	38,3	23,6	23,6	574,32	574,32
P10-3/2 x P-2	**29,4 +h**	25,2 pd	**15,5 +h**	11,4 pd	**289.55 +h**	182,54 i
P10-3/2 x YK 48	24,5 i	23,3 pd	12,3 i	11,8 -d	191,48 i	174,70 pd
P10-3/2 x FO	33,2 i	32,8 i	19,2 i	15,3 pd	405,03 i	318,87 pd
P-2 x YK 48	**25,7 +h**	21,9 +d	**14,8 +h**	11,8 +d	**241,68 +h**	164,20 +d
P-2 x FO	34,1 pd	29,8 i	20,4 pd	17.7 i	442,01 pd	335,15 i
YK 48 x FO	32,0 i	31.6 i	18,3 i	16.9 i	372,09 i	339,33 i

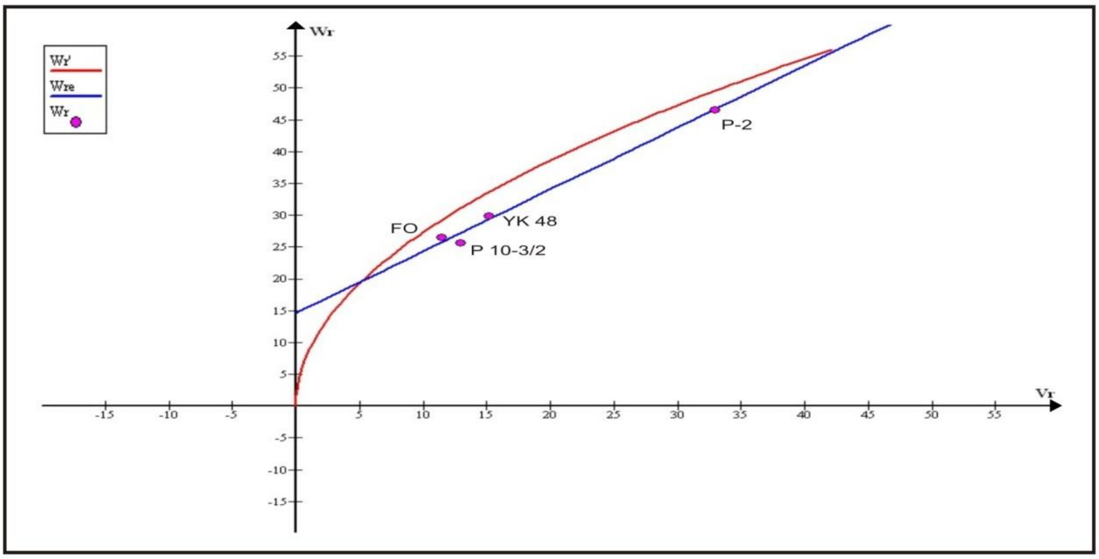
The graph of regression (VR, WR) for middle belt leaf length in F1 and F2 almost equals to 1 and differs significantly from 0, which indicates absence of interallelic interaction. The expected regression line is close to the limiting parabola (especially for F2 generation), which indicates predominance 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.

The position of the varieties FO, P 10-3/2 and YK 48 in the coordinate system shows significantly higher number of dominant than recessive genes in F1 generation (Fig.1). 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.

From the graphic analysis of F2 generation (Graph 2), the position of FO and P 10-3/2 indicates that dominant genes prevail, whereas in YK 48 and P-2 additive genes prevail in inheritance of this character.

Values obtained in Graphs 1 and 2 are also presented in Table 2.

Graph 1- Graphic presentation of the inheritance of leaf length in F1 generation



Graph 2- Graphic presentation of the inheritance of leaf length in F2 generation

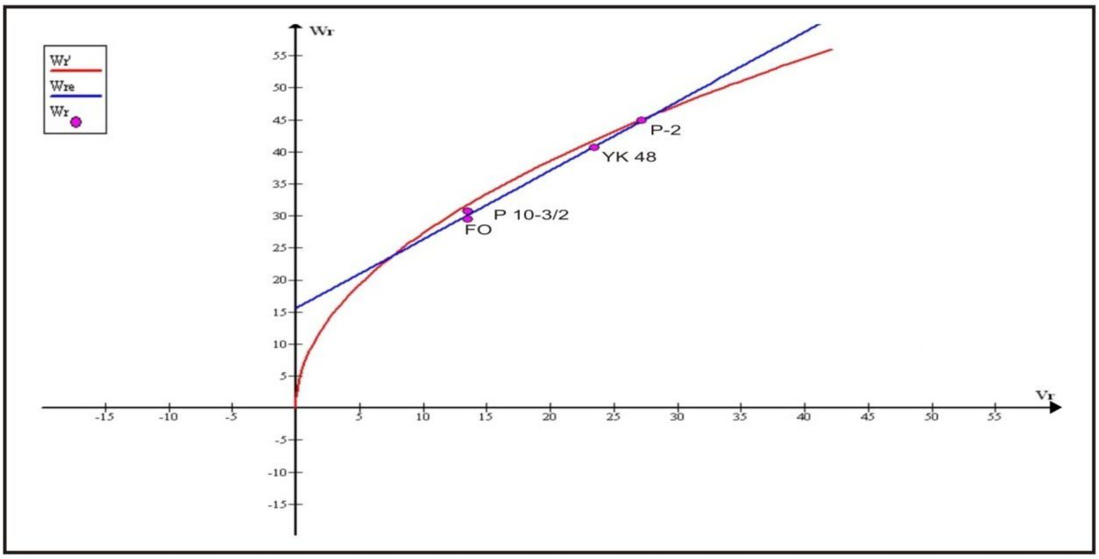


Table 2. The values for graphic presentation of inheritance for leaf length in F1 and F2 generations (Graph 1 and 2)

Parents	Generations	Coordinate System					
		Limiting parabola		Expected regression line		Distribuition points in the diagram	
		VR (x)	WR' (y)	VR (x)	WRE (y)	VR (x)	WR (y)
1. P 10-3/2	F1	13.01	31.03	13.01	27.12	13.01	25.65
2. P-2		32.93	49.55	32.93	46.62	32.93	46.61
3. YK 48		14.92	33.52	14.92	29.14	14.92	29.89
4. FO		11.43	29.19	11.43	25.72	11.43	26.56
Vp=74.56	Vm=14.57	a=1.726	b=0.972				
1. P 10-3/2	F2	13.49	31.77	13.49	30.10	13.49	30.78
2. P-2		27.14	44.99	27.14	44.82	27.14	44.91
3. YK 48		23.42	41.81	23.42	40.83	23.42	40.72
4. FO		13.52	31.75	13.52	30.13	13.52	29.49
Vp=74.56	Vm=18.22	a=1.824	b=1.078				

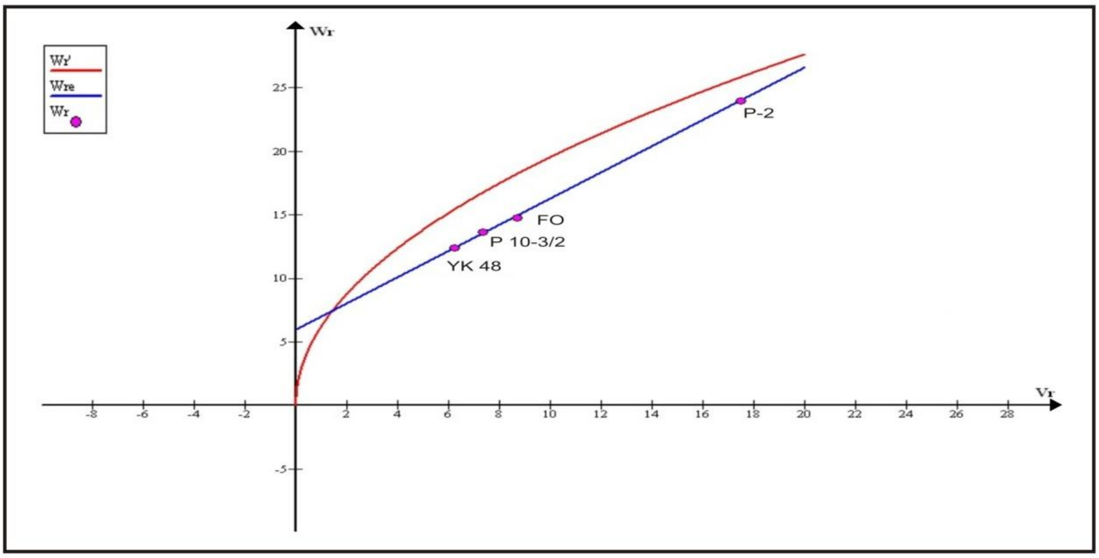
The regression graphs for the caharacter **middlebeltleaf width** in both generations has coefficient of regresionalmost equal to 1, and the position of regression line is very close to the limiting parabola (especially that of F2 generation). It denotes absence of interallelic interaction and dominance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

Distribution of points for F1 generation (Graph 3) shows that P 10-3/2 is closest to the point where parabola intersects the regression line on the side of ordinate. Accordingly, this variety has mostly dominant genes and neglectable number of recessive genes in inheritance of this character. YK 48, as well as P 10-3/2 and FO are positioned on the opposite side, which reveals presence of higher number of additive then dominant genes, indicating that additive gene effect prevails in inheritance of this character.

Distribution of points along the expected regression line for F2 (Graph 4) shows the distance of parents in relation to this character. The sequence of varieties is not identical to that of F1. Varieties YK 48, P 10-3/2 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.

Values of Graphs 3 and 4 are presented in Table 3.

Graph 3- Graphic presentation of the inheritance of leaf width in F1 generation



Graph 4- Graphic presentation of the inheritance of leaf width in F2 generation

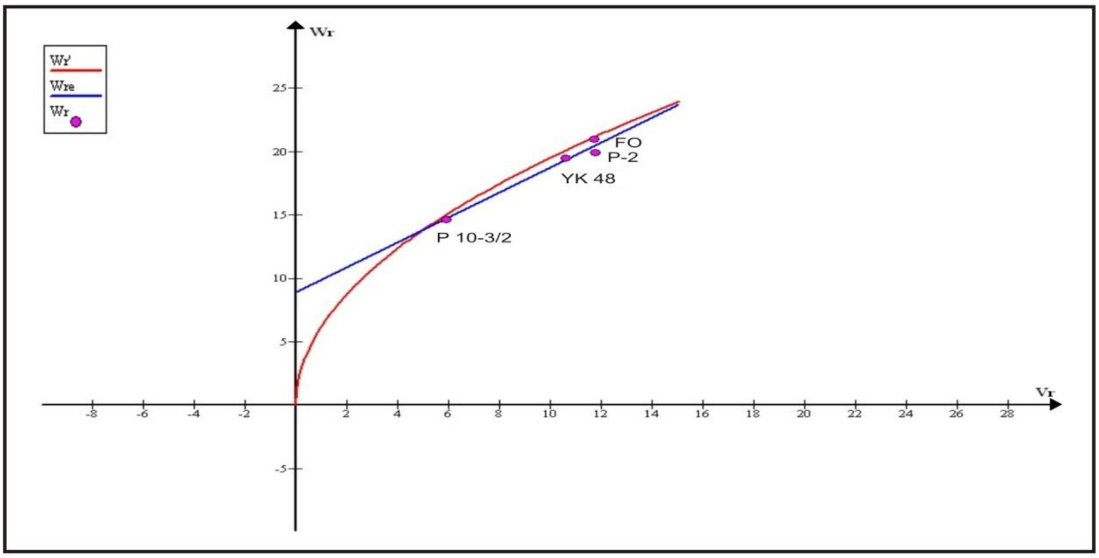


Table 3. The values for graphic presentation of inheritance for leaf width in F1 and F2 generations (Graph 3 and 4)

Parents	Generations	Coordinate System					
		Limiting parabola		Expected regression line		Distribuition points in the diagram	
		VR (x)	WR' (y)	VR (x)	WRE (y)	VR (x)	WR (y)
1. P10-3/2	F1	7.33	16.81	7.33	13.48	7.33	13.62
2. P-2		17.47	25.81	17.47	23.97	17.47	23.99
3. YK 48		6.19	15.41	6.19	12.39	6.19	12.41
4. FO		8.7	18.21	8.7	14.91	8.7	14.76
Vp=38.14	Vm=7.54	a=1.525	b=1.032				
1. P 10-3/2	F2	6.01	14.97	6.01	14.68	6.01	14.70
2. P-2		11.74	21.16	11.74	20.49	11.74	20.97
3. YK 48		10.59	20.11	10.59	19.37	10.59	19.51
4. FO		11.78	21.20	11.78	20.53	11.78	19.95
Vp=38.14	Vm=8.49	a=1.776	b=0.993				

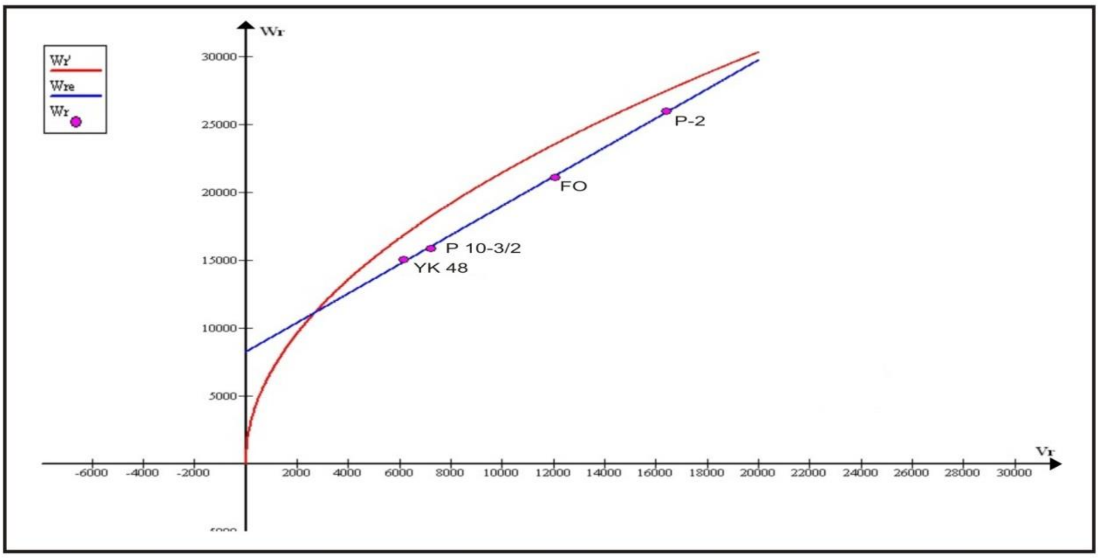
The coefficient of the regression graph for **middle belt leaf area** in F1 and F2 is almost equal to 1 and significantly different from 0, which indicates the absence of interallelic interaction. The expected regression line is close to the limiting parabola (especially the one for F2 generation) which 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 partially dominant type of inheritance. Distribution of points in the diagram gives genetic picture of parental genotypes for the character investigated.

The position of YK 48 and P10-3/2 in the coordinate system for F1 generation shows the presence of significantly higher number of dominant genes over the recessive ones. 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 indicates 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 Graph 5.

From the graphic analysis of F2 generation presented in Graph 6 it can be concluded that in P 10-3/2 dominant gene effect prevails, in YK 48 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 obtained in Graph 5 and 6 are presented in Table 4.

Graph 5- Graphic presentation of the inheritance of leaf area in F1 generation



Graph 6- Graphic presentation of the inheritance of leaf area in F2 generation

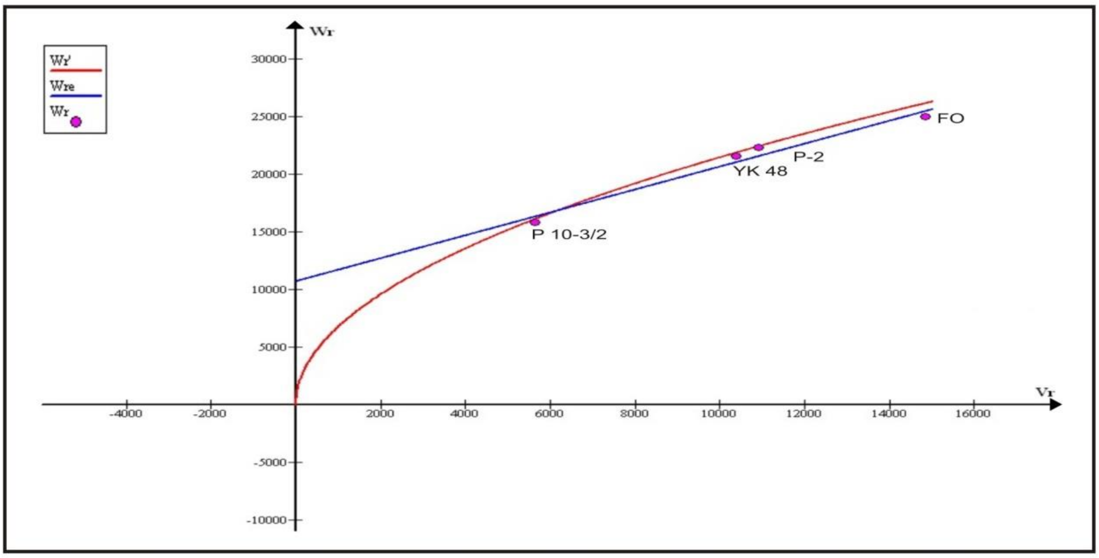


Table 4. The values for graphic presentation of inheritance of leaf area in F1 and F2 generations (Graph 5 and 6)

Parents	Generations	Coordinate System					
		Limiting parabola		Expected regression line		Distribuition points in the diagram	
		VR (x)	WR' (y)	VR (x)	WRE (y)	VR (x)	WR (y)
1. P10-3/2	F1	7236.05	18253.98	7236.05	16032.87	7236.05	15859.12
2. P-2		16389.31	27472.19	16389.31	25884.21	16389.31	25978.63
3. YK 48		6143.14	16819.32	6143.14	14857.05	6143.14	15068.09
4. FO		12068.57	23574.41	12068.57	21234.21	12068.57	21103.11
Vp=46049.60 Vm=8718.11 a=1.864 b=1.076							
1. P10-3/2	F2	5638.07	16113.20	5638.07	16322.13	5638.07	15802.45
2. P-2		10899.94	22403.97	10899.94	21627.10	10899.94	22340.25
3. YK 48		10390.05	21873.90	10390.05	21113.00	10390.05	21553.19
4. FO		14859.20	26158.37	14859.20	25619.26	14859.20	24985.34
Vp=46049.60 Vm=9862.29 a=2.026 b=1.008							

CONCLUSIONS

- Parental genotypes are homogenous, with significant differences among them.
- The inheritance of leaf size in F1 and F2 progenies differs, but the most represented type is intermediate inheritance. Positive heterosis in F1 progeny was observed in P 10-3/2 x P-2 and in P-2 x YK 48.
- All 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 line differs significantly from 1, which denotes absence of interallelic interaction. The patterns of distribution points along the regrssion line of the diagram reveal prevalence of dominant gene effect in P 10-3/2 for inheritance of length, width and area of the middle belt leaves. In P-2 recesive genes prevail in inheritance of the above characters. In YK 48 has both dominant and additive genes, with small prevalence of one over the other, depending on the character or on generation. The semi-oriental FO is governed mostly by dominant genes in inheritance of length and width and recesive genes in inheritance of area of the middle belt leaves.

REFERENCES

1. Borojević S., 1981. Principi i metode oplemenjivanja bilja. Ċirpanov, Novi Sad.
2. Butorac J., Vasilj Đ., Kozumplik V., Beljo J.,1999. Quantitative parameters of some Burley tobacco traits. ROSTLINNÁ VÝROBA, 45, (4), 149-156.
3. Dobhal V. K., Nageswara RaoC.R., 1988. Variability and character associations for certain economic traits in hookah and chewing tobacco (Nicotiana rustica L.). Tob. Res., 14-2, 88-97.
4. Hayman B.I., 1963. Models in quantitative genetics. Statis. Gen. and Pl. Breed. Nat. Acad. of Sci. Publ.
5. Ibrahim H.A., AvratovscukovaN., 1982. Diallel crosses among flue-cured varieties of tobacco. Bul. Spec. CORESTA, Simposium Winston-Salem, 77.
6. Jinks J.L., 1954. The analysis of continuous variation in diallel cross of Nicotiana rustica varieties. Genetics, 39.
7. Jung S.H., Hwang J.K., Son S.H., 1982. The analysis of inheritance of quantitative characters with oriental tobacco varieties (Nicotiana tabacum L.) in diallel cross. 2. Gene distribution and analysis of variance for each character in F1 generation. J. Korean Soc. Tob. Sci., 4-1, 15-20.
8. Lee J.D., Chang K.Y., 1984. Heterosis and combining ability in F1 hybrids of Korea local and oriental tobacco varieties (Nicotiana tabacum). J. Korean Soc. Tob. Sci., 6-1, 3-11.
9. Mather K., JinksJ.L., 1974. Biometrical genetics. Champan and Hall, London.
10. Mather K., JinksJ.L., 1977. Introduction to biometrical genetics. Champan and Hall, London.
11. Stell R.G.D., TorrieJ.H., 1960. Principles and Procedures of Statistics. McGraw Hill Book Co., New York.