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TOMATO (*Lycopersicon esculentum* Mill.) BREEDING FOR YIELD

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Abstract

Inheritance of yield has been researched for 12 hybrids originating from diallel crossing of six inbreed lines of tomato. The inheritance mode of fruit yield in tomato has been determined by the mean generation analysis. Eleven hybrids showed significant reaction of additive genes. Six crossing combinations showed interaction dominant x dominant genes, in 6 hybrid epistasis additive x dominant genes; and in 4 hybrids additive x additive genes. Most significant interactions (most often for researched genotypes) were dominant x dominant genes, and within this combination duplicate type of epistasis. This type of gene interaction has unfavourable effect to yield, and in process of selection for better yield it causes the decrease of total yield.

Key words: tomato, inheritance, yield, mean generation analysis

Introduction

Yield is one of the most important selection program parameters. The aim of this paper is to determine and explain the differences in the yield of five tomato hybrids. In this way, it is possible to define which gene effects are more important for the yield expression. The obtained results would suggest that there is possibility for applying such research in plant breeding, which is aimed at selecting high-yield hybrids.

The average fruit weight per plant represent a yield component. In their research, Das et al.1988 pointed out the following facts: 10-20 genes affected the fruit weight, the additive variance was prominent in fruit weight inheritance, there was partial dominance in light fruit weight, and there was no interallele interaction. Conti et al. (1984) established that were significant epistatic gene effects on fruit weight inheritance. Singh and Singh (1984) achieved similar results in their researches. They established the fact apart from additive and dominance gene effects there were also epistatic ones. As for the inheritance of this characteristic, Singh and Singh (1985) concluded the following: additive genes prevailed over dominance ones in inheriting fruit weight, additive gene values were higher than dominance gene values, and (j) and (l) epistatic types were established. Dhaliwal and Nandpuri (1988) found out that one out of the three investigated combinations did not suggest the existence of the digenic interaction in inheriting this feature, but the other two combinations had additive x dominance gene effects. Applying the 6-parameter model, proved additive activity epistatic gene effects on fruit weight and earliness as their features.

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Material and method

Six parental tomato genotypes that differed in fruit yield have been selected. Their crossing has been performed by applying the method of diallele crossing. Four of them (D-150, S-49, S-35 and H-52) were pure lines, one was a cultivar (SP-109) and one was a population (Kg-ž). All of them belonged to the collection of tomato genotypes of the Institute for Vegetable Crops in Smederevska Palanka. The trial was set in 2005 by applying the method of random block system in three replications. The inheritance mode of fruit shape was determined on the basis of the mean generation of crossing the two parents (P1, P2, F1, F2, BC1, and BC2) employing the additive - dominance model (a three-parameter model). Gene effects were marked with the following symbols: mean value (m); additive gene effects (d); dominance gene effects (h); additive x additive (i); additive x dominance (j); dominance x dominance (l). On the basis of testing the adequacy of this model, it was concluded that there was either presence or absence of epistatic gene effects. The adequacy of the additive – dominance model was tested in two ways: by the general test (χ2-test). Applying the six-parameter model (Mather and Jinks, 1982), the estimation of the values of epistatic gene effects was performed. This investigation dealt with digenic epistasis between additive, dominance, and additive x dominance genes.

Results

Variability of the average yield values has been expressed by variation coefficient (V), which was below 10. Variation coefficient in F_1 generation has been moving from 1,84% (H-52 x SP-109) to 6,32% (S-49 x H-52) and has been lower than for parents. In F_2 generation the variation coefficient has been from 7,54% (S-35 x H-52) to 18,91 % (D-150 x S-49) (Tab 1). Common χ^2-test proved that model with three parameters is adequate only for hybrids D-150 x SP-109 and S-49 x H-52. For crossings where no adequate three parameter mode has been established, the model with six parameters has been used in order to evaluate the gene effect. Combination D-150 x SP-109 had significant values of additive and dominant gene effect. The evaluated values of dominant genes have been higher than additive genes, so the dominant genes could be crucial in inheriting the yield component within this combination. Values of additive and dominant gene effect in hybrid S-49 x H-52 have been significant and values of dominant gene effect have been higher than additive. Values of χ^2-test for both hybrids have been compatible and exclude the presence of non allele interactions (epystasis). Testing of other hybrids by using three parameters model proved the epistatic gene reaction. Based on significant χ^2-tests, the presence of two significant genes, the presence of two-gene epistasis has been recorded (Table 2).

Evaluated genetic parameters for these crossings have been calculated by analysing average generation by using six parameters model. Analysing the model of genetic parameters by using the model with six parameters only two-gene epystasis have been found (between additive, dominant and additive and additive x dominant genes – Table 3).

No significant value of epystatic gene effect has been found for hybrid D-150 x S-49, although χ^2 and scaling tests pointed to its presence. It is probable that these were higher gene interaction levels, while this method determinates only two gene epystasis. Heritability level in higher sense, within this hybrid group was from 87,52% (D-150 x Kg-ž) to 97, 56% (D-150 x S-49), which were high values of heritability (Table 2).

Hybrids with common parent S-49 had genetic parameters only for crossing S-49 x SP-109. Additive gene effects and epystasis effect dominant x dominant genes had significant values. Hybrids S-35 x SP-109 had significant interaction dominant x dominant but with opposite

pre-sign than dominant gene values, which proves the dominant type of epystasis. Crossing combination H-52 x Kg-ž had duplicate type of epistasis (Table 3).

Discussion

From 12 researched hybrids including hybrids D-150 x SP-109 and S-49 x H-52, za koje je inheritance has been found by using model with three parameters, the significant level of hybrids has been found only in 7 hybrids. All crossing combinations had additive and dominant gene effect, where dominant values were higher than estimated values of additive genes, except for combination Kg-ž x SP-109 where established values of dominant genes have been negative. Dominant genes usually dominate over additive, which is compatible with Sonone et al. (1986) and Singh and Singh (1989), results.

In our research, the significant level of additive and dominant level has been proved for six hybrids. In S-35 x Sp-109 hybrid, dominant genes values have been higher than additive, while in hybrid Kg-ž x SP-109 value of additive genes have been higher than values of dominant genes. These conclusions are compatible with Singh et al (1988) who proved that both gene effects have significant values and that both gene effects impact the yield expression.

Significant level of additive genes has been found in five hybrids. These results are compatible with many research results proving that additive genes are dominant in yield inheriting: Kale et al. (1988), Sonone et al. (1986), Crill et al. (1987), Das et al. (1988), Singh and Singh (1993), Hegazi et al. (1995).

If genotypes were to be classified according to epiystasys expression frequency, in 12 researched hybrids the most common was (l) type of epistasys (6 times) and (j) type (6 times) and they could be the most significant which is compatible with Singh and Singh (1985), results who proved that (j) and (l) epystasis types are more significant than (i) epistasis in inheriting the yield impact per plant. Important notification in our research is that large number of hybrids had duplicate epistasis. In all combinations with significant values (h) and (l) this type of epistasis has been found, which proves that this type of interactions in stable in yield inheriting. This type of epistasis impacts the lower expression of the researched trait. Practically, this is a negative appearance in tomato breeding for increased yield. Our results have been compatible with Dhaliwal and Nandpuri (1988) who analysed three hybrid combinations with expended two-gene model and found duplicate type of epistasis. They considered that selection in the first generations after crossing would be slow, while in later generations much faster.

Results of interactive gene reaction have not been completely compatible with Singh et al. (1989). Our research proved interaction additive x dominant (j) type of epistasis in three hybrids (S-35 x Kg-ž, S-35 x SP-109 i Kg-ž x SP-109). These hybrids have been connected with the same mother or father components, which lead to a conclusion that this type of epistasic effect could be fixed by selection of parents. These hybrids have had second type of epistasis (duplicate type between dominant and dominant x dominant genes), so they have been the most important in analysing this trait.

Conclusion

From 12 researched hybrids, 11 showed significant reaction of additive genes; in 7 significant reaction of dominant genes. In 6 crossing combinations the interaction dominant x dominant genes has been found in 6, in 6 hybrids epistasis additive x dominant genes; and in 4 hybrids

additive x additive genes. As the most significant interactions the most common for researched genotypes have been dominant x dominant genes and within this combination duplicate type of epistasis. This type of interactive gene effect has unfavourable impact on yield in selection process with the aim to increase yield, since it effects the decrease of total yield.

Acknowledgements

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Table 1: The average value and variability factors for yield per tomato plant (g)

Genotypes		x	± s_x	σ	V	Genotypes		x	± s_x	σ	V
D-150		**907,4**	**36,77**	**63,69**	7,02	S-49 x KG-ž	BC_2	2277,7	25,02	43,34	1,90
D-150 x S-49	F_1	1839,9	27,29	47,27	2,57	S-49 x SP- 109	F_1	1073,5	17,42	30,17	2,81
	F_2	1847,2	201,7	349,4	18,91		F_2	1685,0	105,9	183,50	10,89
	BC_1	1778,0	157,1	272,2	15,31		BC_1	1872,2	129,9	225,08	12,02
	BC_2	1952,9	34,74	60,20	3,08		BC_2	1418,5	81,34	140,9	9,93
D-150 x S-35	F_1	1768,4	29,70	51,45	2,91	**S-35**		**1572,3**	**40,14**	**69,52**	**4,42**
	F_2	1463,6	124,38	215,44	14,72	S-35 x H-52	F1	1383,8	18,34	31,78	2,29
	BC_1	1701,4	71,22	123,36	7,25		F_2	1254,0	54,56	94,49	7,54
	BC_2	1795,4	124,59	215,80	12,02		BC_1	1332,8	84,49	146,34	10,98
D-150 x H-52	F_1	1679,8	29,16	47,05	2,80		BC_2	1484,7	87,58	151,69	10,22
	F_2	1583,5	141,56	245,2	15,48	S-35 x Kg-ž	F_1	1672,2	21,39	37,05	2,22
	BC_1	1779,3	63,55	110,08	6,19		F_2	1364,0	77,97	135,06	9,90
	BC_2	1255,7	36,37	63,00	5,02		BC_1	1303,6	78,49	135,15	10,43
D-150 x Kg-ž	F_1	2090,5	45,62	79,03	3,78		BC_2	1213,3	53,90	93,36	7,69
	F_2	1494,0	112,21	194,36	13,01	S-35 x SP-109	F_1	1568,5	94,66	163,97	10,45
	BC_1	1800,8	10,91	18,89	1,05		F_2	1191,2	65,41	113,3	9,45
	BC_2	1783,6	9,99	16,54	0,93		BC_1	1456,7	102,71	177,91	12,21
D-150 x SP-109	F_1	1585,3	39,56	68,52	4,32		BC_2	1624,8	29,59	51,24	3,15
	F_2	1204,2	123,27	213,51	17,73	**H-52**		**1122,3**	**36,60**	**63,40**	**5,65**
	BC_1	1188,7	33,27	57,45	4,83	H-52 x Kg-ž	F_1	1698,7	21,39	37,05	2,18
	BC_2	1010,0	62,71	108,61	10,73		F_2	1738,6	77,97	135,06	7,78
S-49		**1580,3**	**38,62**	**66,88**	4,23		BC_1	1682,8	78,49	135,95	8,08
S-49 x S-35	F_1	2195,1	45,48	78,77	3,59		BC_2	1213,3	53,9	93,36	7,69
	F_2	1821,9	104,25	180,57	9,91	H-52 x SP-109	F_1	1471,6	15,62	27,05	1,84
	BC_1	2107,2	25,68	44,48	8,11		F_2	1596,4	65,21	112,95	7,08
	BC_2	2190,1	198,29	341,46	16,20		BC_1	1780,3	32,89	56,96	3,20
S-49 x H-52	F_1	2549,6	92,97	161,02	6,32		BC_2	1087,9	56,84	98,46	9,05
	F_2	2048,7	218,82	368,62	17,99	**Kg-ž**		**1528,6**	**35,87**	**62,14**	**4,07**
	BC_1	1937,8	172,7	299,10	15,44	KG-ž x SP-109	F_1	16,54	29,74	51,51	3,11
	BC_2	1776,8	48,33	83,72	4,71		F_2	1534,0	99,93	173,08	11,28
S-49 x Kg-ž	F_1	1987,7	42,82	74,17	3,73		BC_1	1303,7	14,37	250,06	19,18
	F2	1878,1	85,21	147,58	7,86		BC_2	1078,3	34,22	59,28	5,50
	BC_1	1732,8	27,48	47,60	8,75	**SP-109**		**730,5**	**15,84**	**27,45**	**3,76**

$LSD_{(0,05)}$ 77,15

(0,01) 109,76

Table 2: Genetic analysis of gene effect per plant using model with three parameters

Genotypes	(m)	$t_{(m)}$	(d)	$t_{(d)}$	(h)	$t_{(h)}$	χ^2	h^2
D-150 x S-49	1311,43	51,76	-310,34	12,31	601,25	15,61	67,16**	97,58
D-150 x S-35	1264,23	46,65	-311,77	11,46	534,86	13,05	24,64**	91,99
D-150 x H-52	1021,88	40,76	-45,28	1,82	665,39	17,28	58,53**	93,95
D-150 x Kg-z	1291,76	57,03	-62,22	4,92	970,24	21,44	150,10**	87,52
D-150 x SP-109	798,05**	48,27	70,25**	4,32	723,58**	17,21	6,63	93,31
S-49 x H-52	1347,27**	51,33	231,87**	8,88	1145,67**	4,30	1,13	91,42
S-49 x SP-109	1179,91	58,40	440,07	21,73	-84,74	3,10	70,83**	93,96
S-35 x H-52	1337,97	50,29	210,37	7,71	41,27	1,25	10,75**	65,71
S-35 x SP-109	1131,99	52,67	379,15	17,78	963,04	17,12	122,81**	80,56
H-52 x Kg-z	1302,58	23,44	-232,88	9,43	300,34	10,56	173,34**	85,32
H-52 x SP-109	1048,43	57,63	315,361	17,28	466,91	18,67	113,34**	87,18
Kg-ž x SP-109	1125,42	61,02	399,78	21,64	495,68	14,70	14,86**	92,33
$t_{0,05}$		2,228		2,776		2,179		
$_{0,01}$		3,169		4,604		3,055		

Table 3 : Genetic analysis of gene effect of yield per plant by using a model with six parameters

parameters / hybrids	**[m]**	$t_{(m)}$	**[d]**	$t_{(d)}$	**[h]**	$t_{(h)}$	**[i]**	$t_{(i)}$	**[j]**	$t_{(j)}$	**[l]**	$t_{(l)}$
D-150 x S-49	1168,5	1,28	-336,4**	12,59	2043,5	1,05	75,5	0,08	323,6	1,99	-1371,8	1,45
D-150 x S-35	100,8	0,69	-332,6**	11,95	3784,0 *	2,78	1139,1	1,92	475,8	1,59	-2116,4 *	2,69
D-150 x H-52	1278,8	2,17	-107,4 *	4,02	817,3	0,66	-263,1	0,45	1261,9**	7,47	-416,5	0,64
D-150 x KG-ž	2587,0	0,06	-313,3**	12,12	3807,0**	4,21	1191,5 *	2,66	658,7**	11,11	-1744,0**	3,77
S-49 x SP-109	1314,8 *	2,46	424,9**	20,74	1723,4	1,33	-159,4	0,30	57,5	0,17	-1964,3 *	2,52
S-35 x H-52	728,7	1,99	223,9**	8,05	1448,0	1,49	618,8	1,69	-732,4 *	2,54	-793,3	1,29
S-35 x SP-109	-246,8	0,69	420,9**	19,23	3936,3**	4,50	1398,1**	3,91	-1178,1**	5,27	-2121,3 *	3,78
H-52 x KG-ž	2540,4**	8,67	21,871	0,84	-3838,0**	4,68	-990,0 *	3,39	-4509,9**	17,31	2969,0**	29,69
H-52 x SP-109	1575,8**	5,03	195,9**	9,56	186,9	0,27	-649,5	2,08	992,9**	7,12	-290,9	0,74
KG-ž x SP-109	2501,6**	5,05	399,1**	21,39	-3023,0 *	2,55	-1371,9 *	2,77	-347,34	1,18	2176,3**	3,06
$t_{0,05}$		2,228		2,776		2,179		2,447		2,306		2,179
$t_{0,01}$		3,169		4,604		3,055		3,707		3,350		3,055

СЕЛЕКЦИЈА НА ПРИНОС ПАРАДАЈЗА (*Lycopersicon esculentum Mill.*)

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Резиме

Парадајз спада у једну од напрофитабилнијих повртарских врста. Величина и квалитет приноса, поред раностасности, односно динамике сазревања плодова, дају привредни значај парадајзу. Познавање начина наслеђивања у селекцији ове врсте може да представља умногоме скраћивање времена које је потребно да се селекционише комерцијални хибрид и осигурати ми стабилност у његовој експресији. Наслеђивање приноса испитивано је код 12 хибрида пореклом из диалелног укрштања шест инбред линија парадајза (Д-150, С-49, С-35 и Х-52). Код 11 хибрида се испољило сигнификантно деловање адитивних гена; у 7 сигнификантно деловање доминантних гена на принос плодова парадајза. Код 6 комбинација укрштања утврђена је интеракција доминантни х доминатни гени, у 6 хибрида епистаза адитивни х доминантни гени; и у 4 хибрида адитивни х адитивни гени. Као најзначајније интеракције (најчешће се појављују код испитиваних генотипова), могу се издвојити доминантни х доминантни гени, и у оквиру њих дупликатни тип епистаза. У прктичној селекцији парадајза треба одабрати линије које усливљавају већи број позитивних генетских ефеката у потомству, а који ће у комерцијалним комбинацијама дати перспективне хибриде.

Кључне речи: парадајз, принос, наслеђивање, анализа просека генерација

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