

**INHERITANCE OF EAR YIELD AND ITS COMPONENTS IN SWEET
CORN (*Zea mays L. saccharat*)**

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Srdić J., Z. Pajić, M. Filipović, M.Babić and M. Sečanski (2011):
Inheritance of ear yield and its components in sweet corn (Zea mays L. saccharat). - Genetika, Vol 43, No. 2, 341-348.

Sweet corn is mutation of field corn in which greater accumulation of sugars and water soluble polysaccharides provide specific taste and texture. It is consumed in the milky stage of the endosperm, so the product's quality and its appearance are important as well as ear yield. That is why breeders pay the same attention to these traits in breeding process.

In this paper we analyzed combining ability and mode of inheritance of ear yield and yield components in sweet corn, such as kernel-row number, and ear length, by the use of diallel crosses of six sweet corn inbred lines. ANOVA showed that estimates of general (GCA) and specific (SCA) combining abilities were highly significant ($p < 0.01$) for all observed

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traits. Nonadditive gene effects were more significant in the expression of ear yield and ear length, while additive gene effects were more important for kernel-row number. Analysis of components of genetic variance was in agreement with the results of ANOVA of combining ability. The mode of inheritance of kernel-row number was partial dominance, while overdominance was of greater importance for ear yield, and ear length.

Inbred line L₄ was indicated as the most desirable, among the examined set of inbreds, in the further sweet corn breeding programs, due to its significant GCA effects concerning ear yield and number of kernels per ear, and ear yield performances of the hybrids in which one of the components was this inbred, according to SCA and heterosis estimates.

Key words: diallel analysis, GCA, SCA, sweet corn

INTRODUCTION

Sweet corn differs from field corn by the mutation at the sugary (*Su*) locus on chromosome 4 and so sweet corn has the *su* gene at this locus. This mutation affects the endosperm composition by causing it to accumulate twice as much sugar and eight to ten times more water-soluble polysaccharides, than normal field corn at the milky stage of the endosperm development. This kernel composition provides sweet taste and creamy texture of sweet corn (PAJIĆ *et al.*, 2008).

Breeding of sweet corn has several equally important aims that are directed by the market demands and different mode of consumption than field corn. The ear yield, in sweet corn is not the only and main goal of breeding. Morphological traits of the plant, ear and kernel and chemical composition of the kernel is also very important. Favorable traits for the hybrids that are used in industrial processing are uniformity of ear size, length and shape, proper kernel row configuration, depth, width and color of kernels, as well as quality of the taste (PAJIĆ *et al.*, 2010). Usually yellow kernel types of sweet corn hybrids are more popular for the fresh market consumption. Also nice and healthy appearance of the ear is very important, and the quality of the product such as sweetness, pericarp tenderness and creamy texture of the endosperm are crucial traits for this market.

Studies of the genetic nature and modes of inheritance of traits, especially yield components, are very important in maize breeding. Yield is an important, but very complex trait, whose expression is determined by several major or minor genes, that are influenced by environmental conditions, which additionally mask their action and makes its study more difficult (SRDIĆ *et al.*, 2007).

The method of diallel crosses has been widely used in genetic research to investigate the inheritance of important traits among a set of genotypes (YAN and HUNT, 2002). It was devised especially to investigate combining abilities of the inbred lines for the purpose of identification of superior parents for use in hybrid breeding. Diallel cross analysis has been used most extensively by breeders to obtain information about genetic control of quantitative traits (JINKS and HAYMAN, 1953; WALTERS and MARTON, 1978), identification of heterotic groups and prediction of traits in a new population derived by diallel crosses (HALLAUER and MIRANDA, 1995).

This diallel study was undertaken with the objective to determine genetic nature and inheritance of ear yield and its components in sweet corn, and to evaluate breeding potential of six sweet corn inbred lines of different origin selected and adapted in the midcontinental environment of Serbia.

MATERIALS AND METHODS

For this study six sweet corn inbred lines were chosen. All of them were selected in Maize Research Institute "Zemun Polje", but they originated from different varieties introduced from Mexico (L₁- ZPL 620/121 and L₂- ZPL ZPL 1/12), Iran (L₄- ZPKŠ 8/1-161 and L₅- ZPKŠ 8/1-153), synthetic populations of sweet corn derived in Maize Research Institute (L₃- ZPL 620/121-25), and F₂ population of hybrid Jubilee (L₅- Jub I-5).

Six sweet corn inbred lines were crossed in a diallel fashion without reciprocal combinations [$n(n-1)/2$] (n-number of parental lines), which produced 15 F₁ combinations. The 15 hybrid combinations and 6 parental lines were included in a randomized block design with three replications in three treatments. The treatments were: 1. no irrigation, 2. with irrigation, 3. late sowing. Hybrids and inbreds were sown at the same time in separate plots with two border rows for each plot. The experimental unity was one row for each entry, with 20 plants and density of approximately 50.000 plants/ha. Harvest was done 23-24 days after silking, for each genotype. Ear yield was observed without husk, and for ear length and kernel-row number sample of 10 ears were analyzed.

General (GCA) and specific (SCA) combining abilities were analyzed according to the GRIFFING (1956) mathematical model I, method 2. Components of the genetic variance and heritability in narrow and broad sense were calculated according to JINKS (1954), HAYMAN (1954) and MATHER and JINKS (1971).

RESULTS AND DISCUSSION

The analysis of variance of the diallel crosses showed highly significant estimates ($p < 0.01$) of both GCA and SCA for all observed traits. The non additive gene effects were predominant in the expression of ear yield and ear length, which was indicated by GCA to SCA ratio < 1 (table 1). This value was only in the case ear length- treatment 1 slightly above unity which pointed to the almost the same effect of additive and non additive effects for this trait. Significance of the non additive effects was also found in the research of VOICHITA (2001) both for sweet corn ear yield with or without husk and ear length. On the other hand BORDALLO *et al.* (2005) observed the same significance of the GCA and SCA in the inheritance of the ear yield and ear length in sweet corn. Additive gene effect had greater influence on the kernel row number which is in accordance with the results obtained both on the sweet corn (DUTTA *et al.*, 2004) and standard grain quality corn (SEČANSKI *et al.*, 2005; ŽIVANOVIĆ *et al.*, 2007; BOĆANSKI *et al.*, 2010).

Table 1. ANOVA of combining ability for ear yield, ear length and kernel row number

Sources of Var.	D.F	Mean Square								
		ear yield			ear length			kernel row number		
		Treat. 1	Treat. 2	Treat. 3	Treat. 1	Treat. 2	Treat. 3	Treat. 1	Treat. 2	Treat. 3
GCA	5	8,87**	2,95**	1,28**	3,60**	1,75**	1,96**	18,88**	23,69**	22,22**
SCA	15	14,33**	7,36**	12,64**	3,53**	4,85**	9,98**	0,57**	0,90**	1,36**
Error	40	0,62	0,34	0,27	0,11	0,17	0,08	0,15	0,10	0,12
GCA/SCA		0,62	0,40	0,10	1,02	0,36	0,20	33,34	26,18	16,29

*,** - significant at the 0,05 and 0,01 probability level

The GCA effects of six sweet corn inbred lines for three examined traits are given in the table 2. L₄ is the only inbred line with significant estimates of GCA for ear yield. For ear length two inbreds with significant GCA were found – L₅ and L₆. Also, two inbreds had significant estimates for kernel row number – L₄ and L₅. Following the presumption that parental lines with significant GCA can be used to improve the trait of interest, three inbreds are distinguished – L₄, L₅ and L₆. Out of those three inbreds, line L₄ is probably the most desirable one in sweet corn breeding, because it had highly significant estimates of GCA for ear yield and number of kernels per row.

Table 2. GCA for ear yield, ear length and kernel row number of six sweet corn inbred lines

Inbred lines	Ear yield			Ear length			Kernel row number		
	Treat. 1	Treat. 2	Treat. 3	Treat. 1	Treat. 2	Treat. 3	Treat. 1	Treat. 2	Treat. 3
L ₁	-0,43	-0,56	-0,34	-0,01	0,46*	0,11	-0,50*	-0,97**	-0,88**
L ₂	0,41	0,41	0,22	-1,10**	-0,08	-0,38*	-1,97**	-2,30**	-2,06**
L ₃	-0,93	-0,48	-0,23	-0,42*	-0,74**	-0,52**	-0,58*	-0,19	-0,62**
L ₄	1,95**	1,00**	0,68*	0,32	-0,32	-0,36*	2,40**	2,63**	2,51**
L ₅	-0,55	-0,10	0,02	0,51**	0,31	0,65**	1,15**	1,22**	1,42**
L ₆	-0,45	-0,35	-0,34	0,71**	0,36	0,50**	-0,51*	-0,40*	-0,37**
SE	0,39	0,29	0,26	0,16	0,20	0,14	0,20	0,16	0,17

*,** - absolute estimate two, three times larger than SE

SCA and heterosis estimates were high and significant for ear yield (Tab. 3). Hybrid potential was mostly expressed in this trait, because hybrids yielded 2-3 times more than their parental lines. High and significant estimates of heterosis are

the result of non additive gene action (dominance and epistasis). This was confirmed in both on the sweet corn fresh ear yield (SRDIĆ *et al.*, 2011) and standard grain quality corn yield (SRDIĆ *et al.*, 2007). Those estimates were also high and significant for ear length but not to that extent such as in ear yield (data not shown), which was in accordance with the genetic nature of inheritance of these traits, also presented by ANOVA of combining ability. On the other hand only few hybrid combinations had significant SCA and heterosis estimates for kernel row number, which was caused by the additive gene action in the inheritance of this trait.

Table 3. SCA and heterosis for ear yield of six sweet corn inbred lines

Hybrid combinations	Treatment 1		Treatment 2		Treatment 3	
	SCA	Heterosis	SCA	Heterosis	SCA	Heterosis
L ₂ x L ₁	3,95**	201,26 **	2,11*	146,03 **	1,36*	192,73 **
L ₃ x L ₁	-0,48	70,39	1,21	102,41 **	-0,16	130,78 *
L ₄ x L ₁	3,47**	65,73	1,2	26,91	2,21**	92,54 **
L ₅ x L ₁	-0,53	45,06	0,08	38,67 *	2,00**	99,61 *
L ₆ x L ₁	1,76	132,02 **	1,22	77,89 *	3,04**	227,96 **
L ₃ x L ₂	1,23	134,22 *	2,47**	152,03 **	1,99**	234,6 **
L ₄ x L ₂	3,52**	75,96 *	2,31**	51,86 *	3,25**	121,48 *
L ₅ x L ₂	2,03*	107,73 **	2,11*	68,10*	2,74**	126,14 *
L ₆ x L ₂	4,11**	257,02 **	2,01*	111,64 *	1,73*	222,58 **
L ₄ x L ₃	1,21	33,84 **	1,43*	30,55	2,50**	99,69 **
L ₅ x L ₃	3,19**	104,38 **	0,75	35,05	2,78**	117,78 **
L ₆ x L ₃	1,23	113,95 *	1,12	77,52	2,66**	260,09 **
L ₅ x L ₄	-0,15	22,46	-0,58	12,27	-1,46*	32,78
L ₆ x L ₄	1,51	38,68	0,88	25,71	1,36*	77,215 **
L ₆ x L ₅	1,15	75,60	0,88	38,95	0,39	66,67 *
SE	0,96	0,71			0,63	

*, ** - absolute estimate two, three times larger than SE

The results of the analysis of components of genetic variance were in accordance with previously obtained results of ANOVA. Estimates of additive component of variance (D) were in almost all cases significant and lower than dominant components (H₁ and H₂) for ear yield and ear length. As expected, additive component for the number of kernels per row was significant and higher than H₁ and H₂. The average degree of dominance was >1 for ear yield and ear length indicating overdominance as the mode of inheritance of these traits. In the inheritance of kernel row number was <1, which pointed that inheritance of this trait is partial dominance.

Heritability in narrow sense was very low for ear yield and ear length, while its estimate was high for kernel row number (table 4). While this parameter is the indicator of the share of additive component in the phenotypic variability such

results were expected due to the fact that additive gene action was predominant only in kernel row number. Heritability in broad sense was high in all the cases showing the high proportion of genetic variability in the whole phenotypic variability. Those results indicated that only for kernel row number breeding process could lead straight forward from the parental lines with more kernel row number towards such hybrids.

Table 4. Components of genetic variance and heritability in narrow and broad sense for ear yield, ear length and kernel row number

	Ear yield			Ear length			Kernel row number		
	Treat. 1	Treat. 2	Treat. 3	Treat. 1	Treat. 2	Treat. 3	Treat. 1	Treat. 2	Treat. 3
D	4,549**	0,84	3,136**	4,549**	0,84	3,136**	11,636**	13,120**	15,569**
$\sqrt{H_{H_1}} / D$	10,036**	12,117**	27,462**	10,036**	12,117**	27,462**	2,341**	3,590**	4,163**
H ₂	8,652**	11,646**	25,200**	8,652**	11,646**	25,200**	1,506**	2,893**	3,329**
	1,485	3,797	2,959	1,485	3,797	2,959	0,454	0,523	0,517
h ² _{ns}	0,225	0,146	0,034	0,206	0,130	0,058	0,895	0,875	0,838
h ² _{bs}	0,946	0,938	0,970	0,963	0,954	0,987	0,971	0,985	0,980

CONCLUSION

Diallel analysis of six sweet corn inbred lines resulted in following:

Estimates of GCA and SCA were significant for each trait, showing the importance of both additive and non additive gene effect. Based on the higher estimates of the SCA and dominant components of variance (H₁ and H₂), and GCA/SCA ratio lower than unity we found that dominant gene effect played more significant role in the expression of ear yield and ear length in sweet corn. On the other hand additive gene effect was more important for kernel row number. This was validated also by heritability in narrow sense for each trait, were only for the kernel row number estimates of this parameters were high. Estimates of the average degree of dominance revealed overdominance as the mode of inheritance of ear yield and length, while partial dominance of the kernel row number.

Significant GCA effects for the inbred L₄ concerning ear yield and number of kernels per ear, indicted its potential usefulness in sweet corn breeding programs. This was confirmed by the ear yield performances of the hybrids in which one of the components was this inbred, according to SCA and hetrosis estimates.

ACKNOWLEDGMENTS

This study was supported by the Ministry of Education and Science of the Republic of Serbia through the Project TR-31068.

Received, December 22th2010

Accepted, July 05th 2011

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**NASLEĐIVANJE PRINOSA KLIPA I NJEGOVIH KOMPONENTI KOD
KUKURUZA ŠEĆERCA (*Zea mays L. saccharat*)**

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I z v o d

Kukuruz šećerac predstavlja mutaciju kukuruza standardnog kvaliteta zrna, kod koga dolazi do povećanog nakupljanja šećera i u vodi rastvorljivih polisaharda, što njegovom zrnju obezbeđuje specifičan ukus i teksturu. S obzirom da se koristi u mlečnoj fazi razvoja endosperma, kvalitet i izgled klipa i zrna kukuruza šećerca podjednako su važni kao i sam prinos.

U ovom radu proučavane su kombinacione sposobnosti šest samooplodnih linija kukuruza šećerca i način nasleđivanja prinosa klipa i komponenti prinosa, kao što su broj redova zrna i dužina klipa, metodom dialelne analize. Analiza varijanse kombinacionih sposobnosti je pokazala visoko značajne vrednosti ($p < 0.01$) opštih (GCA) i posebnih (PCA) kombinacionih sposobnosti za sve posmatrane osobine. Neadditivno delovanje gena bilo je značajnije za osobine prinos klipa i dužinu klipa, dok je aditivno delovanje gena bilo odlučujuće za ekspresiju broja redova zrna. Analiza komponenti genetičke varijanse bila je u saglasnosti sa rezultatima ANOVA-e kombinacionih sposobnosti. Način nasleđivanja broja redova zrna bila je parcijalna dominacija, dok je za prinos klipa i dužinu klipa to bila superdominacija.

Samooplodna linija L_4 je posmatrajući vrednosti OKS za prinos klipa i broj redova zrna, kao i vrednosti PKS hibridnih kombinacija čija je bila komponenta, ocenjena kao najperspektivnija u daljem procesu oplemenjivanja kukuruza šećerca.

Primljeno 22. XII. 2010.

Odobreno 05. VII. 2011.