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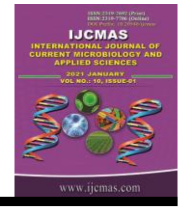

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Combining Ability Effects for De-husked Cob Yield in Baby Corn (*Zea mays* L.)

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A B S T R A C T

The present investigation consisted of a total of 45 hybrids along with 18 parents (15 inbred lines and 3 testers) and 2 checks. A total of 65 entries were evaluated in randomized block design with three replications over three locations (Two during *Kharif*-2019 and one during *Rabi* 2019-20) at Instructional farm, Rajasthan College of Agriculture, Udaipur, Rajasthan (*Kharif*-2019 and *Rabi* 2019-2020) and Agriculture Research Sub Station, Vallabh Nagar, Udaipur, Rajasthan (*Kharif*-2019). Observations were recorded on eighteen characters for combining ability. The inbred lines *viz.*, EIQ-103 (2.297), EIQ-180 (1.534) and EI-1104-1 (1.510) were good general combiners for yield and its contributing characters in all the environments and on pooled analysis. Crosses EI-2177-2 × EI-670-2 (3.25), EI-1104-1 × EI-670-2 (3.41), EI-561-2 × EI-2518-4 (5.08), EI-561-2 × EI-2518-4 (2.15) expressed maximum and significantly (positive) desirable sca effects in E_{1}, E_2, E_3 and on over the environments, respectively for de-husked cob yield.

Introduction

Maize (*Zea mays* L.) 2n=20, is the third most important cereal crop after rice and wheat in the world. By origin, maize is native to South America. Baby corn is a delicious, decorative and nutritious vegetable, without cholesterol. It is a low caloric vegetable which is rich in fibre content. One baby corn can be compared with an ‘egg’ in terms of minerals. Nutritive values of baby corn (per 100 g of edible portion) is Moisture 89.10 %, Carbohydrates 8.20 g, Protein 1.90 g, Calcium 28.00 mg, Phosphorus 86.00 mg, Iron 0.10 mg (Jat *et al.*, 2019).

Worldwide, Thailand is the leading producer and exporter of baby corn. India is emerging as the potential producer of baby corn due to high demand with less cost of production. In India, baby corn is being cultivated in Meghalaya, Western Uttar Pradesh, Haryana, Maharashtra, Karnataka and Andhra Pradesh. Young cob corn has been used by the Chinese as vegetable for generations, and this practice has spread to other Asian countries. It has nutritive value similar to that of non- legume vegetables such as cauliflower, cabbage, tomato, cucumber. This vegetable has versatile use after cooking and for processing as a canned product.

India is emerging as one of the potential baby corn producing country due to low cost of production and high demand within the country. There is a great potential to earn foreign exchange through export of fresh/canned baby corn and its processed products. Another important point is that baby corn is a safe edible vegetable as it is almost free from residual effects of pesticides as the young cob on plant is wrapped with husk and well protected from insect attack and pathogens.

Baby corn has a short growing period (60-75 days), so that a farmer can grow four or more crops per year in a piece of land under tropical climatic conditions. It has a wide range of adaptation and does not need intensive practices for cultivation. The benefit of reaping with baby corn is that even after its harvest, the total herbage of maize plant can be utilized as green fodder. It generates more nutrition per unit area with the shortest crop duration and has the potential of being an excellent cash crop.

Materials and Methods

The present investigation consisted of a total of 45 hybrids along with 18 parents (15 inbred lines and 3 testers) and 2 checks. A total of 65 entries were evaluated in randomized block design with three replications over three locations (Two during *Kharif*-2019 and one during *Rabi* 2019-20) at Instructional farm, Rajasthan College of Agriculture, Udaipur, Rajasthan (*Kharif*-2019 and *Rabi* 2019-2020) and Agriculture Research Sub Station, Vallabh Nagar, Udaipur, Rajasthan (*Kharif*-2019). Observations were recorded on eighteen characters for combining ability. The experimental material comprised of 15 inbred lines *viz.*,EI-2311-4, EI-2449-2, EI-2403, EIQ-103, EIQ-104, EI-1104-1, EI-561-2, EI-2173, EI-2177-2, EI-2509, EI-2518-2, EI-11-3, EIQ-180, EIQ-225, EIQ-235 and 3 testers EI-670-2, EI-2518-4, EI-2156 their 45 F_{1s} and two checks *viz.*, HM-4 and VL Baby Corn-2. These 45 F_{1s} were obtained by crossing 15 inbred lines and 3 testers in line × tester mating design. The combining ability effects for line x tester mating design was performed as per method suggested by Kemthorne (1957) for individual environments as well as over the environments.

Combining ability effects for individual environment

$$\mu = \frac{\sum_{i=1}^{t}\sum_{j=1}^{l}\sum_{k=1}^{r} X_{ijk}}{ltr}$$

$$GCA\ line = \frac{\sum_{i=1}^{t}\sum_{k=1}^{r} X_{ijk}}{tr} - \mu$$

$$GCA\ tester = \frac{\sum_{i=1}^{l}\sum_{k=1}^{r} X_{ijk}}{lr} - \mu$$

$$SCA = \frac{\sum_{k=1}^{r} X_{ijk}}{r} - \frac{\sum_{j=1}^{t}\sum_{k=1}^{r} X_{ijk}}{tr} - \frac{\sum_{j=1}^{l}\sum_{k=1}^{r} X_{ijk}}{lr} + \mu$$

Standard error of combining ability effects:

S.E. (GCA line)	=	**$(MSE/rt)^{1/2}$**
S.E. (GCA tester)	=	$(MSE/rl)^{1/2}$
S.E. (SCA)	=	$(MSE/r)^{1/2}$
S.E. (GCA_i - GCA_j) line	=	$(2 \times MSE/rt)^{1/2}$
S.E. (GCA_i - GCA_j) tester	=	$(2 \times MSE/rl)^{1/2}$
S.E. (SCA_{ij} - SCA_{kl})	=	$(2 \times MSE/r)^{1/2}$

Where,		
X_{ijk}	=	Value of hybrid between i^th^ and j^th^ parent in k^th^ replication
t	=	Number of testers
l	=	Number of lines
r	=	Number of replications
MSE	=	Error mean square i.e. $M_{14.}$

Combining ability effects for over the environments

Over the environments general combining ability effects of parents and specific combining ability effects of hybrids were calculated for all the characters same manner as for individual environments except the number of environments was an additional divisor.

$$\mu = \frac{\sum_{m=1}^{s}\sum_{i=1}^{t}\sum_{j=1}^{l}\sum_{k=1}^{r} X_{ijkm}}{sltr}$$

$$GCA\ line = \frac{\sum_{m=1}^{s}\sum_{i=1}^{t}\sum_{k=1}^{r} X_{ijkm}}{str} - \mu$$

$$GCA\ tester = \frac{\sum_{m=1}^{s}\sum_{i=1}^{l}\sum_{k=1}^{r} X_{ijkm}}{slr} - \mu$$

$$SCA = \frac{\sum_{m=1}^{s}\sum_{k=1}^{r} X_{ijkm}}{sr} - \frac{\sum_{m=1}^{s}\sum_{j=1}^{t}\sum_{k=1}^{r} X_{ijkm}}{str} - \frac{\sum_{m=1}^{s}\sum_{j=1}^{l}\sum_{k=1}^{r} X_{ijkm}}{slr} + \mu$$

The effects of individual environments were subtracted from above effects to estimates of the deviation of effects in individual environments from effects of over the environments.

The standard error of effects was worked out as follows:

S.E. (GCA line)	=	$\mathbf{(MSE/rts)^{1/2}}$
S.E. (GCA tester)	=	$(MSE/rls)^{1/2}$
S.E. (SCA)	=	$(MSE/rs)^{1/2}$
S.E. (GCA_i - GCA_j) line	=	$(2 \times MSE/rts)^{1/2}$
S.E. (GCA_i - GCA_j) tester	=	$(2 \times MSE/rls)^{1/2}$
S.E. (SCA_{ij} - SCA_{kl})	=	$(2 \times MSE/rs)^{1/2}$
S.E. (GCA_{ij} – GCA_i) line	=	$[(1+s)\ MSE/rts]^{1/2}$
S.E. (GCA_{ij} – GCA_i) tester	=	$[(1+s)\ MSE/rls]^{1/2}$
S.E. (SCA_{ijk} – SCA_{ij})	=	$[(1+s)\ MSE/rs]^{1/2}$

Where,		
X_{ijkm}	=	Value of hybrid between i^th^ and j^th^ parent in k^th^ replication and m^th^ environment.
t	=	Number of testers
l	=	Number of lines
r	=	Number of replications
s	=	Number of environments
MSE	=	Error mean square i.e. M_{27}.

Results and Discussion

Two lines (EI-1104-1 and EIQ-180) in E_1, Five lines (EI-2403, EIQ-103, EIQ-104, EIQ-180 and EIQ-235) in E_2, four lines (EIQ-103, EI-1104-1, EI-2173 and EI-11-3) in E_3 and three lines (EIQ-103, EI-1104-1 and EIQ-180) on over the environments, exhibited significantly positive gca effects for de-husked cob yield per plant. In E_1, female line EIQ-180 (1.88) showed significantly maximum positive desirable gca effects followed by EI-1104-1 (1.64). In E_2, the female line EIQ-104 (3.06) expressed maximum positive GCA effects followed by EIQ-235 (2.59) and EIQ-103 (2.77). In E_3, the female line EIQ-103 (3.19) exhibited maximum positive GCA effects followed by EI-1104-1 (2.35) and EI-2173 (1.88). On pooled basis, the female line EIQ-103 (2.29) indicated maximum positive gca effects followed by EIQ-180 (1.53) and EI-1104-1 (1.51). None of the male parent in any environment was found with positive significant gca effects for de-husked cob yield per plant.

Table.1 Analysis of variance for combining ability on over the environments

Source of variation	d. f.	Mean squares																	
		Days to first cob silking	Days to last cob silking	Days to first cob picking	Days to last cob picking	Days to first and last cob picking interval	Number of cobs per plant	Husked cob weight	De-husked cob weight	Baby corn cob length	Baby corn cob girth	Husked cob yield per plant	De-husked cob yield per plant	De-husked to husked cob yield ratio per	Plant height	Moisture content	Crude protein content	TSS	Green fodder yield per plant
Replications (r)	2	0.906	79.055	8.718*	10.476**	0.195	0.11	1.133	0.066	0.726	0.229	2.921	1.82	0	56.461	2.322	0.432	0.531	3840.436*
Environments (e)	2	12133.4**	21508.6**	13846.34**	27315.1**	2357.662**	5.763**	2662.071**	101.028**	124.684**	63.322**	59280.7**	2137.058**	0.001**	18373.51**	95.958**	118.104**	0.486	1038739**
Rep. × Env.	4	9.939	23.75	4.088	1.83	1.143	0.01	4.796	0.292	0.07	0.179	9.187	3.043	0	43.654	1.167	0.167	0.413	754.27
Crosses	44	22.967**	29.382	14.521**	11.390**	14.859**	0.117**	71.290**	2.034**	1.948**	0.494**	766.358**	22.093**	0	736.222**	10.102**	2.30**	4.051**	20336.940**
line (l)	14	30.722	33.009	22.379	15.634	20.134	0.189*	134.611*	3.679**	3.465**	0.686	1373.182**	43.456**	0	1892.390**	16.114*	5.530**	7.238*	52330.460**
tester (t)	2	12.458	1.819	2.539	26.859	38.866*	0.02	37.616	0.767	4.472*	0.889	561.505	10.739	0	41.873	1.852	0.638	0.473	10642.8
line × tester	28	19.840**	29.541	11.449**	8.163**	10.507**	0.087**	47.035**	1.303**	1.010**	0.370**	477.578**	12.222**	0	207.735**	7.685**	0.804**	2.712**	5032.628**
Environment × Crosses	88	17.98**	37.808*	15.125**	10.666**	13.173**	0.137**	43.711**	1.330**	1.603**	0.519**	649.470**	21.175**	0.00**	271.695**	8.282**	3.673**	4.457**	20971.170**
Environment × Line effects	28	21.163	57.070*	27.167**	19.554**	22.126**	0.244**	74.234**	2.520**	2.550**	0.857**	941.536*	31.122*	0.00**	629.133**	10.205**	9.498**	8.123**	49034.58**
Environment × tester effects	4	21.582	22.138	21.691	4.408	20.629	0.025	9.518	0.231	2.158	0.26	86.212	4.472	0	38.254	1.918	0.738	3.804	3533.936
Environment × Line × tester effects	56	14.631**	29.296	8.635**	6.669**	8.164**	0.092**	30.891**	0.813**	1.089**	0.368**	543.669**	17.394**	0.000*	109.651**	3.755**	0.971**	2.671**	8184.976**
Error	264	7.849	27.741	2.386	2.092	2.821	0.026	4.908	0.286	0.366	0.146	99.547	4.347	0	42.851	2.119	0.228	0.486	852.714
Total	404	71.716	136.668	75.065	140.224	18.015	0.088	33.724	1.201	1.422	0.579	583.558	20.477	0	259.035	4.787	1.788	1.739	12508.86

*, ** Significant at 5% and 1% level of significance, respectively

One cross (EI-2177-2 × EI-670-2) in E_1, six crosses (EI-2311-4 × EI-2518-4, EI-2403 × EI-2156, EI-1104-1 × EI-670-2, EI-2509 × EI-670-2, EI-2518-2 × EI-2518-4 and EI-11-3 × EI-670-2) in E_2, five crosses (EI-2311-4 × EI-2156, EI-561-2 × EI-2518-4, EI-2173 × EI-670-2, EI-11-3 × EI-2156 and EIQ-235 × EI-670-2) in E_3 and two crosses (EIQ-103 × EI-2156 and EI-561-2 × EI-2518-4) on pooled analysis, showed significantly positive sca effects for de-husked cob yield per plant. Maximum significantly positive sca effects were depicted by cross EI-2177-2 × EI-670-2 (3.25) in E_1. In E_2, cross EI-1104-1 × EI-670-2 (3.41) expressed maximum significantly positive desirable sca effects for this trait followed by EI-11-3 × EI-670-2 (2.59) and EI-2509 × EI-670-2(2.49). In E_3, cross EI-561-2 × EI-2518-4 (5.08) showed maximum significant positive sca effects for this trait followed by EI-2311-4 × EI-2156 (3.38) and EI-2173 × EI-670-2(2.81). On pooled basis, crossEI-561-2 × EI-2518-4 (2.15) indicated maximum significantly positive desirable sca effects followed by EIQ-103 × EI-2156 (1.40). In the present study, combining ability indicated that mean sum of squares due to crosses were significant for all the traits in all the environments as well as over the environments (Table-1). Partitioning of these mean sum of squares into lines, testers and line x tester interaction revealed that the mean sum of squares due to line, tester and line x tester were found to be significant for most of the traits in all the environments as well as in data pooled over environments.

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