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Identification of transgressive segregants among newly derived F₄ inbred maize lines (*Zea mays* L.) for baby corn characteristics

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Abstract

Baby corn is high demand nutritional vegetable in India. Although its demand among consumers and growers was increasing day by day, it is noted that only few available inbreds and hybrids available in both public and private sector with respect to baby corn. Even though the initiation of research programmes for baby corn started in early 1990s, still there is a dearth of population improvement programmes with respect to baby corn in India. In this regard a population improvement programme was initiated by considering two diverse heterotic populations *viz.*, PDM 4441 × PDM 53 (Population A) and HKI 1105 × HKI 323 (Population B) following modified reciprocal recurrent selection. The derived test single cross hybrids were evaluated for baby corn traits.

The inbred lines P11 and P27 were considered as potential transgressive segregants with HKI 1105 and HKI 323 as testers respectively for the traits namely baby corn yield per plant without husk (g), baby corn yield per plant with husk (g) and number of cobs per plant. In population B, with respect to PDM 4441 as tester, line H13 transgressed positively for various important baby corn traits such as baby corn yield per plant without husk (g), baby corn weight per plant with husk (g) and number of cobs per plant. Considering PDM 53 as tester, lines H61 and H94 were regarded as best transgressive segregants for baby corn yield per plant without husk (g), baby corn weight per plant with husk (g) and number of cobs per plant. While the lines H99, H94 and H6 transgressed superiorly in desirable direction with common tester PDM 260-1 for the traits *viz.*, baby corn weight per plant without husk (g), baby corn yield per plant with husk (g) and number of cobs per plant.

Keywords: Newly derived F₄, *Zea mays*, baby corn

Introduction

Maize (*Zea mays* L.), is an important cereal crop belonging to the tribe Maydeae of the grass family Poaceae. It is globally known as the “Queen of Cereals” as it is physiologically more efficient and has higher yield potential compared to other Poaceae family members. It has its origin in Southern Mexico. It is one of the important staple food crops. It is the most versatile photo insensitive crop with high adaptability, hence it is also referred to as a “Miracle crop”. In the world, maize is cultivated in an area of 182 million ha, with a production of 1040 million tonnes and productivity of 5820 kg ha⁻¹. The USA is the largest producer of maize in the world followed by China, Brazil and India contribute nearly 35% of the total production in the world. The USA has the highest productivity of 11.2 t ha⁻¹ which is double the global average of 5.5 t ha⁻¹. In India, it is cultivated in an area of 9.18 million ha with a production of 27.23 million tonnes and productivity of 2965 kg ha⁻¹. Major growing states in India include Karnataka, Andhra Pradesh, Maharashtra, Tamil Nadu, Rajasthan, Uttar Pradesh, Bihar, and Madhya Pradesh accounting for more than 80 percent of total area and production. In Karnataka, it is cultivated in an area of 1.34 million ha with production of 3.73 mt and average productivity is 2777 kg ha⁻¹ (Anon. 2019) [3].

In India maize is principally grown for grain purpose which is mostly consumed as food and partly as animal feed and industrial uses. With a change in food pattern and significant shift in cropping system maize assumes tremendous potentiality in Indian agriculture. Baby corn (*Zea mays* L.) is one of the dual purpose crop widely grown throughout the year for both its cob and green fodder. It can be eaten raw or cooked form because of its delicious taste and sweetness. Baby corn is harvested two or three days after the emergence of the silk.

Moreover, it contains 17 amino acids and nine essential amino acids, including lysine, was found in baby corn (Yu *et al.*, 1993) [14]. Baby corn fetches high demand and market value in cosmopolitan cities and metro cities in India as food commodity in domestic market.

Baby corn now becoming an ideal ingredient in various continental and indigenous foods such as crispy vegetable in salad, soup, pickles, pakodas, vegetable biryani, pasta, chutney, cutlets, kofta curry, manchurian, raita, candy, jam, burfi, halwa, kheer, deep fried baby corn with meat and rice (Asaduzzaman *et al.*, 2014) [5].

It produces high biomass which serves as fresh fodder for which there is a high dearth. To sustain the cattle population, baby corn can provide a valuable supplementary source of green fodder particularly for milking animals in the summer months due to its high succulence, palatability and digestibility (Singh *et al.*, 2006) [12].

In a hybrid breeding program meant to support development of hybrids, the objective is to identify a new lines that, when crossed will produce hybrids with superior performance. However, with increased number of genotypes this is practically impossible to make all possible crosses and evaluate them. Therefore, a breeder must essentially identify a limited number of lines with sufficient genetic potential (combining ability) before their evaluation is done in specific hybrid combinations (Fehr, 1987) [6]. New dimension for the use of progeny test or top cross test were suggested after Sprague and Tatum (1942) [13] introduced the concept of general and specific combining ability effects. Different recurrent selection procedures were proposed in the context of improvement of general and or specific combining ability effects. Jensen (1970) [7] gave a method to broaden variability for *per se* performance by introducing matings in segregating generations.

Response to selection for any character is dependent on the existence of variability for that character. Emphasis is not laid on creation of variability and assessing the nature and magnitude of the variability for combining ability. Like other characters, even for combining ability, variability can be created by crossing genotypes and generating recombinational variation and evaluating the recombinants in segregating generations for combining ability. In cross pollinated crops like maize, this principle is involved in breeding procedures like recurrent selection for general and specific combining ability.

Because of recombination some of the lines have accumulated more dominant or recessive favourable alleles distributed between the two parents. As a result of this, the lines revealed improved *per se* performance with tester/s in concern. Conversely some lines have accumulated dominant or recessive unfavourable alleles distributed between the parents; as a result these lines turn out to be transgressing on the negative side for their ability to combine with the testers. A line accumulating such favourable alleles is expected to be good in performance with different testers. However the genotypic background of the tester further influences the potentiality finally realized in the derived F₁.

The property of progeny falling outside or exceeding the range of the parents is called transgressive segregation. It is caused due to dispersion of favourable alleles between parents. Unlike heterosis, extreme phenotypes caused by transgressive segregation are heritably stable (Mackay *et al.*, 2021) [9].

Therefore, transgressive breeding aims at improving yield or its contributing characters through transgressive segregation. The intensity of a character absent in the original parents may appear in the segregating generation. Such plants are produced by an accumulation of the plus or favourable genes from both the parents as a consequence of recombination. Obviously, the parents involved in hybridization must

combine well with each other and preferably be genetically diverse. In such a situation, each parent is expected to contribute different positive genes, which when brought together by recombination gives rise to transgressive segregation. As a result, the intensity of the character in the transgressive segregants in the new derivative is greater than that in either of the parents.

In this line, an attempt was made to identify potential transgressive segregants in early segregating lines (F₄ inbreds) for baby corn traits *viz.*, baby corn yield per plant without husk (g), baby corn yield per plant with husk (g) and number of cobs per plant.

Materials and Methods

The material comprised of 26 and 26 F₄ generation inbred lines of genetically diverse populations *viz.*, Population A (HKI 1105 × HKI 323) and Population B (PDM 53 × PDM 4441) respectively. The F₄ inbreds were selected based on *per se* performance and combining ability for baby corn traits.

The crossing programme was taken up during *Kharif* 2018 at Botanical garden, Department of genetics and Plant breeding, University of agricultural sciences, Dharwad. The F₄ lines of the two populations *i.e.*, Population A and Population B, testers HKI 1105, HKI 323 (reciprocal testers for Population A), PDM 4441, PDM 53 (reciprocal testers for Population B) and one common tester, PDM 260-1 along with parents of diverse populations were sown on staggered dates and crosses were made between the lines and testers, a total of 78 test F₁ hybrids representing Population A and 78 test F₁ hybrids representing Population B were developed.

The bench mark crosses (BMCs) were developed for Population A by crossing original parental inbreds *viz.*, PDM 53 and PDM 4441 of Population A with testers' *viz.*, HKI 1105, HKI 323 and PDM 260-1. For Population B by crossing parental inbred lines *viz.*, HKI 1105 and HKI 323 with corresponding testers PDM 53, PDM 4441 and PDM 260-1. The generated test single cross F₁s of Population A, Population B, parents, bench mark crosses along with check hybrid were evaluated in randomized complete block design with two replications at Botany garden, Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Dharwad, Karnataka, India. To estimate the transgressive segregation, comparison was made between the test F₁'s and their respective superior bench mark cross (SBMC).

Observations on baby corn traits *viz.*, baby corn yield per plant with husk (g), baby corn yield per plant without husk (g), days to 50 % silking, number of cobs per plant, baby corn weight with husk (g), baby corn weight without husk (g), baby corn length (cm) and baby corn girth (cm) were recorded by average value of randomly chosen five plants from each entry.

Results and discussion

ANOVA of Population A (26 × 3 line × tester design)

Analysis of variance for Population A indicated the existence of significant differences among parents for all the eight baby corn traits *viz.*, baby corn yield per plant with husk (g), baby corn yield per plant without husk (g), days to 50 % silking, number of cobs per plant, baby corn weight with husk (g), baby corn weight without husk (g), baby corn length (cm) and baby corn girth (cm).

Among parents, lines showed significant differences for yield per plant with husk and corn girth whereas significant differences were observed for yield per plant with and without

husk, number of cobs per plant, and corn weight with husk among testers. The mean sum of squares with respect to

interaction between lines and testers and derived hybrids were significant for all the characters (Table 1).

Table 1: Analysis of variance for combining ability involving Population A (F₄ lines of PDM 4441 × PDM 53) and its derived crosses for baby corn features.

Source of Variation	DF	Baby corn yield per plant without husk (g)	Baby corn yield per plant with husk (g)	Days to 50% silking	Number of cobs per plant	Baby corn Weight without husk	Baby corn Weight with husk	Baby corn length	Baby corn girth
Replicates	1	0.34	4.63	0.23	0.003	0.001	0.003	0.00	0.002
Crosses	77	119.91**	1929.89**	10.91**	0.47**	4.67**	57.73**	0.93**	0.02**
Parents	28	5265.97**	62281.10**	709.66**	24.50**	103.35**	2497.56**	79.91**	0.62**
Line Effect	25	137.79	2524.47*	12.52	0.61	4.73	74.80	1.11	0.03**
Tester Effect	2	442.45*	10283.44**	15.01	1.65*	4.42	150.13*	0.09	0.02
Line * Tester Eff.	50	98.07**	1298.46**	9.94**	0.36**	4.65**	45.41**	0.83**	0.01**
Error	77	0.303	5.382	0.867	0.002	0.005	0.037	0.040	0.001
Total	155	59.72	961.42	5.85	0.24	2.32	28.61	0.48	0.01

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

ANOVA of Population B (26 × 3 line × tester design)

ANOVA for line × tester analysis of Population B revealed the existence of significant differences among parents for all baby corn traits studied. The lines exhibited significant difference only for baby corn length. Among testers significant differences were observed for all the traits except

for number of cobs per plant, baby corn length and baby corn girth. The interaction between lines and testers were significant for all the characters. The mean squares with respect to test hybrids were found to be significant for all the characters (Table 2).

Table 2: Analysis of variance for Line × Tester analysis involving Population B (F₄ lines of HKI1105 × HKI 323) and its derived crosses for baby corn features

Source of Variation	DF	Baby corn yield per plant without husk (g)	Baby corn yield per plant with husk (g)	Days to 50% silking	Number of cobs per plant	Baby corn weight without husk	Baby corn weight with husk	Baby corn length	Baby corn girth
Replicates	1	2.48**	13.58**	1.44	0.004	0.037**	0.004*	0.049**	0.001
Crosses	77	137.55**	2501.81**	19.78**	0.32**	5.40**	106.78**	1.11**	0.01**
Parents	28	3083.02**	65384.37**	793.35**	18.74**	151.61**	2326.60**	65.25**	0.20**
Line Effect	25	175.18	2680.04	17.96	0.32	6.44	104.34	1.68*	0.01
Tester Effect	2	419.67*	10035.620*	94.67**	0.55	20.81*	345.98*	0.37	0.009
Line * Tester Eff.	50	107.44**	2111.35**	17.69**	0.32**	4.27**	98.43**	0.85**	0.01**
Error	77	0.01	1.29	1.40	0.001	0.002	0.001	0.001	0.001
Total	155	68.13	1300.63	10.53	0.16	2.69	57.11	0.55	0.01

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

Transgressive segregants in early generation F₄ derived inbred lines of Population A (PDM 53 × PDM 4441)

The improvement in combining ability of F₄ lines of Population A *i.e.*, F₄ lines of PDM 53 × PDM 4441 and F₄ lines of Population B *i.e.*, HKI 1105 × HKI 323 upon crossing with their respective reciprocal testers and common tester was assessed by comparing the test single cross hybrids (F₄ lines × testers) with their respective superior bench mark crosses (SBMC). The test hybrids were generated by crossing of F₄

lines with two reciprocal testers (parents of opposite base population F₁) and a common tester, which were compared with their superior bench mark crosses as a base. The details of transgressive segregants produced by Population A and B are described for various important traits *viz.*, baby corn yield per plant without husk (g), baby corn yield per plant with husk (g) and number of cobs per plant in Table 3, 4, 5 and 6, 7, 8 respectively.

Table 3: Measure of transgressive segregation for combining ability of derived F₁s involving Population A (F₄ lines of PDM 4441 × PDM 53) for baby corn yield per plant without husk (g)

Sl. No.	F ₄ lines of population A	Reciprocal testers				Common tester			
		HKI 1105 (T1)		F ₄ lines of population A	HKI 323 (T2)		F ₄ lines of population A	PDM 260-1	
		Mean (grams per plant)	% imp over SBMC		Mean (grams per plant)	% imp over SBMC		Mean (grams per plant)	% imp over SBMC
1	P11	51.05	95.42**	P27	59.80	93.86**	P38	46.40	46.20**
2	P14	46.52	78.1**	P36	58.72	90.32**	P27	44.37	39.79**
3	P12	45.91	75.77**	P34	51.93	68.31**	P17	43.70	37.68**
4	P17	45.69	74.94**	P47	50.00	62.07**	P45	43.66	37.56**
5	P45	43.72	67.38**	P40	49.87	61.65**	P41	42.02	32.40**
6	P36	42.72	63.53**	P4	47.12	52.74**	P10	40.67	28.12**
7	P34	41.08	57.25**	P11	46.92	52.11**	P15	40.34	27.11**
8	P10	40.65	55.65**	P10	46.72	51.43**	P44	39.07	23.11**
9	P32	39.77	52.26**	P17	44.50	44.25**	P4	38.61	21.66**

10	P19	37.11	42.06**	P24	41.66	35.04**	P32	37.22	17.25**
11	P41	37.09	42.00**	P8	41.18	33.48**	P13	36.96	16.45**
12	P38	35.11	34.42**	P19	40.52	31.35**	P8	36.66	15.50**
13	P15	34.32	31.37**	P37	39.36	27.60**	P36	35.47	11.74**
14	P27	34.27	31.22**	P14	39.15	26.89**	P40	35.42	11.59**
15	P8	32.40	24.04**	P41	37.77	22.43**	P48	33.18	4.54*
16	P44	31.91	22.19**	P12	36.60	18.64**	P34	33.08	4.24*
17	P39	30.66	17.36**	P48	36.34	17.8**	P30	32.90	3.67*
18	P30	30.38	16.33**	P45	35.52	15.54**	P14	30.41	-4.17*
19	P24	29.21	11.85**	P39	35.03	13.53**	P47	30.37	-4.33*
20	P40	29.12	11.49**	P38	34.87	13.01**	P39	29.63	-6.65**
21	P37	29.02	11.08**	13.00	32.27	4.62*	P11	29.51	-7.03**
22	P4	29.02	11.12**	P50	32.14	4.17*	P24	29.16	-8.13**
23	P47	28.33	8.46**	P30	31.02	0.57	P19	28.81	-9.22**
24	P48	28.17	7.85**	P44	29.61	-4.04*	P50	28.47	-10.32**
25	P50	27.83	6.53**	P32	28.64	-7.18**	P37	27.18	-14.38**
26	P13	23.32	-10.72**	P15	26.28	-14.81**	P12	26.77	-15.67
	SBMC	(PDM 53 × HKI 1105) 26.12			(PDM 4441 × HKI 323) 30.85		SBMC	(PDM 4441 × PDM 260-1) 31.74	
	CD (5%)	0.78							
	CD (1%)	1.03							
Transgression for combining ability									
Significant positive	25			22			17		
Non significant positive	0			1			0		
Non significant negative	0			0			0		
Significant negative	1			3			9		

Transgressive segregants in early generation F₄ lines of Population A (PDM 53 × PDM 4441)

Baby corn yield per plant without husk (g)

The *per se* performance and per cent improvement of test hybrids of Population A (PDM 53 × PDM 4441 F₄ lines) over their respective superior bench mark crosses for baby corn yield per plant without husk (g) are presented in Table 3. With respect to reciprocal testers HKI 1105 and HKI 323, recorded 25 and 22 positive transgressive segregants for the trait

whereas for common tester (PDM 260-1), 17 positive transgressive segregants were observed (Table 3). Top three significant positive transgressive segregants with respect to tester HKI 1105 were *viz.*, P11 (95.42%), P14 (78.10%) and P12 (75.77%). Contrary to tester HKI 323 F₄ lines *viz.*, P27 (93.86%), P36 (90.32%) and P34 (68.31%) were superior over bench mark cross (PDM 4441 × HKI 323) for the trait. Top three lines with respect to common tester PDM 260-1 were P38 (46.20%), P27 (39.79%) and P17 (37.68%).

Table 4: Measure of transgressive segregation for combining ability of derived F₁s involving Population A (F₄ lines of PDM 4441 × PDM 53) for baby corn yield per plant with husk

Sl. No.	F ₄ lines of population A	Reciprocal testers				Common tester			
		HKI 1105 (T1)		F ₄ lines of population A	HKI 323 (T2)		F ₄ lines of population A	PDM 260-1	
		Mean (grams per plant)	% imp over SBMC		Mean (grams per plant)	% imp over SBMC		Mean (grams per plant)	% imp over SBMC
1	P11	221.93	108.81**	P47	233.65	129.20**	P36	212.43	51.38**
2	P45	194.04	82.57**	P27	227.93	123.60**	P38	188.26	34.16**
3	P14	193.76	82.30**	P4	219.71	115.53**	P44	183.04	30.44**
4	P41	191.19	79.88**	P15	216.89	112.76**	P14	179.44	27.87**
5	P40	190.03	78.80**	P10	214.26	110.18**	P30	174.37	24.26**
6	P30	188.13	77.01**	P36	212.27	108.23**	P41	171.86	22.47**
7	P10	185.47	74.50**	P34	203.06	99.19**	P17	168.25	19.90**
8	P48	181.22	70.50**	P40	201.41	97.58**	P10	166.03	18.32**
9	P37	172.81	62.59**	P17	201.22	97.39**	P32	164.29	17.08**
10	P36	172.47	62.28**	P19	191.96	88.31**	P40	161.11	14.82**
11	P44	168.35	58.39**	P11	190.49	86.86**	P45	160.71	14.52**
12	P12	159.39	49.96**	P45	190.07	86.45**	P11	159.67	13.78**
13	P47	159.34	49.92**	P14	187.61	84.04**	P24	156.61	11.61**
14	P4	155.4	46.22**	P38	185.12	81.59**	P4	156.41	11.46**
15	P34	149.89	41.02**	P8	184.68	81.16**	P15	154.28	9.94**
16	P50	143.78	35.28**	P39	176	72.66**	P34	153.35	9.28**
17	P24	142.41	33.99**	P30	167.35	64.17**	P13	150.44	7.21**
18	P19	140.49	32.18**	P37	164.02	60.90**	P48	145.18	3.46*
19	P17	136.35	28.29**	P24	159.07	56.04**	P27	144.33	2.85
20	P15	135.61	27.59**	P13	151.06	48.18**	P37	144.04	2.65
21	P27	133.47	25.58**	P48	148.81	45.98**	P8	142.22	1.35
22	P8	131.74	23.95**	P44	142.93	40.21**	P12	134.99	-3.80*
23	P39	128.17	20.60**	P12	141.4	38.71**	P39	118.55	-15.52**
24	13	127.57	20.03**	P41	139.38	36.72**	P47	117.03	-16.60**

25	P38	110.57	4.03	P32	121.24	18.93 **	P50	109.36	-22.07 **
26	P32	100.72	-5.24*	P50	121.22	18.91 **	P19	99.89	-28.82 **
	SBMC	(PDM 53 × HKI 1105) 106.29		SBMC	(PDM 53 × HKI 323) 101.94		SBM,C	(PDM 53 × PDM 260-1) 140.33	
	CD (5%)	3.26							
	CD (1%)	4.32							
Transgression for combining ability									
Significant positive	24			26					18
Non significant positive	1			0					3
Non significant negative	0			0					0
Significant negative	1			0					5

Baby corn yield per plant with husk (g)

With reciprocal tester HKI 1105, the improvement of test single crosses over its SBMC (PDM 53 x HKI 1105) revealed 24 positive transgressive segregants (Table 4). Among 24 positive segregants, three F₄ lines *viz.*, P11 (108.81 %), P45 (82.57 %) and P14 (82.30 %) produced highest significant transgressive segregants. With reciprocal tester HKI 323, the per cent improvement of test hybrids over its superior bench mark cross (PDM 4441 x HKI 323) registered 26 positive transgressive segregants of which P47 (129.20 %), P27 (123.60 %) and P4 (115.53 %), produced significant transgressive segregants with highest improvement over SBMC. In case of common tester PDM 260-1, the per cent improvement over superior bench mark cross (PDM 4441 x PDM 260-1) registered 18 positive transgressive segregants many among them were numerically superior over their SBMC.

Number of cobs per plant

The test single cross hybrids corresponding to positive transgressive segregants for number of cobs per plant were

presented in Table 5. The F₄ lines *viz.*, P12 (72.05 %), P11 (68.11 %) and P32 (65.35 %) recorded top three positions corresponding to reciprocal tester HKI 1105 over their respective bench mark cross PDM 53 x HKI 1105. With respect to reciprocal tester HKI 323, 23 positive transgressive segregants over their corresponding superior bench mark cross PDM 4441 x HKI 323, of these, F₄ lines *viz.*, P47 (63.32 %), P40 (54.11 %) and P36 (51.48 %) produced top three significant transgressive segregants. Considering the common tester PDM 260-1, all the F₄ lines except P50 produced positive transgressive segregants, among which top three positions were occupied by lines *viz.*, P36 (55.89 %), P17 (50.36 %) and P41 (47.86 %) over their corresponding SBMC PDM 4441 x PDM 260-1.

The identified top 5 inbred lines transgressing positively in Population A were P17, P41, P27, P11 and P45 can be used in any hybridisation programme as parents for deriving potential single cross hybrid with respect to baby corn yield and its component traits.

Table 5: Measure of transgressive segregation for combining ability of derived F₁s involving Population A (F₄ lines of PDM 4441 × PDM 53) for number of cobs per plant

Sl. No.	Reciprocal testers						Common tester		
	F4 lines of population A	HKI 1105 (T1)		F4 lines of population A	HKI 323 (T2)		F4 lines of population A	PDM 260-1	
		Mean (grams per plant)	% imp over SBMC		Mean (grams per plant)	% imp over SBMC		Mean (grams per plant)	% imp over SBMC
1	P12	4.37	72.05 **	P47	4.97	63.32 **	P36	4.37	55.89 **
2	P11	4.27	68.11 **	P40	4.68	54.11 **	P17	4.21	50.36 **
3	P32	4.2	65.35 **	P36	4.61	51.48 **	P41	4.14	47.86 **
4	P36	4.2	65.35 **	P27	4.56	50.00 **	P24	4.08	45.54 **
5	P17	4.03	58.86 **	P19	4.52	48.68 **	P44	3.9	39.29 **
6	P34	3.99	57.09 **	P17	4.46	46.88 **	P45	3.83	36.79 **
7	P10	3.98	56.69 **	P39	4.4	44.74 **	P37	3.79	35.36 **
8	P45	3.96	55.91 **	P8	4.2	38.16 **	P14	3.79	35.36 **
9	P44	3.96	55.91 **	P4	4.2	38.32 **	P 30	3.78	35.00 **
10	P14	3.88	52.95 **	P34	4.06	33.55 **	P10	3.69	31.79 **
11	P19	3.71	45.87 **	P11	3.96	30.26 **	P40	3.66	30.89 **
12	P27	3.66	44.09 **	P38	3.79	24.67 **	P47	3.63	29.64 **
13	P4	3.61	42.13 **	P41	3.79	24.67 **	P13	3.58	28.04 **
14	P15	3.58	40.94 **	P12	3.77	24.18 **	P8	3.58	28.04 **
15	P39	3.38	33.07 **	P37	3.72	22.20 **	P32	3.57	27.68 **
16	P 30	3.38	33.07 **	P45	3.7	21.71 **	P11	3.56	27.14 **
17	P47	3.27	28.74 **	P24	3.69	21.22 **	P27	3.5	24.82 **
18	P37	3.26	28.35 **	P44	3.68	21.05 **	P34	3.49	24.64 **
19	P13	3.25	27.95 **	P 30	3.62	19.08 **	P4	3.48	24.29 **
20	P8	3.23	27.17 **	P13	3.6	18.42 **	P15	3.31	18.39 **
21	P38	3.2	25.79 **	P15	3.59	18.26 **	P38	3.3	18.04 **
22	P24	3.17	24.80 **	P10	3.58	17.93 **	P48	3.3	17.86 **
23	P48	3.13	23.23 **	P14	3.56	17.11 **	P12	3.28	17.14 **
24	P40	3.1	22.05 **	P48	2.98	-1.97	P19	3.02	8.04 **
25	P41	3.1	22.05 **	P50	2.89	-4.93 **	P39	2.96	5.71 **
26	P50	2.87	12.99 **	P32	2.88	-5.10 **	P50	2.38	-15.00 **

	SBMC	(PDM 53 × HKI 1105) 2.54	SBMC	(PDM 4441 × HKI 323) 3.04	SBM,C	(PDM4441 × PDM 260-1)2.80
	CD (5%)			0.07		
	CD (1%)			0.09		
Transgression for combining ability						
	Significant positive	26		23		25
	Non significant positive	0		0		0
	Non significant negative	0		1		0
	Significant negative	0		2		1

Transgressive segregants in early generation F₄ lines of Population B (HKI 1105 × HKI 323).

Baby corn yield per plant without husk (g)

Baby corn yield per plant without husk of 25 derived F₁sof Population B with reciprocal tester PDM 4441 produced a total of 23 positive transgressive segregants over their superior bench mark cross HKI 323 x PDM 4441, top three lines among them were viz., H94 (73.92 %), H99 (60.37 %) and H13 (60.16 %) (Table 6). With reciprocal tester PDM 53,

the improvement of test hybrids over its superior bench mark cross HKI 1105 x PDM 53 registered 22 positive transgressive segregants. Among them, F₄ line H61 (132.70 %) registered highest significant value. F₄ lines viz., H99 (151.03 %), H94 (120.94 %) and H6 (117.60 %) produced top three significant positive transgressive segregants with respect to common tester PDM 260-1 over superior bench mark cross HKI 1105 x PDM 260-1.

Table 6: Measure of transgressive segregation for combining ability of derived F₁s involving Population B (F₄ lines of HKI 1105 × HKI 323) for baby corn yield per plant without husk (g)

Sl. No.	F4 lines of population B	Reciprocal testers				Common tester			
		PDM 4441 (T1)		F4 lines of population B	PDM 53 (T2)		F4 lines of population B	PDM 260-1	
		Mean (grams per plant)	% imp over SBMC		Mean (grams per plant)	% imp over SBMC		Mean (grams per plant)	% imp over SBMC
1	H94	53.81	73.92 **	H61	62.26	132.70 **	H99	57.85	151.03 **
2	H99	49.62	60.37 **	H94	45.74	70.96 **	H94	50.92	120.94 **
3	H13	49.56	60.16 **	H8	41.28	54.31 **	H6	50.15	117.60 **
4	H29	49.16	58.89 **	H 49	40.26	50.48 **	H22	47.02	104.04 **
5	H 91	49.06	58.56 **	H99	39.15	46.33 **	H 5	43.41	88.35 **
6	H22	47.81	54.52 **	H13	38.48	43.82 **	H35	41.48	80.00 **
7	H20	47.72	54.22 **	H16	38.1	42.42 **	H8	40.99	77.85 **
8	H8	46.22	49.37 **	H6	36.49	36.37 **	H20	40.93	77.63 **
9	H41	45.47	46.96 **	H106	36.02	34.63 **	H95	35.75	55.15 **
10	H35	44.17	42.78 **	H35	35.61	33.10 **	H106	35.67	54.78 **
11	H 46	41.06	32.71 **	H28	35.4	32.29 **	H81	35.6	54.50 **
12	H19	40.42	30.64 **	H32	35.11	31.23 **	H97	35.12	52.40 **
13	H16	38.91	25.78 **	H29	34.42	28.65 **	H32	34.18	48.32 **
14	H6	38.22	23.53 **	H 46	33.25	24.28 **	H41	34.18	48.32 **
15	H95	37.1	19.91 **	H19	32.83	22.71 **	H57	33.65	46.00 **
16	H106	36.99	19.57 **	H81	31.7	18.50 **	H13	33.61	45.85 **
17	H51	36.97	19.49 **	H97	31.56	17.94 **	H51	33.49	45.35 **
18	H32	36.31	17.34 **	H 5	31.39	17.32 **	H29	33.14	43.81 **
19	H61	34.83	12.57 **	H 91	31.1	16.24 **	H 91	32.64	41.61 **
20	H59	34.33	10.96 **	H51	29.52	10.35 **	H61	31.93	38.53 **
21	H57	33.33	7.72 **	H57	29.46	10.11 **	H 46	30.84	33.83 **
22	H81	33.12	7.03 **	H22	28.4	6.15 **	H28	29.88	29.66 **
23	H 49	32.12	3.81 **	H41	27.36	2.26	H19	25.93	12.50 **
24	H97	30.65	-0.92	H95	25.06	-6.32 **	H59	25.83	12.09 **
25	H28	28.11	-9.13 **	H59	24.51	-8.41 **	H 49	24.79	7.57 **
26	H 5	24.6	-20.49 **	H20	21.15	-20.95 **	H16	21.74	-5.66 **
	SBMC	(PDM 4441 × HKI 323) 30.94	SBMC	(PDM 53 × HKI 1105) 26.75	SBM,C	(HKI 1105 × PDM 260-1) 23.05			
	CD (5%)								
	CD (1%)								
Transgression for combining ability									
	Significant positive	23			22		25		
	Non significant positive	0			1		0		
	Non significant negative	1			0		0		
	Significant negative	2			3		1		

4.3.2.2 Baby corn yield per plant with husk (g)

Considering the reciprocal tester PDM 4441, F₄ lines of Population B viz., H8 (108.36 %), H13 (106.86 %), and H91 (105.96 %) produced top three significantly positive transgressive segregants over its superior bench mark cross

HKI 1105 x PDM 4441 (Table 7). Whereas, with reciprocal tester PDM 53, F₄ lines H61 (111.69 %), H94 (103.78 %) and H32 (103.65 %) were the transgressive segregants with highest significant improvement over their corresponding superior bench mark cross HKI 1105 x PDM 53. Considering

common tester PDM 260-1, F₄ lines viz., H99 (89.74 %), H6 (87.95 %) and H94 (86.65 %) produced top three significantly

positive transgressive segregants over its superior bench mark cross HKI 1105 x PDM 260-1.

Table 7: Measure of transgressive segregation for combining ability of derived F₁s involving Population B (F₄ lines of HKI 1105 × HKI 323) for baby corn yield per plant with husk

Sl. No.	Reciprocal testers						Common tester		
	F ₄ lines of population B	PDM 4441 (T1)		F ₄ lines of population B	PDM 53 (T2)		F ₄ lines of population B	PDM 260-1	
		Mean (grams per plant)	% imp over SBMC		Mean (grams per plant)	% imp over SBMC		Mean (grams per plant)	% imp over SBMC
1	H8	227.29	108.36 **	H61	230.05	111.69 **	H99	230.37	89.74 **
2	H13	225.65	106.86 **	H94	221.46	103.78 **	H6	228.2	87.95 **
3	H 91	224.68	105.96 **	H32	221.32	103.65 **	H94	226.63	86.65 **
4	H94	223.34	104.74 **	H 49	199.1	83.20 **	H 5	220.65	81.73 **
5	H41	217.43	99.32 **	H97	198.29	82.46 **	H51	178.6	47.09 **
6	H20	217.25	99.15 **	H 46	196.53	80.84 **	H22	175.19	44.29 **
7	H32	211.01	93.44 **	H106	195.19	79.61 **	H8	172.1	41.74 **
8	H29	210.56	93.02 **	H8	194.81	79.25 **	H35	165.73	36.50 **
9	H99	209.4	91.96 **	H13	194.78	79.23 **	H 46	157.38	29.62 **
10	H35	193.12	77.04 **	H51	192.19	76.85 **	H81	156.48	28.88 **
11	H95	186.65	71.11 **	H99	188.29	73.26 **	H95	147.48	21.46 **
12	H16	181.29	66.19 **	H16	185.19	70.41 **	H61	146.72	20.85 **
13	H 46	178.52	63.65 **	H6	183.58	68.92 **	H20	139.8	15.14 **
14	H6	176.72	62.01 **	H19	176.25	62.18 **	H28	136.25	12.22 **
15	H22	175.44	60.83 **	H35	164.6	51.46 **	H32	135.81	11.85 **
16	H59	170.8	56.58 **	H 91	162.45	49.48 **	H 91	135.2	11.35 **
17	H97	161.51	48.06 **	H59	158.99	46.29 **	H19	134.28	10.60 **
18	H81	158.73	45.51 **	H29	154.33	42.02 **	H13	132.57	9.19 **
19	H51	156.84	43.78 **	H28	151.99	39.86 **	H41	130.7	7.65 **
20	H 49	154.56	41.69 **	H57	150.84	38.80 **	H106	130.39	7.39 **
21	H61	153.14	40.39 **	H 5	147.49	35.72 **	H16	124.59	2.62 *
22	H57	141.9	30.08 **	H81	140.85	29.60 **	H57	124.56	2.59 *
23	H19	141.72	29.92 **	H22	138.13	27.10 **	H29	123.79	1.96
24	H106	140.81	29.08 **	H41	131.93	21.40 **	H97	123.51	1.73
25	H28	135.29	24.02 **	H95	116.5	7.20 **	H 49	110.42	-9.05 **
26	H 5	119.47	9.52 **	H20	107.31	-1.26	H59	106.97	-11.90 **
	SBMC	(PDM 4441 × HKI 323) 109.08		SBMC	(PDM 53 × HKI 1105) 108.67		SBM,C	(HKI 1105 × PDM 260-1) 121.42	
	CD (5%)								
	CD (1%)								
Transgression for combining ability									
Significant positive	26				25			22	
Non significant positive	0				0			2	
Non significant negative	0				1			0	
Significant negative	0				0			2	

4.3.2.3 Number of cobs per plant

With respect to the reciprocal testers (PDM 4441 and PDM 53) and common tester 9PDM260-1), the F₄ lines recorded 23, 26 and 25 positive transgressive segregants respectively (Table 8). Top three positive transgressive segregants with respect to tester PDM 4441 were viz., H13 (42.97 %), H91 (38.49 %) and H35 (24.42 %); with respect to reciprocal tester PDM 53 were viz., H61 (68.75 %), H16 (68.57 %) and H8 (59.19 %). Top three lines with respect to common tester PDM 260-1 were H99 (67.72 %), H5 (50.37 %) and H94

(50.19 %). The identified single cross hybrids which are outperforming parental inbreds for baby corn yield and its related traits can be evaluated further at multi-location trails. Any single cross hybrid performing better can be released for cultivation.

The identification of transgressive segregants in early generations was reported by Alkuddsi *et al.* (2013)^[2], Ajay *et al.* (2014)^[1], Kencharaddi *et al.* (2014)^[8], Mohan *et al.* (2018)^[10], Anusha *et al.* (2019)^[4] and Pattar and Deshpande (2019)^[11].

Table 8: Measure of transgressive segregation for combining ability of derived F₁s involving Population B (F₄ lines of HKI 1105 × HKI 323) for number of cobs per plant

Sl. No.	Reciprocal testers						Common tester		
	F ₄ lines of population B	PDM 4441 (T1)		F ₄ lines of population B	PDM 53 (T2)		F ₄ lines of population B	PDM 260-1	
		Mean (grams per plant)	% imp over SBMC		Mean (grams per plant)	% imp over SBMC		Mean (grams per plant)	% imp over SBMC
1	H13	4.63	42.97 **	H16	4.59	68.57 **	H99	4.5	67.72 **
2	H 91	4.48	38.49 **	H61	4.59	68.75 **	H 5	4.03	50.37 **
3	H35	4.03	24.42 **	H8	4.33	59.19 **	H94	4.03	50.19 **

4	H41	3.94	21.79 **	H99	4	46.88 **	H22	3.94	46.83 **
5	H99	3.94	21.64 **	H 49	3.91	43.57 **	H6	3.92	46.27 **
6	H8	3.91	20.71 **	H32	3.89	43.01 **	H13	3.89	45.15 **
7	H29	3.9	20.56 **	H19	3.8	39.71 **	H61	3.83	42.91 **
8	H 46	3.83	18.39 **	H97	3.79	39.52 **	H51	3.78	41.23 **
9	H97	3.82	18.08 **	H 46	3.71	36.21 **	H32	3.66	36.57 **
10	H20	3.8	17.62 **	H94	3.69	35.66 **	H81	3.65	36.19 **
11	H51	3.8	17.62 **	H6	3.68	35.29 **	H35	3.64	35.82 **
12	H94	3.78	16.85 **	H106	3.66	34.38 **	H41	3.61	34.70 **
13	H57	3.75	15.77 **	H 5	3.65	34.19 **	H106	3.6	34.51 **
14	H6	3.75	15.77 **	H 91	3.61	32.72 **	H95	3.59	33.96 **
15	H19	3.71	14.53 **	H29	3.58	31.62 **	H29	3.55	32.46 **
16	H32	3.64	12.67 **	H35	3.5	28.86 **	H57	3.51	30.97 **
17	H61	3.64	12.67 **	H28	3.44	26.29 **	H20	3.5	30.78 **
18	H16	3.63	12.06 **	H95	3.42	25.55 **	H 91	3.38	26.12 **
19	H106	3.51	8.50 **	H57	3.42	25.74 **	H8	3.3	23.13 **
20	H22	3.51	8.50 **	H51	3.42	25.55 **	H28	3.22	19.96 **
21	H95	3.5	8.04 **	H22	3.34	22.98 **	H 49	3.02	12.87 **
22	H59	3.48	7.57 **	H41	3.3	21.32 **	H16	3.01	12.50 **
23	H81	3.3	2.01 *	H13	3.22	18.38 **	H19	2.97	10.63 **
24	H28	3.23	-0.15	H59	3.18	16.91 **	H59	2.96	10.26 **
25	H 5	3.22	-0.46	H20	2.93	7.54 **	H97	2.94	9.70 **
26	H 49	3.22	-0.46	H81	2.91	6.99 **	H 46	2.58	-3.54 **
	SBMC	(PDM 4441 × HKI 323)	3.24	SBMC	(PDM 53 × HKI 323)	2.72	SBM,C	(HKI 1105 × PDM 260-1)	2.68
	CD (5%)								
	CD (1%)								
Transgression for combining ability									
Significant positive	23			26			25		
Non-significant positive	0			0			0		
Non-significant negative	3			0			0		
Significant negative	0			0			1		

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