

## Elucidating Combining Ability through Line x Tester Analysis for Yield and its Contributing Traits in Isabgol [*Plantago ovata* (Forsk.)]

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**ABSTRACT:** In order to explore the genetic architecture of isabgol (*Plantago ovata* Forsk.) through combining ability studies, the present investigation was carried out using 45 crosses which were produced using fifteen lines and three testers in a Line x Tester mating design at experimental farm of Plant Breeding and Genetics, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur (Rajasthan). The experimental material assessed in three environments: E1 (*Rabi-2020-21*, Instructional Farm, RCA, Udaipur), E2 (*Rabi-2020-21*, Krishi Vigyan Kendra, Badgaon) and E3 (*Rabi-2020-21*, Krishi Vigyan Kendra, Banswara) using a randomized block design with three replications in each environment. One of the important reasons for nearly stagnant yields of isabgol may be limited genetic improvement. This might have been due to a narrow genetic base and use of traditional breeding techniques with little or no understanding of the genetic architecture of the target populations. The good general combiner parental lines for seed yield per plant were L<sub>1</sub>, L<sub>5</sub>, L<sub>14</sub> and L<sub>15</sub>. SCA effects revealed that out of 45 crosses, 13 hybrids exhibited significant positive SCA effects for seed yield per plant on pooled basis. The crosses, L<sub>10</sub> × T<sub>3</sub>, L<sub>11</sub> × T<sub>1</sub>, L<sub>5</sub> × T<sub>2</sub> and L<sub>1</sub> × T<sub>3</sub> showed positive and significant SCA effects in all the environments and over the environments for seed yield per plant. Cross L<sub>10</sub> × T<sub>3</sub> showed highest positive and significant SCA effects in all the three environments as well as on pooled basis for seed yield and other yield attributing traits.

**Keywords:** Combining ability, Isabgol, Line x Tester and Environment.

### INTRODUCTION

Isabgol (*Plantago ovata* Forsk.) is an important medicinal plant commercially cultivated in India and being exported in the world market. India holds monopoly in the trade of Isabgol seed and husk. It is a *Rabi* season crop, usually matures in 120 to 140 days after sowing. The seed husk, the seed epidermis having muco-polysaccharide layers are responsible for medicinal properties and are widely used against constipation, diarrhoea and intestinal irritation. The swelling property of the mucilaginous polysaccharide of husk is responsible for the medicinal property (Rohilla *et al.*, 2012).

It is also known as “blond psyllium” belonging to the family plantaginaceae and genus *Plantago* (Kumar *et al.*, 2014). It has narrow genetic base (Kaswan *et al.*, 2013) on account of small genome size (621Mb) based on 4 (2n=2x=8) heterochromatin rich chromosomes, low chiasmata frequency and recombination index and

predominantly a cross-pollinated annual herb (Kour *et al.*, 2016).

The seeds of *Plantago ovata* contains 17.4% protein, 6.7% fat, 24.6% fibre, 19.6% insoluble fibre, 5% soluble fibre and combustion dietary heat of 4.75% kcal/g. The One of the important reasons for nearly stagnant yields of isabgol may be limited genetic improvement. This might have been due to a narrow genetic base and use of traditional breeding techniques with little or no understanding of the genetic architecture of the target populations (Singh and Lal 2009).

The combining ability studies provide useful information regarding the selection of suitable parents for effective hybridization programme and at the same time elucidates the nature and magnitude of gene action (Hallauer, 1990). Combining ability is the relative ability of a genotype to transmit its desirable performance to its crosses. It is very important to screen out the parent materials for their genetic diversity and

combining ability. Since, the nature of gene action varies with genetic architecture of population involved in hybridization, it is necessary to evaluate the parents for their combining ability.

## MATERIAL AND METHODS

The experimental material comprised 15 parental lines, 3 testers, 45 F<sub>1</sub> and two checks viz., VI-1 and Niharika. The lines, testers and checks were obtained from AICRP M & AP, Udaipur. These 45 F<sub>1</sub> were obtained by crossing 15 parental lines and 3 testers in Line × Tester mating design. These 18 parents (15 lines and 3 testers) along with 45 F<sub>1</sub> crosses and two checks were evaluated using a Randomized Block Design with three replications at three different locations (Instructional Farm, Rajasthan College of Agriculture-

Udaipur, Krishi Vigyan Kendra- Badgaon and Krishi Vigyan Kendra- Banswara) during *Rabi*, 2020-2021 (Table 1).

The method of random sampling was adopted for recording the observations of various characters in isabgol. The observations for important morphological traits were recorded on randomly selected ‘ten’ plants excluding the border plants at both the extreme ends in each row. Replication wise collected data of ‘ten’ plants were averaged and resultant mean data were used further for statistical analysis. Only two observations viz., days to 50 per cent flowering and days to 75 per cent maturity were recorded on plot basis, whereas all the remaining observations were recorded on plant basis.

**Table 1: Details of Inbred lines, testers and checks.**

Sr. No.	Symbol / Code	Inbred Lines	Source
1	L <sub>1</sub>	UI-1	AICRP M & AP, Udaipur
2	L <sub>2</sub>	UI-2	AICRP M & AP, Udaipur
3	L <sub>3</sub>	UI-6	AICRP M & AP, Udaipur
4	L <sub>4</sub>	UI-7	AICRP M & AP, Udaipur
5	L <sub>5</sub>	UI-10	AICRP M & AP, Udaipur
6	L <sub>6</sub>	UI-11	AICRP M & AP, Udaipur
7	L <sub>7</sub>	UI-16	AICRP M & AP, Udaipur
8	L <sub>8</sub>	UI-25	AICRP M & AP, Udaipur
9	L <sub>9</sub>	UI-29	AICRP M & AP, Udaipur
10	L <sub>10</sub>	UI-62	AICRP M & AP, Udaipur
11	L <sub>11</sub>	UI-121	AICRP M & AP, Udaipur
12	L <sub>12</sub>	UI-130	AICRP M & AP, Udaipur
13	L <sub>13</sub>	HI-1	AICRP M & AP, Udaipur
14	L <sub>14</sub>	HI-8	AICRP M & AP, Udaipur
15	L <sub>15</sub>	HI-9	AICRP M & AP, Udaipur
16	T <sub>1</sub>	UI-2-1	AICRP M & AP, Udaipur
17	T <sub>2</sub>	UI-3	AICRP M & AP, Udaipur
18	T <sub>3</sub>	UI-124	AICRP M & AP, Udaipur
19	C <sub>1</sub>	VI-1	AICRP M & AP, Udaipur
20	C <sub>2</sub>	Niharika	AICRP M & AP, Udaipur

**Statistics:** The data was subjected to ANOVA following the standard procedures. Analysis of variance (ANOVA) for all treatments was carried out by the method Panse and Sukhatme, (1985) and combining ability analysis and test of significance of different genotypes was based on the procedure suggested by Kempthorne (1957).

## RESULT AND DISCUSSION

The analysis of variance for combining ability revealed significant differences between crosses for all the characters in all the three environments. Significant mean squares due to lines and testers indicated that lines and testers contributed significantly to the GCA effects. Similarly, significant mean squares due to lines x testers indicated that hybrids contributed significantly to SCA effects.

The results on pooled basis revealed that mean squares due to lines, testers and lines x testers were significant for all traits except plant height in all the environments, seed yield and biological yield in E1, 1000 seed weight in E3 and harvest index in E2 due to testers.

Parents were classified as good, average and poor combiners on the basis of their GCA effects (Table 2). Parents with desirable and significant GCA effects were considered good combiners while parents showing non-significant estimates but in desirable direction were classified as average combiners. Poor combiners possess undesirable GCA effects. The estimates of GCA effects for yield and yield contributing characters revealed that good general combiner inbred lines for seed yield per plant were L<sub>1</sub>, L<sub>5</sub>, L<sub>14</sub> and L<sub>15</sub>.

**Table 2: Classification of parents based on general combining ability (GCA) effects for various traits over the environments.**

Sr. No.	Parents Traits	T1	T2	T3	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15
		1	Days to 50 per cent flowering	G	P	P	P	G	A	P	P	P	G	A	A	G	P	P	G
2	Days to 75 per cent maturity	G	G	G	A	A	P	P	P	P	P	G	P	G	A	P	A	G	G
3	Plant height (cm)	P	P	A	A	P	P	P	P	P	G	P	G	P	A	G	G	G	A
4	Number of branches per plant	P	G	G	P	P	P	P	P	P	G	P	G	G	G	G	G	A	P
5	Number of effective spikes per plant	G	A	G	P	P	A	G	G	A	G	G	P	G	P	G	G	G	P
6	Spike length (cm)	G	P	G	P	P	G	P	P	P	G	A	G	A	G	G	A	P	P
7	Length of peduncle (cm)	P	P	G	P	P	P	P	P	P	G	A	P	G	P	G	P	G	G
8	Length of leaves per plant (cm)	P	P	G	P	G	G	A	P	A	P	P	G	A	P	P	A	P	G
9	1000 Seed weight (g)	P	P	G	P	G	A	P	A	P	P	G	G	A	P	P	A	P	G
10	Number of leaves per plant	P	A	G	A	P	P	A	G	P	P	P	G	P	P	G	P	G	G
11	Number of florets per spike	P	P	G	G	G	P	P	P	P	P	A	P	G	P	P	A	G	A
12	Seed yield per plant (g)	P	A	A	P	P	G	G	G	G	P	P	P	G	G	G	P	P	P
13	Biological yield per plant (g)	P	P	G	G	G	G	A	A	P	P	G	P	A	P	P	P	A	A
14	Harvest index (%)	P	P	G	P	P	P	P	G	P	G	G	G	G	P	P	P	G	G
15	Husk yield per plant (g)	A	A	P	G	P	G	P	P	P	P	P	P	P	P	P	P	G	P

Good (G) = Desirable significant (+ or -) GCA effect, Average (A) = Desirable non-significant (+ or -) GCA effect, Poor (P) = Undesirable significant (+ or -) GCA effect

The maximum significant GCA effects in positive direction were exhibited by line L<sub>14</sub> for number of effective spikes per plant and husk yield per plant. The line L<sub>15</sub> exhibited maximum significant GCA effects in positive direction for number of branches per plant, spike length, 1000-seed weight, number

of florets per spike, biological yield per plant and for harvest index. For maturity related traits, inbred lines L<sub>2</sub>, L<sub>7</sub>, L<sub>10</sub>, L<sub>13</sub>, L<sub>14</sub> and L<sub>15</sub> were good general combiners for day to 50 per cent flowering and lines L<sub>8</sub>, L<sub>10</sub>, L<sub>14</sub> and L<sub>15</sub> for days to 75 per cent maturity. Among three testers, the maximum

significant GCA effects in positive direction were exhibited by tester parent T<sub>2</sub> for seed yield per plant. For other yield contributing traits, tester parent T<sub>1</sub> was considered good general combiner for number of branches per plant, spike length, length of leaves, husk yield per plant, the tester parent T<sub>2</sub> for number of leaves per plant, the tester parent T<sub>3</sub> for length of peduncle, length of leaves, 1000-seed weight. For maturity related traits, tester T<sub>1</sub> for days to 50 per cent flowering and days to 75 per cent maturity and tester T<sub>2</sub> for days to 75 per cent maturity was good general combiner. The high

general combining ability effects were due to additive gene effects and additive x additive gene effects (Griffing, 1956 and Sprague, 1966).

A perusal of SCA effects among hybrids revealed that maximum magnitude of positive SCA effects for seed yield per plant were exhibited by cross L<sub>10</sub> × T<sub>3</sub> in E1 (41.60), E2, E3 and as well as over the environment. 13 crosses showed significantly superior SCA effects in which the crosses L<sub>11</sub> × T<sub>1</sub>, L<sub>5</sub> × T<sub>2</sub> and L<sub>1</sub> × T<sub>3</sub> showed positive significant SCA effects in all the three environments as well as over the environments.

**Table 3: Significant specific combining ability (SCA) effect estimates of crosses in desirable directions for various traits over the environments.**

Sr. No.	Traits Crosses	Days to 50 % flowering	Days to 75 % maturity	Plant height (cm)	No. of branches per plant	No. of effective spikes per plant	Spike length (cm)	Length of peduncle (cm)	Length of leaves (cm)	1000 Seed weight (g)
1	L <sub>1</sub> × T <sub>1</sub>	**	**			**		**	**	
2	L <sub>2</sub> × T <sub>1</sub>								**	**
3	L <sub>3</sub> × T <sub>1</sub>									
4	L <sub>4</sub> × T <sub>1</sub>									
5	L <sub>5</sub> × T <sub>1</sub>				**	**	**	**		
6	L <sub>6</sub> × T <sub>1</sub>			*			**			**
7	L <sub>7</sub> × T <sub>1</sub>									
8	L <sub>8</sub> × T <sub>1</sub>	**		*	**	**			*	
9	L <sub>9</sub> × T <sub>1</sub>				**					
10	L <sub>10</sub> × T <sub>1</sub>				**		**	**		
11	L <sub>11</sub> × T <sub>1</sub>				**	**	**	**		
12	L <sub>12</sub> × T <sub>1</sub>		**	**		**	**	**	**	
13	L <sub>13</sub> × T <sub>1</sub>		**			**	**	**		**
14	L <sub>14</sub> × T <sub>1</sub>						*			**
15	L <sub>15</sub> × T <sub>1</sub>	*		*		**	**	**		**
16	L <sub>1</sub> × T <sub>2</sub>						**			
17	L <sub>2</sub> × T <sub>2</sub>	**		**		**		**		**
18	L <sub>3</sub> × T <sub>2</sub>	**		*		**				
19	L <sub>4</sub> × T <sub>2</sub>				**	*		**		
20	L <sub>5</sub> × T <sub>2</sub>							*		**
21	L <sub>6</sub> × T <sub>2</sub>							**		
22	L <sub>7</sub> × T <sub>2</sub>	**								**
23	L <sub>8</sub> × T <sub>2</sub>						**	**		**
24	L <sub>9</sub> × T <sub>2</sub>					**	*			
25	L <sub>10</sub> × T <sub>2</sub>					**			**	
26	L <sub>11</sub> × T <sub>2</sub>									
27	L <sub>12</sub> × T <sub>2</sub>	**								**
28	L <sub>13</sub> × T <sub>2</sub>		**						**	
29	L <sub>14</sub> × T <sub>2</sub>			**	**	**	**	**	*	**
30	L <sub>15</sub> × T <sub>2</sub>	**	**		**	**	**			
31	L <sub>1</sub> × T <sub>3</sub>				*					
32	L <sub>2</sub> × T <sub>3</sub>						**			
33	L <sub>3</sub> × T <sub>3</sub>						*	**	**	**
34	L <sub>4</sub> × T <sub>3</sub>		*	**			**			
35	L <sub>5</sub> × T <sub>3</sub>			*	**	*	**	*	*	
36	L <sub>6</sub> × T <sub>3</sub>					**				
37	L <sub>7</sub> × T <sub>3</sub>		**		**	**		**		
38	L <sub>8</sub> × T <sub>3</sub>			**				*		
39	L <sub>9</sub> × T <sub>3</sub>	**	**	**	**	**	**	**	*	
40	L <sub>10</sub> × T <sub>3</sub>	**	**					**	**	**
41	L <sub>11</sub> × T <sub>3</sub>						**			
42	L <sub>12</sub> × T <sub>3</sub>					**				
43	L <sub>13</sub> × T <sub>3</sub>	**			**					**
44	L <sub>14</sub> × T <sub>3</sub>			**	**	**	**	**	*	**
45	L <sub>15</sub> × T <sub>3</sub>				**	**		**		**

Table 3. Continued...

Sr. No.	Traits Crosses	No. of leaves per plant	Number of florets per spike	Seed yield (g)	Biological yield (g)	Harvest index (%)	Husk yield per plant (g)
1	L <sub>1</sub> x T <sub>1</sub>	**					
2	L <sub>2</sub> x T <sub>1</sub>		**				
3	L <sub>3</sub> x T <sub>1</sub>						**
4	L <sub>4</sub> x T <sub>1</sub>		**			**	**
5	L <sub>5</sub> x T <sub>1</sub>	**			**		
6	L <sub>6</sub> x T <sub>1</sub>				**		**
7	L <sub>7</sub> x T <sub>1</sub>						**
8	L <sub>8</sub> x T <sub>1</sub>	**		**			*
9	L <sub>9</sub> x T <sub>1</sub>						
10	L <sub>10</sub> x T <sub>1</sub>		*	**			
11	L <sub>11</sub> x T <sub>1</sub>		*			**	
12	L <sub>12</sub> x T <sub>1</sub>	*					**
13	L <sub>13</sub> x T <sub>1</sub>			**			
14	L <sub>14</sub> x T <sub>1</sub>		*				
15	L <sub>15</sub> x T <sub>1</sub>		**			**	
16	L <sub>1</sub> x T <sub>2</sub>		**				**
17	L <sub>2</sub> x T <sub>2</sub>			**	**	*	**
18	L <sub>3</sub> x T <sub>2</sub>						
19	L <sub>4</sub> x T <sub>2</sub>				**		
20	L <sub>5</sub> x T <sub>2</sub>		**	**		**	**
21	L <sub>6</sub> x T <sub>2</sub>						
22	L <sub>7</sub> x T <sub>2</sub>	**		**			
23	L <sub>8</sub> x T <sub>2</sub>				**	**	
24	L <sub>9</sub> x T <sub>2</sub>		*		**	**	
25	L <sub>10</sub> x T <sub>2</sub>						**
26	L <sub>11</sub> x T <sub>2</sub>	*	**				**
27	L <sub>12</sub> x T <sub>2</sub>					**	
28	L <sub>13</sub> x T <sub>2</sub>	**					**
29	L <sub>14</sub> x T <sub>2</sub>	**			**	**	
30	L <sub>15</sub> x T <sub>2</sub>						**
31	L <sub>1</sub> x T <sub>3</sub>	**					
32	L <sub>2</sub> x T <sub>3</sub>		**		**	**	
33	L <sub>3</sub> x T <sub>3</sub>					**	
34	L <sub>4</sub> x T <sub>3</sub>			**	**		
35	L <sub>5</sub> x T <sub>3</sub>	**	**	**	**	**	**
36	L <sub>6</sub> x T <sub>3</sub>	**			**		**
37	L <sub>7</sub> x T <sub>3</sub>	**			**		
38	L <sub>8</sub> x T <sub>3</sub>	*				*	
39	L <sub>9</sub> x T <sub>3</sub>	**	**	**	**	**	**
40	L <sub>10</sub> x T <sub>3</sub>	**				**	
41	L <sub>11</sub> x T <sub>3</sub>				**		
42	L <sub>12</sub> x T <sub>3</sub>						
43	L <sub>13</sub> x T <sub>3</sub>						**
44	L <sub>14</sub> x T <sub>3</sub>	**	**	**	**	**	**
45	L <sub>15</sub> x T <sub>3</sub>	**				**	

(\* , \*\* significant at 0.05 and 0.01 probability level, respectively)

On pooled basis, the maximum positive SCA effects were exhibited by cross L<sub>9</sub> x T<sub>3</sub> for plant height, cross L<sub>10</sub> x T<sub>3</sub> for number of branches per plant, husk yield per plant and 1000-seed weight, cross L<sub>4</sub> x T<sub>2</sub> for number of effective spikes per plant and spike length, cross L<sub>5</sub> x T<sub>3</sub> for length of peduncle, cross L<sub>2</sub> x T<sub>2</sub> for length of leaves, cross L<sub>9</sub> x T<sub>2</sub> for number of leaves per plant, cross L<sub>1</sub> x T<sub>3</sub> for number of florets per spike and biological yield per plant, cross L<sub>13</sub> x T<sub>3</sub> for harvest index.

For maturity related traits, cross T<sub>9</sub> x T<sub>3</sub> showed maximum negative significant SCA effects for days to 50 per cent flowering and days to 75 per cent maturity, respectively (Table 3). Similar findings for identification of superior hybrids based on SCA effects for seed yield and its components were also reported by Ardelean *et al.* (2006) in foxglove, Singh and Lal (2009), Sarkar and Lal (2018a) and Singh and Saxena (2019) in isabgol. In the present investigation, crosses with significant high SCA effects for different traits were found from either poor or average (or both) general combiner parents. The combination of desirable

genes from the parents for the corresponding traits might have resulted in high SCA effects. It is also observed that many of these hybrids with high SCA effects were from either average x average or good x average general combiner parents. Hence, it is evident that the parents with either good GCA or poor GCA would have greater probability to have good complementarily with other parents. Venkateshwarlu and Singh (1982) suggested that cross combinations which involved G x A and G x P general combiners and having higher heterosis values beside higher *per se* performance suggested the possibility of exploiting these crosses for yield improvement through heterosis breeding.

On the basis of above criteria, out of 45 crosses, four promising crosses *viz.*, L<sub>15</sub> x T<sub>1</sub>, L<sub>14</sub> x T<sub>1</sub>, L<sub>15</sub> x T<sub>2</sub> and L<sub>5</sub> x T<sub>2</sub> were selected with higher *per se* performance along with high GCA and SCA effects for seed yield and yield contributing traits over the environments (Table 4). Ahmad *et al.* (2017) and Divya *et al.* (2022) also reported similar findings.

**Table 4: Four promising crosses identified on the basis of highest *per se* performance along with significantly positive useful heterosis as well as GCA and SCA effects for seed yield per plant and husk yield per plant on pooled basis.**

Sr. No.	Crosses	Seed yield per plant (g)			Husk yield per plant (g)		
		Mean value (g)	SCA effects	GCA effects	Mean value (%)	SCA effects	GCA effects
1	L <sub>15</sub> x T <sub>1</sub>	6.41	0.55**	1.19** x 0.10* H H	1.94	0.34**	0.40** x 0.03** H H
2	L <sub>14</sub> x T <sub>1</sub>	6.38	0.79**	0.91** x 0.10* H H	1.75	0.13**	0.42** x 0.03** H H
3	L <sub>15</sub> x T <sub>2</sub>	6.29	0.41*	1.19** x 0.12** H H	1.64	0.06	0.40** x 0.02 H L
4	L <sub>5</sub> x T <sub>2</sub>	5.88	0.90*	0.29** x 0.12** H H	1.62	0.33**	0.10** x 0.02 H L

(\* , \*\* significant at 0.05 and 0.01 probability level, respectively)

(# best check *i.e.*, Niharika for seed yield and VI-1 for husk yield, on pooled basis) (GCA effect of parents *i.e.*, H: high, L: low)

## CONCLUSION

The crosses, L<sub>10</sub> x T<sub>3</sub>, L<sub>11</sub> x T<sub>1</sub>, L<sub>5</sub> x T<sub>2</sub> and L<sub>1</sub> x T<sub>3</sub> showed positive and significant SCA effects in all the environments and over the environments for seed yield per plant. Cross L<sub>10</sub> x T<sub>3</sub> showed highest positive and significant SCA effects in all the three environments as well as on pooled basis for seed yield and other yield attributing traits. However, due to non-significant economic heterosis and low *per se* performance for seed yield, the hybrid cannot be selected only on the basis of significant SCA without high *per se* as a result, high *per se* performance and significant economic heterosis, as well as a good GCA of parents, should be used to select promising hybrids.

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