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Genetic divergence in Isabgol (*Plantago ovata* Forsk.) genotypes

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Abstract
Genetic divergence among 42 genotypes of Isabgol (*Plantago ovata* Forsk.) was estimated by Mahalanobis D^2 statistics during *Rabi* 2022-23 at the Instructional Research Farm, Rajasthan College of Agriculture, MPUAT, Udaipur for 15 characters. The mean squares due to genotypes for all the traits were significant except days to 75 percent maturity, indicated the presence of sufficient variability among the genotypes. Genotypes were grouped into XX clusters following Tocher's method (Rao, 1952). Cluster I had maximum number of genotypes *i.e*., 14 genotypes, Cluster II with 3 genotypes, Cluster III to IX each with 2 genotypes and Cluster X to XX each with single genotypes. The maximum intra-cluster distance (D^2) was found for Cluster IX (0.48) followed by cluster VIII (0.45). The maximum inter-cluster distance (D^2) was found in between cluster XIV and cluster XX (1.16) followed by Cluster XVII and Cluster XX (1.13) and cluster X and cluster XIII (1.12). This indicated that the genotypes in these clusters (UI-492, UI-509, UI-481 and UI-490, UI-499, respectively) had a diverse genotype and could be used in a hybridization programme to increase Isabgol yield. The genotypes found in the various clusters can be employed as promising parents in a hybridization program to get a high heterotic response and hence better segregants in Isabgol. The genotypes UI-482, UI-491, UI-497, UI-500, UI-483 and UI-509 were determined to be superior based on this investigation.

Keywords: Genetic divergence, cluster analysis, D^2 analysis, Isabgol

Introduction
Isabgol (*Plantago ovata* Forsk.) is a valuable medicinal crop that belongs to the Plantaginaceae family and the genus *Plantago*. It has a chromosomal number of 2n=8. It is a cross pollinated crop due to Protogynous condition. Due to its diverse ecosystems, India is one of the world's most significant sources of medicinal and aromatic plants. Isabgol is commercially known as "blond psyllium" (Dalal and Sri Ram, 1995) [2], and grown in India for its use in ayurvedic medicines (Bist *et al*. 2001) [1]. The genus *Plantago* includes 200 species (Rhan, 1996), out of which 10 occur in India. Out of 10 *Plantago* species 3 important species are found in India *viz.*, *ovata*, *Psyllium* and *indica*.
The seed husk and seed epidermis with muco-polysaccharide layers are responsible for therapeutic characteristics and are frequently used to treat constipation, diarrhoea, and intestinal discomfort. The swelling property of the mucilaginous polysaccharide of husk is responsible for the medicinal property (Husain *et al*., 1984) [4]. The husk, which accounts for around 25 to 30% of the seed, absorbs and retains water and thus acts as an anti-diarrheal medication (Dhar *et al*., 2011) [3].
The success of any breeding work is determined by the level of genetic diversity in the population. Genetic divergence research is critical for developing cultivars with higher yields, broader adaptability, desirable characteristics, and pest and disease resistance. As a result, for a successful breeding program, a plant breeder must understand genetic divergence and the characteristics employed for discriminating among the population. The most straightforward method for assessing genetic diversity is morphological characterization. D^2 analysis has been proven to be the most successful and, as a result, is commonly employed for paternal line categorization. The D^2 statistics assesses the genetic diversity of a large number of germplasm lines and aids in the identification of genetically varied genotypes for use in hybridization programs.

Materials and Methods
The experimental material consists of 42 promising genotypes of isabgol along with four checks, *i.e.*, VI-1, GI-2, UI-89 and Niharika received from AICRP on Medicinal and Aromatic

Plant, Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, MPUAT, Udaipur. The experiment was laid out in Augmented Design during *Rabi 2022-23* at the Instructional Research Farm, Rajasthan College of Agriculture, MPUAT, Udaipur. 2 rows per genotype were sown with inter row spacing 30 x 10 cm and 3m row length. Another recommended agronomic practice for zone IVA was followed to grow a healthy crop.

Traits observed

The observations were recorded on 5 arbitrarily selected plants for plant height (cm), total number of branches per plant, total number of effective spikes per plant, spike length (cm), length of peduncle (cm), length of leaves (cm), 1000 seed weight (gm), total number of leaves per plant, swelling factor (cc/g), total number of florets per spike, seed yield per plant (gm), biological yield per plant (gm) and harvest index (%). While observations for days to 50 percent flowering and days to 75 percent maturity were noted on plot basis. The mean data for all characters were computed for the statistical analysis.

Statistical analysis

The genetic divergence among 42 genotypes was calculated by Mahalanobis D^2 statistics (generalized distance) as given by Rao (1952) [8]. Based on the estimated inter cluster distances between the genotypes, the genetic divergence between various genotypes is calculated. The steps used to calculate D^2 values was according to Singh and Choudhary, 1985 [9].

Results and Discussion

Cluster Pattern

42 Isabgol genotypes were grouped into 20 clusters based on their relative magnitude of D^2 values. The result of genotypes grouped into different clusters is presented in Table 1. Cluster I was the largest with 14 genotypes followed by cluster II with 3 genotypes, cluster III to IX each with 2 genotype and cluster X to XX each with a single genotype.

Inter and Intra Cluster Distance

The inter and intra cluster average distance among 20 clusters were variable. The maximum intra-cluster distance (D^2) was found for cluster IX (0.48) followed by cluster VIII (0.45), cluster VII (0.45), cluster I (0.45), cluster VI (0.44), cluster V (0.42), cluster II (0.41), cluster IV (0.37) and cluster III (0.35). The intra-cluster distance observed in cluster X to XX were zero due to the presence of only single genotype in every cluster (Table 2).

The maximum inter-cluster distance (D^2) was found in between cluster XIV and cluster XX (1.16) followed by cluster XVII and cluster XX (1.13), cluster X and cluster XIII (1.12), cluster V and cluster XIX (1.11) and cluster II and cluster XX (1.10). The minimum inter-cluster distance was found between cluster X and cluster XI (0.55). The inter-cluster distances were higher than the intra-cluster distances, indicating a high level of genetic variation among the genotypes. As a result, genotypes in these clusters appeared to be divergent and may have different geographical/genetic origins, suggesting that they could be usefully used in the Isabgol enhancement initiative.

Table 1: Grouping of 42 Isabgol genotypes into twenty clusters by Tocher's method

Cluster	Name of genotypes	Number of genotypes
I	UI-477, UI-479, UI-480, UI-484, UI-488, UI-502, UI-503, UI-505, UI-506, UI-507, UI-508, UI-513, UI-514, UI-517	14
II	UI-485, UI-501, UI-515	3
III	UI-478, UI-496	2
IV	UI-476, UI-486	2
V	UI-497, UI-500	2
VI	UI-493, UI-510	2
VII	UI-495, UI-516	2
VIII	UI-498, UI-512	2
IX	UI-482, UI-491	2
X	UI-490	1
XI	UI-489	1
XII	UI-504	1
XIII	UI-499	1
XIV	UI-492	1
XV	UI-487	1
XVI	UI-494	1
XVII	UI-481	1
XVIII	UI-511	1
XIX	UI-483	1
XX	UI-509	1

Table 2: Average inter and intra cluster distance based on corresponding D^2 values in Isabgol

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX
I	0.45	0.60	0.57	0.61	0.67	0.60	0.64	0.59	0.63	0.76	0.67	0.77	0.69	0.57	0.58	0.74	0.65	0.68	0.62	0.83
II		0.41	0.56	0.79	0.72	0.58	0.78	0.76	0.72	0.91	0.66	0.88	0.79	0.74	0.56	0.78	0.77	0.85	1.00	1.10
III			0.35	0.66	0.75	0.63	0.78	0.68	0.76	0.73	0.84	0.72	0.67	0.81	0.79	0.72	0.73	0.58	0.62	0.83
IV				0.37	0.81	0.82	0.83	0.82	0.83	0.77	0.93	0.84	0.66	0.67	0.74	0.85	0.82	1.00	0.86	0.90
V					0.42	0.80	0.67	0.80	0.75	0.97	0.69	0.93	0.88	0.56	0.93	0.90	0.84	0.81	1.11	0.72
VI						0.44	0.70	0.71	0.73	0.83	0.61	0.87	0.87	0.78	0.75	0.78	0.81	1.01	0.59	0.76
VII							0.45	0.71	0.65	0.89	0.91	0.63	0.92	0.77	0.96	0.88	0.62	0.72	0.70	1.03
VIII								0.45	0.78	0.74	0.79	0.90	0.68	0.68	0.73	0.80	0.67	0.79	0.85	0.81
IX									0.48	0.98	0.78	0.85	0.91	0.79	0.79	0.77	0.95	0.74	0.71	0.92
X										0.00	0.55	1.03	1.12	1.06	0.94	0.78	0.84	0.69	0.98	0.99
XI											0.00	0.92	0.69	0.64	0.72	0.97	0.70	0.93	0.92	1.05
XII												0.00	0.55	0.58	0.66	0.85	1.01	0.89	0.72	1.02
XIII													0.00	0.61	0.89	0.95	0.78	0.88	1.04	1.10
XIV														0.00	0.60	0.96	1.03	0.95	0.73	1.16
XV															0.00	0.72	0.93	0.93	0.75	0.77
XVI																0.00	0.74	0.80	1.00	0.88
XVII																	0.00	1.09	0.97	1.13
XVIII																		0.00	0.77	0.96
XIX																			0.00	0.88
XX																				0.00

Cluster Mean

The comparison of the cluster mean value of 15 characters of different clusters has been presented in the table 3. The extent of differences in cluster mean values for different character was found to be prominent.

The difference for days to 50 percent flowering varies from 56 days (cluster VI, XV, XIX) to 60 days (cluster V, XVI), days to 75 percent maturity from 95 days (cluster XIII) to 100 days (cluster VII, XII, XV, XX), plant height from 26.25 cm (cluster XX) to 37.00 cm (cluster XIV), number of branches per plant from 4.90 (cluster XX) to 6.55 (cluster IX), number of effective spikes per plant from 28.80 (cluster XX) to 46.40 (cluster XIV), spike length from 4.24 cm (cluster X) to 6.03 cm (cluster IV), length of peduncle from 15.80 cm (cluster XVI) to 22.00 cm (cluster X), length of leaves from 15.40 cm (cluster XII, XIII) to 19.57 cm (cluster IX), 1000 seed weight from 1.60 gm (cluster XII) to 2.08 gm (cluster X), number of leaves per plant from 61.60 (cluster XVIII) to 96.00 (cluster XIX), swelling factor from 9.20 cc/g (cluster XIX) to 11.50 cc/g (cluster VIII, X), number of florets per spike from 76.20 (cluster XVII) to 106.10 (cluster X), seed yield per plant from 2.99 gm (cluster X, XI) to 4.85 gm (cluster VII), biological yield per plant from 15.65 gm (cluster XI) to 26.78 gm (cluster VII) and harvest index from 15.26 percent (cluster XVII) to 23.25 percent (cluster XIV).

Table 3: Mean values of different characters for 42 Isabgol genotypes grouped into 20 clusters.

Cluster	Days to 50 percent flowering	Days to 75 percent maturity	Plant height (cm)	Number of branches per plant	Number of effective spikes per plant	Spike length (cm)	Length of peduncle (cm)	Length of leaves (cm)	1000 seed weight (gm)	Number of leaves per plant	Swelling factor (cc/g)	Number of florets per spike	Seed yield per plant (gm)	Biological yield per plant (gm)	Harvest index (%)
I	58.07	98.44	31.24	5.51	39.67	5.29	19.85	17.82	1.80	85.67	10.49	87.66	4.23	21.55	19.72
II	56.67	99.67	33.30	5.10	40.97	5.34	17.65	17.39	1.77	79.67	10.50	80.90	3.94	23.19	16.89
III	57.00	99.00	26.91	5.10	35.70	4.93	19.97	17.15	1.68	81.80	9.50	80.40	3.67	20.72	18.01
IV	59.00	99.00	31.63	5.25	38.80	6.03	20.62	18.72	1.67	86.10	9.75	88.90	3.71	20.78	17.85
V	60.00	99.50	34.74	5.20	40.50	5.00	18.44	17.80	1.76	77.60	10.75	82.00	3.78	17.28	21.86
VI	56.00	99.50	29.41	5.50	37.14	5.59	18.48	15.51	1.98	85.20	10.50	83.20	4.18	20.77	20.31
VII	58.50	100.00	36.32	6.40	45.20	5.81	21.15	18.17	2.04	80.90	11.00	92.05	4.85	26.78	18.08
VIII	56.50	96.50	29.05	6.40	45.55	5.60	20.96	17.86	2.05	85.50	11.50	104.80	4.62	23.49	19.97
IX	57.50	98.50	31.40	6.55	41.40	5.75	16.76	19.57	1.73	90.40	11.00	85.60	4.83	24.75	19.59
X	58.00	98.00	30.17	6.30	32.80	4.24	22.00	17.76	2.08	67.60	11.50	106.10	2.99	16.62	17.99
XI	57.00	96.00	35.18	6.30	31.80	4.46	18.42	15.84	1.93	73.80	11.25	87.20	2.99	15.65	19.11
XII	58.00	100.00	35.83	6.10	39.20	5.56	20.40	15.40	1.60	84.80	10.50	101.20	4.56	26.09	17.48
XIII	58.00	95.00	32.37	5.90	37.60	5.94	20.82	15.40	1.66	76.20	10.50	86.60	4.21	24.97	16.86
XIV	59.00	98.00	37.00	5.90	46.40	5.64	19.15	16.20	1.70	83.60	10.00	103.60	4.72	20.30	23.25
XV	56.00	100.00	34.50	5.10	37.40	5.08	17.24	18.40	1.67	94.60	10.50	102.40	3.85	21.63	17.80
XVI	60.00	99.00	29.67	5.30	38.20	4.90	15.80	16.94	1.92	78.60	10.00	103.80	4.15	24.13	17.20
XVII	59.00	97.00	31.70	5.70	40.20	5.00	20.20	17.40	2.01	88.40	10.50	76.20	3.41	22.35	15.26
XVIII	58.00	98.00	33.15	5.90	33.60	4.48	21.34	19.40	1.94	61.60	10.50	102.80	4.23	23.78	17.79
XIX	56.00	99.00	29.50	6.10	34.40	5.26	20.40	17.40	1.85	96.00	9.20	94.00	4.51	21.11	21.36
XX	57.00	100.00	26.25	4.90	28.80	4.98	18.80	18.44	1.77	93.80	11.00	90.40	3.45	15.94	21.64

Relative Contribution of different Character towards total Divergence

The percent contribution of independent characters in the direction of total divergence has been presented in Table 4. The number of florets per spike was found to be the most important character in contributing to overall divergence, accounting for 49.38 percent followed by number of leaves per plant (24.33%), number of effective spikes per plant (11.72%), plant height (6.02%), biological yield per plant (2.42%), length of peduncle (1.81%), days to 75% maturity (1.37%), days to 50 percent flowering (1.22%), length of leaves (1.12%) and remaining characters with minute contribution.

Table 4: Percent contribution of different characters towards total divergence in Isabgol

S. No.	Character name	Percent contribution
1.	Days to 50 percent flowering	1.22
2.	Days to 75 percent maturity	1.37
3.	Plant height (cm)	6.02
4.	Number of branches per plant	0.15
5.	Number of effective spikes per plant	11.72
6.	Spike length (cm)	0.11
7.	Length of peduncle (cm)	1.81
8.	Length of leaves (cm)	1.12
9.	1000 seed weight (gm)	0.01
10.	Number of leaves per plant	24.33
11.	Swelling factor (cc/g)	0.25
12.	Number of florets per spike	49.38
13.	Seed yield per plant (gm)	0.07
14.	Biological yield per plant (gm)	2.42
15.	Harvest index (%)	0.02

Conclusion

Genotypes from distantly located clusters could be exploited to generate desirable transgressive segregants and improved genotypes for those traits with high mean values in these clusters for future isabgol development programs. Cluster XIV and cluster XX having highest inter-cluster distance; therefore, selection of parents should be done from these 2 clusters to get more variability and heterotic effect. Cluster XIV and cluster XX having highest divergence between them so that they can be used in recombinant as well as heterotic breeding, whereas between cluster X and XI lowest inter-cluster distance was found, indicates lesser divergent genotypes from each other.

Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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