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Exploring genetic variability parameters for seed yield and its component traits in isabgol (*Plantago ovata* Forsk.) genotypes

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Abstract

A research trial was conducted during 2023-24 (*Rabi*) to evaluate the genetic variability parameters of 58 isabgol genotypes. The experiment was laid out in Augmented Randomised Complete Block Design (ARCBD) at Instructional Research Farm, MPUAT, Udaipur. The mean sum of squares due to genotypes for all the characters were significant except for days to 50% flowering, harvest index and husk recovery, as revealed from ANOVA indicating the existence of enormous genetic variability among different genotypes for these traits studied. The marginal difference between GCV and PCV suggested least influence of environment in the expression of traits. Moderate values of GCV and PCV were recorded for number of branches plant^{-1}, husk yield plant^{-1}, biological yield plant^{-1} and seed yield plant^{-1}. High heritability coupled with high genetic gain was displayed by husk yield plant^{-1} followed by number of branches plant^{-1}, biological yield plant^{-1}, seed yield plant^{-1}, number of florets spike^{-1}, length of spike, number of effective spike plant^{-1}, test weight, number of leaves plant^{-1} and plant height indicating predominance of additive gene action hence, improvement based on phenotypic value may be efficacious through direct selection.

Keywords: Isabgol, genetic variability, heritability, genetic gain

Introduction

Isabgol (*Plantago ovata* Forsk.) is a significantly important medicinal crop having more than 200 species (Rahn, 1996) [23], among them 10 occurs in India. Three significant species of these ten *Plantago* species are found in India *viz*., *ovata, psyllium and indica*. It belongs to the family Plantaginaceae and genus *Plantago* and also named as "blond psyllium" commercially (Dalal and Sri Ram, 1995) [7] and cultivated in India for its ayurvedic treatment purposes (Bist *et al*., 2001) [3]. It is preponderantly cross-pollinated species possessing a narrow genetic base (Kaswan *et al*., 2013) [16] with chromosomal number of 2n=2x=8 and genome size of about 621 Mb (Pandita, 2013) [21]. Although it is autochthonous to the Persia and West Asia but was introduced by Muslim settlers in India during the middle age (Lal *et al*., 1999) [20].

Flower favours outcrossing because they are bisexual, tetramerous, anemophilous and protogynous in nature (Punia, *et al*., 1985) [22]. The muco-polysaccharide layers are present on seed husk and seed epidermis which has therapeutic properties such as relieving intestinal discomfort, diarrhoea and chronic constipation. Seeds are also believed to have cooling, excellent demulcent effect and are useful in alleviating inflammation (Beara *et al*., 2010) [2] and bilious disorders of digestive organs. They are also applied as a poultice for rheumatic and gouty swelling. The mucilaginous polysaccharide of husk which has swelling characteristics is responsible for therapeutic qualities. (Husain *et al*., 1984) [12]. It is also used in calico printing, dyeing, agar-agar media preparation, making of gums and jellies, as a binder in tablets, as thickener and fixative in ice-creams, confectionaries and in cosmetics industries.

Seeds of psyllium decreases the level of blood cholesterol remarkably and locally utilized in medicines which are classified as Unani and Ayurvedic medicines (Dhar *et al*., 2011) [8]. In paper and textile manufacturing industries it has been used as a deflocculant, as an emulsifying agent, as a binder or lubricant in meat products and as a replacement of fat in low-calorie foods

(Dhar *et al*., 2011) [8]. Isabgol species are used in both traditional and conventional systems of medicine throughout Asia, Europe, and North America (Sarihan *et al*., 2005) [25].

The isabgol productivity is way below the preferred level and India is incapable to meet our global demands. There is an ample scope to increase the productivity of isabgol through genetic enhancement. Primarily, genetic improvement depends upon the nature and magnitude of genetic variability in plant characters, overall genetic and genotypic diversity and relationship between characters. The major constraint for the improvement of psyllium crop is limited existing genetic variability. Crop enhancement programmes rely upon genetic variability as a key element to achieve high-yielding and improved varieties. This involves assessing diverse genetic traits like variance components, coefficient of genotypic and phenotypic variation, inheritance pattern and genetic advancement. Hence, the present research was carried out to appraise genetic variability parameters among 58 isabgol genotypes.

Materials and Methods

The experimental material consists of 58 promising genotypes of isabgol accompanying four checks, *i.e*., UI-89, VI-1, GI-2 and Niharika procured from AICRP on Medicinal and Aromatic Plants & Betelvine (MAP&B), Department of Genetics and Plant Breeding, MPUAT, Udaipur. The experiment was laid out in Augmented Randomised Complete Block Design (ARCBD) at Instructional Research Farm, MPUAT, Udaipur. Observations were recorded for 17 characters *viz*., days to 50% flowering(DF), days to 75% maturity(DM), plant height(PH), number of branches plant^{-1}(NB/P), number of effective spikes plant^{-1}(S/P), length of spike(SL), length of peduncle(PL), length of leaf(LL), test weight(TW), number of leaves plant^{-1}(L/P), number of florets spike^{-1}(F/S), seed yield plant^{-1}(SY/P), biological yield plant^{-1}(BY/P), harvest index(HI), husk recovery(HR), husk yield plant^{-1}(HY/P), swelling factor (SF)on five arbitrarily opted plants for each genotype, although days to 50% flowering and days to 75% maturity traits were recorded on a per-plot basis. The husk recovery was estimated according to process suggested by Thanki and Talati, (1983) [27] and swelling factor was determined by an improved method suggested by Kokate, (1982) [18]. Husk yield plant^{-1} was figured out utilizing formula suggested by Kalyansundaram *et al.* (1999) [15]. The analysis of variance was worked out separately for each character as per the method suggested by Federer (1956) [9] in order to test the difference among the genotypes. The coefficient of genotypic and phenotypic variation was calculated by using the formula suggested by Burton (1952) [5]. Estimates of heritability (h^2BS) was figured out as per the equation suggested by Burton and Devane (1953) [4] and Hanson *et al.* (1956) [11]. Genetic advance and genetic gain were computed as per the formula described by Johnson *et al*. (1955) [14].

Results and Discussion

Mean sum of squares from ANOVA for characters under study are displayed in Table-1. The mean sum of squares due to genotypes for all the characters were significant except for days to 50% flowering, harvest index and husk recovery, as revealed from ANOVA suggesting the existence of high genetic variability among different genotypes for these traits studied. Genetic variability analysis may not be appropriate for the trait *viz*., days to 50% flowering, harvest index and husk recovery as they revealed non-significant mean sum of squares due to genotypes. Almost similar findings were also reported by Singh and Lal (2009) [26], Jain and Paul (2011) [13] and Kumar *et al.* (2013) [19], Yousaf *et al*. (2022) [29] for most of the traits.

The parameters of genetic variability *viz*., mean, range, phenotypic and genotypic coefficient of variation (%), heritability (%) in broad sense, genetic advance (%) and genetic gain (%) for each trait are given in Table 2. GCV and PCV are depicted graphically in Fig.1 and heritability in broad sense and genetic gain are depicted graphically in Fig.2, respectively.

In this study, the marginal difference between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) indicated least influence of environmental conditions, so selection for these traits will be efficacious. Moderate coefficient of variation in terms of both genotypic and phenotypic value was reported for number of branches plant^{-1}, husk yield plant^{-1}, biological yield plant^{-1} and seed yield plant^{-1}. Almost similar outcomes were reported by Yousuf *et al*. (2022) [29], Choudhary *et al*. (2017) [6] for biological yield plant^{-1}. The outcomes were comparable to Jain and Paul (2011) [13], Kaswan *et al*. (2018) [17], Choudhary *et al*. (2017) [6] for seed yield plant^{-1}. Low GCV and PCV were obtained for days to 75% maturity and swelling factor.

Table 1: ANOVA for yield and its component traits in isabgol

SN	Character	Block	Treatment	Check	Germplasm	C v/s G	Error
		[2]	[61]	[3]	[57]	[1]	[6]
1.	Days to 50% flowering	6.08*	2.80	0.53	2.17	45.57**	0.86
2.	Days to 75% maturity	0.08	5.98*	3.19	5.42*	46.31**	1.19
3.	Plant height (cm)	0.52	12.35**	2.04**	13.11**	0.01	0.16
4.	Number of branches plant^{-1}	0.13	0.96**	0.56	0.99**	0.18	0.12
5.	Number of effective spikes plant^{-1}	2.13	27.22**	18.18**	27.87**	17.51*	1.33
6.	Length of spike (cm)	0.04	0.53**	1.12**	0.51**	0.00	0.01
7.	Length of peduncle (cm)	0.01	3.89**	11.08**	3.36**	12.43**	0.01
8.	Length of leaf (cm)	0.00	3.11**	9.40**	2.83**	0.01	0.05
9.	Test weight (g)	0.01**	0.04**	0.00	0.05**	0.05**	0.00
10.	Number of leaves plant^{-1}	3.61	107.30**	19.07	113.21**	35.07	7.77
11.	Number of florets spike^{-1}	4.29	136.52**	131.03**	134.13**	288.76**	1.16
12.	Seed yield plant^{-1} (g)	0.01	0.35**	0.09**	0.32**	2.70**	0.01
13.	Biological yield plant^{-1} (g)	0.47	12.34*	0.58	13.16*	0.99	1.96
14.	Harvest index (%)	1.17	6.94*	3.75	6.2	58.24**	1.77
15.	Husk Recovery (%)	0.22	1.63	2.23	1.59	1.88	0.76
16.	Husk yield plant^{-1} (g)	0.00	0.05**	0.00	0.05**	0.22**	0.00
17.	Swelling factor (ccg^{-1})	0.07	0.52**	0.80**	0.52**	0.09	0.07

*, ** Significant at 5% and 1% respectively.

[] Degrees of freedom

The coefficient of variation only predicts the degree of heterogeneity for various characters, but it provides no information on the heritable part of the variability. Selection can be effective where there is a moderate to high amount of heritability followed by a moderate to high genetic gain. This indicates that additive gene action is involved in the inheritance of the characters in question. The majority of the characters projected high heritability such as peduncle length (99.59%) followed by number of florets spike^{-1} (99.14%), test weight (99.11%), plant height (98.79%), leaf length (98.14%), length of spike (98.08%), husk yield plant^{-1} (97.74%), seed yield plant^{-1} (96.41%), number of effective spikes plant^{-1} (95.24%), number of leaves plant^{-1} (93.14%), number of branches plant^{-1} (87.99%), swelling factor (86.42%), biological yield plant^{-1} (85.13%), days to 75% maturity (77.98%). The outcomes were comparable to Jain and Paul (2011) [13] for length of spike and test weight, number of florets spike^{-1}, Kaswan *et al*. (2018) [17] for days to 75% maturity, number of effective spikes plant^{-1}, seed yield plant^{-1}, biological yield plant^{-1}, Ahmed and Lal (2021) [1] for seed yield plant^{-1}, husk yield plant^{-1}, swelling factor.

Table 2: Mean, Range and Genetic variability parameters of yield and its component traits in isabgol

SN	Character	Mean	Range (Min.- Max.)	GCV (%)	PCV (%)	h^2BS (%)	GA (%)	GG (%)
1	Days to 50% flowering	60.70	57.00-63.00	1.89	2.43	60.28	1.83	3.02
2	Days to 75% maturity	101.74	97.00-105.00	2.02	2.29	77.98	3.75	3.69
3	Plant height (cm)	32.18	25.25-38.80	11.18	11.25	98.79	7.38	22.93
4	Number of branches plant^{-1}	5.62	3.70-7.00	16.61	17.71	87.99	1.81	32.14
5	Number of effective spikes plant^{-1}	42.60	29.20-51.70	12.12	12.42	95.24	10.37	24.40
6	Length of spike (cm)	5.50	3.70-6.85	12.79	12.91	98.08	1.44	26.13
7	Length of peduncle (cm)	21.39	15.90-23.25	8.59	8.60	99.59	3.77	17.68
8	Length of leaf (cm)	20.34	15.55-22.20	8.19	8.27	98.14	3.41	16.74
9	Test weight (g)	1.81	1.43-2.13	11.72	11.77	99.11	0.44	24.07
10	Number of leaves plant^{-1}	85.02	64.90-98.70	12.06	12.50	93.14	20.44	24.01
11	Number of florets spike^{-1}	89.10	69.90-105.70	12.89	12.95	99.14	23.69	26.48
12	Seed yield plant^{-1} (g)	4.14	2.97-5.17	13.25	13.50	96.41	1.12	26.85
13	Biological yield plant^{-1} (g)	22.60	15.30-27.50	14.82	16.06	85.13	6.37	28.21
14	Harvest index (%)	18.57	14.69-25.75	11.24	13.30	71.43	3.67	19.60
15	Husk Recovery (%)	33.23	31.10-35.40	2.74	3.80	51.90	1.35	4.07
16	Husk yield plant^{-1} (g)	1.38	0.96-1.83	16.57	16.74	97.94	0.47	33.83
17	Swelling factor (ccg^{-1})	11.01	9.70-12.10	6.06	6.52	86.42	1.28	11.62

Maximum genetic gain was observed for husk-yield plant^{-1} (33.83%) followed by number of branches plant^{-1} (32.14%), biological yield plant^{-1} (28.21%), seed yield plant^{-1} (26.85%), number of florets spike^{-1} (26.48%), spike length (26.13%), number of effective spikes plant^{-1} (24.40%), test weight (24.07%), number of leaves plant^{-1} (24.01%), plant height (22.93%) and peduncle length (17.68%), leaf length (16.74%), swelling factor (11.62) exhibited moderate genetic gain. Whereas, low genetic gain was noted for days to 75% maturity (3.69%). The outcomes were comparable to Jain and Paul (2011) [13] for length of spike and test weight, number of florets spike^{-1}, Kaswan *et al*. (2018) [17] for days to 75% maturity, number of effective spikes plant^{-1}, seed yield plant^{-1}, biological yield plant^{-1}, Ahmed and Lal (2021) [1] for seed yield plant^{-1}, husk yield plant^{-1}, swelling factor.

High heritability coupled with high genetic gain was noted for husk yield plant^{-1} followed by number of branches plant^{-1}, biological yield plant^{-1}, seed yield plant^{-1}, number of florets spike^{-1}, length of spike, number of effective spike plant^{-1}, test weight, number of leaves plant^{-1} and plant height indicating predominance of additive gene action hence, improvement based on phenotypic value may be effective through direct selection. Comparable findings were suggested in earlier reports by Singh and Lal (2009) [26], Choudhary *et al*. (2017) [6] and Kaswan *et al*. (2018) for biological yield plant^{-1} and seed yield plant^{-1}. The outcomes were comparable to Jain and Paul (2011) [13] for length of spike and test weight, number of florets spike^{-1}, Kaswan *et al*. (2018) [17] for days to 75% maturity, number of effective spikes plant^{-1}, Ahmed and Lal (2021) [1] for seed yield plant^{-1}, husk yield plant^{-1}, swelling factor.

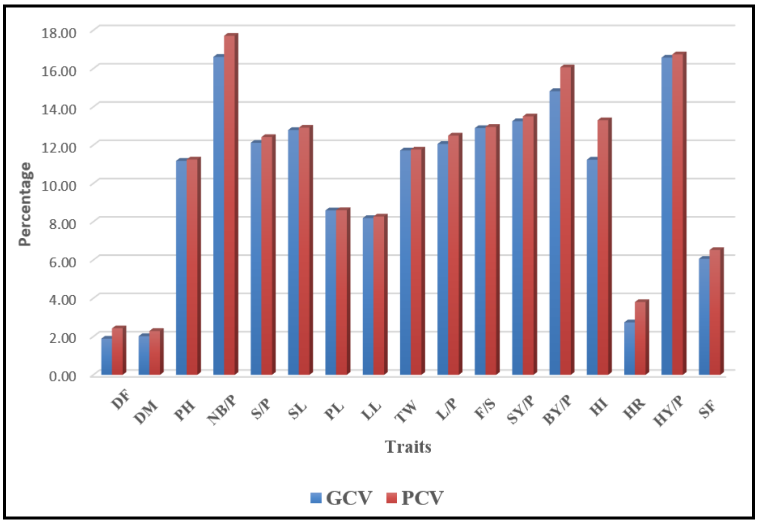

Fig 1: Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV)

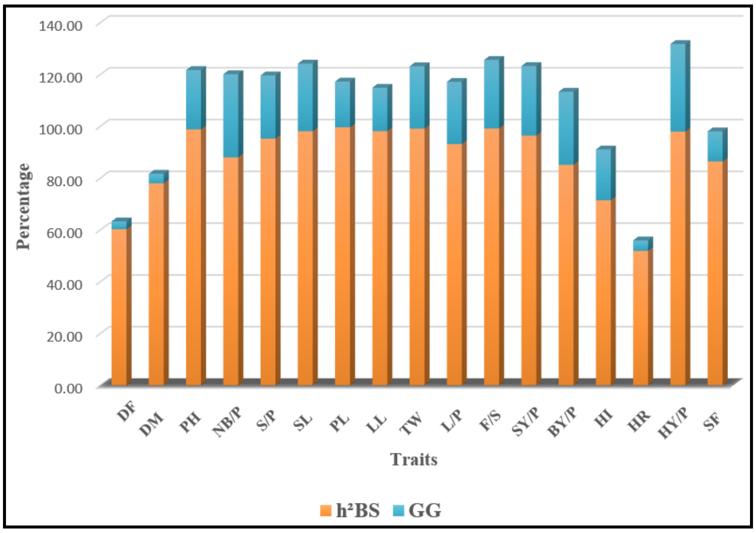

Fig 2: Heritability in broad sense and genetic gain

Conclusion

In the present investigation, genotypes *viz*., UI-519, UI-532, UI-533, UI-543, UI-546, UI-565 and UI-570 were superior not only in term of seed-yield plant^{-1} but also in terms of traits like plant height, number of branches plant^{-1}, number of effective spikes plant^{-1}, length of spike, length of peduncle, length of leaf, test weight, number of florets spike^{-1}, biological yield plant^{-1}, husk recovery, husk yield plant^{-1}, swelling factor. These diverse genotypes could be used in the future breeding programme for the genetic improvement of isabgol.

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