



Research Article

Assessment of Heritability, Variability and Genetic Advance for Yield Linked Factors Related to Diversify Psyllium (*Plantago ovate* L.) Germplasm in Arid Conditions

Malik Muhammad Yousaf¹, Wali Muhammad¹, Muhammad Mohsin Raza^{1*}, Mumtaz Hussain¹, Muhammad Jahangir Shah¹, Bashir Ahamad¹, Annum Sattar², Hera Gull³, Sonia Sumreen⁴, Malik Waqar Yousaf⁵, Nazakat Nawaz⁶ and Nazim Hussain⁷

¹Pakistan Agricultural Research Council, Arid Zone Research Institute Bahawalpur, Pakistan; ²Soil and Water Testing Laboratory, Sheikhupura, Soil Fertility Research Institute, Punjab, Pakistan; ³Department of Horticultural Science, Faculty of Agriculture and Environmental Sciences, The Islamia University of Bahawalpur, Pakistan; ⁴Land Resources Research Institute, National Agricultural Research Center Islamabad, Pakistan; ⁵Department of Plant Breeding and Genetics, Faculty of Agriculture and Environmental Sciences, The Islamia University Bahawalpur, Pakistan; ⁶Pakistan Agriculture Research Council Islamabad, Pakistan; ⁷Department of Agronomy, Faculty of Agricultural Sciences and Technology BZU, Multan, Pakistan.

Abstract | *Plantago ovate* (Psyllium), an important medicinal herb at the global level, grown in winter season. Determination of heritability and genetic variability within Psyllium is a baseline strategy for the improvement of psyllium improving program. This investigation was designed to assess the heritability and genetic diversity among fifty-eight (58) psyllium genotypes. Data on eight yield linked factors, i.e., Days to floral initiation (DFI), Days to 50% flowering (DF), number of tillers per plant (NTPP), plant height (PH), spike length (SPL), number of spikes per plant (NSPP), days to maturity (DM) and seed yield per plant (SYPP) were recorded. Estimates of heritability values were high in SYPP and DF ranged from 0.998 to 0.930, respectively, like all characters except DFI noted as 0.658 whereas genetic advance ranged between 16.3069 in the parameters i.e., NTPP and 1.4473 for the character of SYPP. Highest coefficient of variation (CV=11.53%) was estimated for SPL followed by SYPP (CV=8.04%), while minimum (CV=1.41%) for DM. Likewise, seed yield per plant also reflected significant results among the fifty-eight genotypes. In all trails genotypic coefficient of variability (GCV) was found lesser than phenotypic coefficient of variability (PCV). Principal component analysis showed that first three PCs reflected eigen values more than one where cumulative value was 61.78% of the total variability. The first one accounted as highest proportional value of total variability in all PCs and in remaining PCs lesser amount of variation. High values of heritability referred to broad sense genetic advance possessing higher values in plant attributes under study witnessed that these parameters abide by the effects of additive genes, concluding that sorting of superior germplasm may direct the quick heritable improvement of the material.

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***Correspondence** | Muhammad Mohsin Raza, Pakistan Agricultural Research Council, Arid Zone Research Institute Bahawalpur, Pakistan; Email: mohsinraza@parc.gov.pk

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Keywords | *Plantago ovate* germplasm, ANOVA, Genotypic correlations GCV, PCV, Genetic advance, Heritability



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Introduction

Plantago ovate (Psyllium) is locally known as Isphghol belongs to family Plantaginaceae which is native to Iran and later came from Asia to Europe and then widely distributed to Egypt, Middle East, Afghanistan, and north India. In Pakistan, it was grown in southern areas of Punjab, Sindh and Balochistan (Anonymous, 2001). Isabgol is a short-statured annual herb its height ranged from 30 to 40 cm. Many shoots bearing flowers emerges from the origination end of plant. The isabgol word is a Persian which is a combination of “isap” and “ghol” resembling shape of horse ear. Its seeds are embedded in capsules later on open at maturity. Seed husk is thin, white, ferry shaped, lucent, and odorless with mucilaginous taste. It has well developed tap root system with few fibrous secondary roots. The seeds are sweet in taste, laxative and anti-inflammatory. The husk of isabgol is extensively utilized for treatment of upset stomach and other medical issues i.e., dysentery, colonic and gastritis. It is also used as industrial purposes like for making ice cream, candy etc. (Anonymous, 2016). In Pakistan, maximum species of *Plantago* are grown in Sindh. The crop life cycle comprises of four months in rabi season. In the areas of Sindh province, the crop is grown in Mirpurkhas, Umerkot, Jamshoro, and other districts. There is less authentic and incomplete crop statistics of isabgol. However, as per unofficial data, in 2014, isabgol was sown in 3200 acres in Umerkot, Kunri, Samaro, and Pithoro talukas, which is increased to 5000 acres during the year 2015. This plant could be successfully cultivated in Sindh and Punjab as a cash crop, under water scarce conditions. Pakistan imports a huge quantity of psyllium seed from other neighboring countries. The demand of isabgol is increasing day by day in Pakistan also (Anonymous, 2016).

Seeds of *P. ovata* decreases the levels of blood cholesterol remarkably and locally utilized in medicines which are categorized as Unani and Ayurvedic medicines (Dhar *et al.*, 2011). It is predominantly cross pollinated specie possessing a narrow genetic base carrying number of chromosome ($2n=2x=8$), size of small chromosome (621 Mb), (Pandita, 2013). The productivity of isabgol is affected by biotic and abiotic elements leading decrease in seed and its quantitative and qualitative parameters. *Plantago* is a wild specie carrying important genes for the tolerance of biotic and abiotic stresses, which can create a revolution

in psyllium production (Dhar *et al.*, 2011). Keeping in view the previous research and before initiating a comprehensive breeding program, it is necessary to know about the status and level of heritability, genetic advance and variability related to existing breeding commodity while defining the heritability is to explore differences recorded among individuals leading diversification in genetic makeup or some other factors like environment. Genetic advance explore an idea carrying a new population possessing improved traits through selections as its original germplasm. Present investigation was commenced with the aim to probe the level of variability due to genetic point of view and expected genetic advance persisting.

Materials and Methods

Research trial was executed at agricultural farm of Pakistan Agricultural Research Council Arid Zone Research Institute, Bahawalpur, having latitude 29.22°, longitude 71.38° and altitude 367 ft, while field temperature was recorded 6°C to 40.7°C, with relative humidity recorded from 76.5 to 80.4% and rainfall was observed 6 to 13 mm, in 2019-20. The study comprising the germplasm of fifty-eight different accessions (Table 1), obtained from IABGR, NARC, Islamabad, Pakistan, and laid down in RCBD with three replications in the season of rabi, 2019-21. Single row method was adopted for sowing of each genotype in the field with three replications. The two meter length of each row consists of 30 plants and 45 cm distance was maintained between plots. All cultural practices recommended for the cultivation of psyllium were practiced. The data was recorded for eight genetic parameters viz; (DFI), (DF), (PH), (NTPP), (NSPP), (SPL), (DM) and (SYPP). Observations were conducted on five randomly existing plants. Heritability referred to broad sense and it was explained as the ratio between the total genetic variance to the phenotype variance. Probable genetic advance was measured following Johnson *et al.* (1955). Variation is the point difference for diversity between individuals because of diversification in their genetic constitution or environmental factor. Heritable diversity is useable for long term genetic development (Singh, 2000). Low heritability is an important reducing factor in progress of plant breeding. Heritability as broad sense indicates relevancy of total genetic advance containing dominance, additive and epistatic variance referred to the phenotypic variance (Falconer and Mackay, 1996; Riaz and Chowdhry,

2003). Significant operation of the heritability in the genetic investigation of measurable parameters in estimate able contribution to hint trust worthiness of phenotypic values as a leading role to breeding value. (Dabholkar, 1992; Falconer and Mackay, 1996).

Table 1: *Isphagol* germplasms used in study.

S. No.	Accession No.	S. No.	Accession No.	S. No.	Accession No.
1	20571	26	20683	51	IHGM-1
2	20573	27	20684	52	IMGH-2
3	20582	28	20685	53	IMGH-3
4	20597	29	20709	54	IHGM-4
5	20617	30	20714	55	IHGM-5
6	20640	31	20758	56	IHGM-6
7	20658	32	20835	57	IHGM-7
8	20664	33	20856	58	IHGM-8
9	20665	34	20857		
10	20666	35	20905		
11	20667	36	20972		
12	20668	37	20987		
13	20670	38	20996		
14	20671	39	21162		
15	20672	40	21445		
16	20673	41	21213		
17	20674	42	21216		
18	20675	43	21260		
19	20676	44	21281		
20	20677	45	21301		
21	20678	46	IH-901		
22	20679	47	ISH-902		
23	20680	48	IMI-903		
24	20681	49	IMP-904		
25	20682	50	ISU-905		

Results and Discussion

The appraisal of genetic assortment plays a key role in breeding process but also for proficient execution, categorization and defense mechanism of genetic resources. Plantago germplasm under cultivation has less diversity and have intolerance to numerous stresses i.e., biotic and abiotic.

Eight number of plant parameters were noticed for screening of fifty-eight Plantago genotypes accounted for ANOVA with other genetic attributes revealed highly significant results among all characters under observation showing that selection for related

attributes may be feasible. All the parameters related to phenotype having minimum, maximum mean and CV values are allocated (Table 3) in which estimates of Heritability values were high in SYPP and DF ranged from 0.998 to 0.930, respectively like all characters except DFI noted as 0.658 (Table 3). Exhibition of Genetic advance values were between 16.3069 in the parameters i.e., NTPP and 1.4473 for the character of SYPP. Highest coefficient of variation (CV=11.53%) was estimated for SPL followed by SYPP (CV=8.04%), while minimum (CV=1.41%) for DM. Likewise, seed yield per plant also reflected significant results among fifty-eight genotypes. These results are in congruous with earlier information (Patel and Saravanan, 2010). The phenotypic differences among genotypes were due to factor and magnitude of out-crossing is a capable factor (Singh *et al.*, 2009). Abbreviation used in Static mention in (Table 2).

Table 2: *Plant attributes and other abbreviations.*

S. No	Abbreviations used	Name of characters
1	DFI	days to floral initiation
2	DF	days to 50% flowering
3	PH	plant height
4	NTPP	number of tillers per plant
5	NSPP	number of spikes per plant
6	SPL	spike length
7	DM	days to maturity
8	SYPP	seed yield per plant
9	ANOVA	Analysis of variance
10	SLCA	Single linkage cluster analysis

Table 3: *ANOVA for 58 genotypes of isphagol.*

Parameters	MS(R)	MS (V)	MS (E)	Mean +SE	h ²	GA	CV (%)
DFI	12.8506						4.94
DF	6.879						3.60
PH	2.1583						6.31
NTPP	2.950						6.16
NSPP	2.431						7.00
SPL	0.10420						11.53
DM	1.4885						1.41
SYPP	0.0024						8.04

Genotypic and phenotypic correlation

Correlation investigations were begun with idea of interaction of different traits, their forms and contributing magnitude to yield. This relationship was observed in eight parameters mentioned in Table

4, in which genotypically, DFI is significant and has positive effect with DF, DM and SYPP but non-significant and found positive with PH whereas non-significantly and negatively associated with NTPP while phenotypically, DFI is significant at high level and positively associated with DF and DM while this is non-significant but positive with PH and SYPP while have negatively effect and non-significant with NTPP, NSPP and SPL in contrast, the trait DFI is significant and negatively correlated with NSPP.

With respect to trait DF as per genotypic instance this trait is found in significantly positive correlation with PH, NTPP and DM while negative with NSPP while it is non-significant and negatively correlated with SYPP. On the other hand, phenotypically, this character is highly significant and has a positive relation with DM but has a significant correlation with PH and NTPP whereas negative and non-significant association with NSPP and SPL.

Genotypic parameter PH has positive and significant correlation with the traits NTPP, NSPP, SPL DMM and SYPP while positive and highly significant with NTPP and DM but significant with one-character

NSPP whereas it has non-significant with SPL and SYPP with respect to phenotypic point of view.

According to genotypic point of view the trait NTPP is significant and it is positively associated with NSPP, SPL but negative with DM though it is non-significant and positively associated with SYPP. Phenotypically, NTPP parameter is highly significant and positively associated with NSPP but it is positive and non-significant association with SPL and SYPP however, it is negatively and non-significantly associated with DM.

As per genotypic point of view the trait NSPP is significant but negatively correlated with DM while positively with the character SPL but negatively correlated with SYPP, in contrast phenotypically the trait NSPP is found negatively and non-significantly correlated with DM and SYPP while found positive and non-significant association with trait SPL.

Genotypic parameter SPL is found positive and significantly correlated with DM while non-significantly and negatively associated with SYPP, whereas it has a non-significant and positive correlation with

Table 4: Genotypic (r_g) and phenotypic (r_p) correlation.

Traits	DFI	DF	PH	NTPP	NSPP	SPL	DM	SYPP
DFI								
r_g	1	0.4861*	0.0068	-0.0171	-0.2049*	-0.0833	0.3579*	0.1326*
r_p		0.3660**	-0.0165	-0.0111	-0.1619*	-0.0580	-0.3042**	-0.1087
DF								
r_g		1	0.1379*	0.0668*	-0.0250*	-0.0098	0.4524*	-0.0385
r_p			0.1311	0.0628	-0.0243	-0.0102	0.4318**	-0.0366
PH								
r_g			1	0.2323*	0.1592*	0.0840*	-0.2574*	0.0812*
r_p				0.2244**	0.1518*	0.0800	0.2475**	0.0755
NTPP								
r_g				1	0.9057*	0.1204*	-0.0891*	0.0207
r_p					0.8930**	0.1204**	-0.0869	0.0204
NSPP								
r_g					1	0.0133	-0.0844*	-0.0152*
r_p						0.0155	-0.0829	-0.0157
SPL								
r_g						1	0.0678*	-0.1060
r_p							0.0639	-0.1022
DM								
r_g							1	0.0583
r_p								0.0578
SYPP								
r_g								1
r_p								

DM, while negatively correlated with SYPP as per phenotypic point of view. According to genotypic and phenotypic characteristics DM is non significantly and negatively correlated with SYPP. This Positive and significant mutual relationship were analyzed for genotypic and phenotypic relations in link with DFI, DF, PH, NTPP, NSPP, SPL, DM and SYPP for phenotypic characteristics and for genetic additive level similar to the studies (Ochi-e-Ardabili *et al.*, 2009; Selim *et al.*, 2003).

Principal component analysis

According to outcomes of Principal component analysis first three PCs reflected eigen values were more than one where cumulative value of the total variation was 61.78%. In 1st value PC explored 25.05% of total variation and the rest of two PCs exposed 22.70 and 14.01% variability, correspondingly, (Table 5). The 1st reading in considered for highest proportional value of total variation in all PCs and rest of PCs have lower variability. And almost similar finding was recorded from Indian mustard by Zada *et al.* (2013) mustard; Avtar *et al.* (2014) in toria and Neeru *et al.* (2015) in analysis. Four different principle factor of eight various no of traits under studies as discussed in (Table 6).

Table 5: Eigenvalues of correlation matrix, and related statistics.

Principal components	Eigen value	Percent variance	Percent cumulative variance
1	2.0048	25.0595	25.0595
2	1.8165	22.7067	47.7662
3	1.1214	14.0171	61.7833

Table 6: Factor coordinates of the variables, based on correlations.

Traits	PF1	PF2	PF3
DFI	0.2796	0.6211	-0.2128
DF	0.1226	0.7571	0.0824
PH	-0.2870	0.4590	0.0955
NTPP	-0.9331	0.2149	-0.0800
NSPP	-0.9415	0.0969	-0.1120
SPL	-0.1557	0.0665	0.7276
DM	0.2168	0.7533	0.1376
SYPP	0.0283	0.1397	-0.7020

Analysis without axes rotation is not sufficient to fill the all variables signifying that it lacks much information

related to concept of correlation among the variables and PCs. This was implemented with the results of all variables on various PCs. In Table 3 factors obtained from loadings of numerous variables are mentioned. First principal factor (PF1) which attributed to total four parameters are considered as relating to yield, enabling high weight age of seed yield with two of its most important component traits viz. DFI, DF, DM and SYPP. PF2 had high loadings of all variables i.e., DFI, DF, PH, NTPP, NSPP, SPL DM and SYPP and could be designated as maturity factor, On the other hand the parameters DF and DM has the greatest weight as a whole contributing more variation. PF3 had high weight age of four variables i.e., SPL, DM, PH and DF. Avtar *et al.* (2014) in toria and Singh *et al.* (2014) in Indian mustard also reflected the results of similar type of variables in same principal factor (PF).

It reveals that traits like DFI, DF, PH, NTPP, NSPP, SPL, DM and SYPP were salient variables reflecting the total variation (61.78%) in the set of 58 accessions. The prosperous implementation of 8 structural variables into 3 PCs by categorizing the same variables on different PCs described 61.78% of variability of original one. This is according to Neeru *et al.* (2015) in Indian mustard.

Conclusions and Recommendations

Heritability values were high in SYPP and DF ranged from 0.998 to 0.930, respectively like all characters except DFI noted as 0.658 whereas genetic advance ranged between 16.3069 in the parameters i.e., NTPP and 1.4473 for the character of SYPP. Highest coefficient of variation (CV=11.53%) was estimated for SPL followed by SYPP (CV=8.04%), while minimum (CV=1.41%) for DM. Likewise, seed yield per plant also reflected significant results among the fifty-eight genotypes. Phenotypic coefficient of variability (PCV) was higher than genotypic coefficient of variability (GCV) for all the traits. According to principal component analysis 1st three PCs showed that the eigen values is more than one where cumulative value was 61.78% of the total variability. The first one accounted for highest proportional extent of variability in all PCs and rst of PCs lesser amount of variation. High values of broad sense heritability with higher genetic advance in plant attributes witnessed these types of parameters abide by the effects of additive genes, concluding that

selection procedure give rise a quick improvement of the material.

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Novelty Statement

To the best of our Knowledge this is the first study conducted on ispaghol yield link traits in arid condition.

Author's Contribution

Malik Muhammad Yousaf: Conceived the idea, principal investigator of the project, overall management of the article.

Wali Muhammad: Did analysis.

Muhammad Mohsin Raza: Wrote abstract.

Mumtaz Hussain: Technical input

Muhammad Jahangir shah: Collected data.

Bashir Ahmad: Data entry.

Annum Sattar: Methodology.

Hera Gul: Wrote introduction.

Sonia Sumreen: Wrote references.

Malik Waqar Yousaf: Data entry in SPSS and dis SPSS analysis.

Nazakat Nawaz: Conclusion.

Nasim Hussain: Wrote result and discussion.

Conflict of interest

The authors have declared no conflict of interest.

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