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Genetic variability spectrum and correlation among agro-morphological traits in linseed (*Linum usitatissimum* L.) genotypes

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Abstract

Twelve genotype are evaluated in the experimental field of AICRP on oilseed at college of agriculture, Tikamgarh to generate scientific information, nature and magnitude of genetic variability and correlation. The experiment conducted with three replication in RBD design and the data were recorded for days to flowering initiation, days to 50% flowering, plant stand per hectare, plant height, primary branches per plant, capsules per plant, number of seeds per capsule, biological yield per plant, days to maturity, 1000 seed weight, yield per plant, yield per ha., protein content (%) and oil content (%). The trait, 1000 seed weight showed the highest estimates of both phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) and significant Genetic advance as percent of mean whereas higher heritability with high genetic advance observed for seed yield per plant. Seed yield per plant showed highest degree of positive association- ship with 1000 seed weight.

Keywords: Variance, GCV, PCV, heritability, genetic advance, correlation

Introduction

Linseed (Linum usitatissimum L.) is one of the most important Rabi oilseed crop after rapeseed and mustard. India produced 120.7 thousand tons linseed from 179.9 thousand ha. Area in 2019-2020 with average productivity 671 kg/ha. While Madhya Pradesh harnessed 45 thousands ton from 5 thousand ha. Area with average productivity 867 kg/ha. In 2019-2020 (Anonymous, Ministry of Agriculture and Farmer Welfare, 2019)^[6]. The extent of pace in any breeding programme depends upon the amount of variability present in breeding material. The exploitation of genetic variability is an important for continuous improvement in the desirable traits. The first person that provides the idea of partitioning the variation in different components like genotypic, phenotypic and environmental variation was Fisher (1918) ^[16]. The knowledge on the nature and extent of genetic variability in any crop species play an important role in framing a successful breeding programme. The genetic variability is the raw material of the plant breeding industry on which breeder works to evolve superior genotypes, therefore, thorough understanding is very important for swift and efficient crop improvement. Heritability is the quantitative measure, which provides information about the role of genotypes and environment involved in expression of traits. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimate alone. However, it is not necessary that a character showing high heritability also exhibit high genetic advance. Thus in cases where heritability is mainly due to non-additive gene effects, the expected gain will be low and vice-versa. Hence, any quantitative character can be predicted when genetic advance is considered along with heritability.

Material and Methods

The experimental material consisted of 12 genotypes of linseed were grown in a randomized block design with three replications at experimental field of AICRP on Oilseeds, college of agriculture Tikamgarh Madhya Pradesh during rabi 2021-22. Experiment was conducted in November 2021 with 3.0×3.0 m plot size and row to row and plant to plant distance was maintained 30 cm and 10 cm, respectively. The recommended agronomic practices were followed for growing healthy crop. The observations were recorded on ten randomly selected plants from each genotype in each replication on fourteen agro-morphological characters *viz*;

days to flowering initiation, days to 50% flowering, plant stand per hectare, plant height, primary branches per plant, capsules per plant, number of seeds per capsule, biological yield per plant, days to maturity,1000 seed weight, yield per plant, yield per ha., protein content, oil content. The treatment means for all the characters were subjected to compute the analysis of variance on the basis of model proposed by Panse and Sukhatme (1985) [20]. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed as per Burton and Devane, (1953) method. Heritability in broad sense h^2 (b) and genetic advance as percent of mean were estimated by the formula as suggested by Johnson *et al.* (1955) ^[17]. Genotypic correlation coefficient and phenotypic correlation coefficient were estimated as per Al-jibouri (1958)^[4]. Statistical software INDOSTAT was used for this correlation analysis.

Results and Discussion

Genetic Variability: The estimates of variance were recorded for fourteen yield and quality traits on twelve linseed genotypes (Table 1). Result of analysis of variance showed that all the characters viz., days to flower initiation, days to 50% flowering, plant stand, number of primary branches/plant, number of capsules/plant, number of seeds/capsule, biological yield per plant, days to maturity, 1000 seed weight, seed yield per plant, plant height, yield per hectare, protein content exhibited highly significant except only oil content which was recorded non-significant in mean sum of squares. This indicates that sufficient variability is present in most of the important characters among different genotypes other than oil content. These results were in conformity with Dubey et al. (2006)^[14], Belete and Yohannes (2013)^[8], Paul et al. (2018)^[24] and Chauhan et al. (2018)^[11]. According to estimates of genotypic and phenotypic variation, phenotypic variance was typically higher than genotypic variance, showing the influence of environmental factors on the manifestation of characters (Table 2). Moderately higher magnitude of PCV and GCV were observed for the traits viz 1000 seed weight (16.80, 16.08), yield per plant (15.75, 15.28), plant height (12.76, 12.56), biological yield per plant (12.46, 12.06), days to flower initiation (11.32, 11.14) respectively, while moderate PCV recorded with yield per hectare (10.78). Moreover, lower measure of PCV and GCV recorded with capsule per plant (10.15, 8.39), days to 50% flower (8.83, 8.65), plant stand (6.47, 6.16), protein content in percent (6.12, 6.12), oil content in percent (4.57, 4.13), primary branch per plant (3.25, 2.06), seed per capsule (2.81, 2.75), days to maturity (2.43, 2.25) whereas, low GCV recorded for yield per hectare (9.93). In prior art of research, similar trends of results for genotypic and phenotypic coefficient of variation were also observed by Bibi et al. (2013)^[9], Pali and Mehta (2013)^[19], Kanwar et al. (2014)^[18]

and Upadhyay et al. (2019 b) [28]. The highest heritability was observed for protein content (99%), followed by days to flowering initiation (96%), plant height (96%), seeds per Capsule (96%), days to 50 percent flowering (95%), seed yield per plant (94%), biological yield per plant (93%), 1000 seed weight (91%), and plant stand in numbers (90%). Days to maturity (86%) yield per hectare (84%), oil content (81%). Further moderate heritability was observed only for capsule per plant (68%). The magnitude trend of heritability was in agreement with Akbar et al. (2003) [3], Tyagi et al. (2014) [27], Fida et al. (2015) ^[15] and Upadhyay et al. (2019a). Genetic advance as percent of mean showed the highest values for number of 1000 seed weight (31.71%) followed by yield per plant (30.53%), biological yield per plant (24.04%) and flower initiation (22.57%). Whereas, it was low for primary branch per plant (2.70%). Higher heritability coupled with high genetic advance was recorded in most of the traits taken under study i.e. plant height, days to flower initiation, yield per plant, biological yield per plant,1000 seed weigh and low heritability with low genetic advance recorded in primary branch per plant. Similar results were also observed by Awasthi and Rao (2005) [7]; Ram Jeet et al. (2010) [23], Dandigadasar et al. (2011) [13]; Rajanna et al. (2014) [22], Tyagi et al. (2014) [27]; Choudhary et al. (2017) [12] and Ahmed (2017)^[1]. In study of correlation (Table 3), seed yield per plant exerted positive phenotypic and genotypic correlation with 1000 seed weight (0.605, 0.554) followed by plant stand (0.159, 0.151), seeds per capsule (0.122, 0.104), oil content in percent(0.096, 0.109), primary branches per plant (0.074, 0.087), capsules per plant (0.025, 0.044) respectively while exhibited negative phenotypic and genotypic correlation with days to flower initiation(-0.719, -0.681), days to 50% flowering (-0.706, -0.662), days to maturity(-0.693, -0.579), biological yield per plant(-0.677, -0.637) plant height (-0.660, -0.624), protein content in percent(-0.360, -0.360) and yield per hectare (-0.01, -0.360) recpectively. The results reported by Yadav (2001) [30] were agreement with seed yield per plant which was positively correlated with number of capsules per plant, number of seeds per capsule, 1000 seed weight at both phenotypic and genotypic levels. Further, also reported similar results Akbar et al. (2001)^[2]. Similarly, seed yield of linseed had significant positive correlation for primary branches per plant, capsules per plant (Reddy et al. 2013) [25] and (Ranjana et al. 2018) [24] and 1000 seed weight (Ranjana et al. 2018)^[24] at phenotypic and genotypic Level. Further, results cited by Sahu et al. (2016) ^[26] for number of capsules per plant, Choudhary et al. (2017) ^[12] for plant stand, number of capsules per plant, test weight. And Ankit et al. (2019) [5] for 1000 seed weight had strong positive association-ship with seed yield were similar with results of current study at both genotypic and phenotypic levels.

Table 1: Analysis of variance for yield attributing and quality traits in linseed genotypes

Source of Variation	Degree of freedom		Mean Sum Of Squares														
		Days to flower initiation	Days to 50% flowering	Plant Stand (Numbers)		Primary Branches/ plant	Cancules	seeds/ Capsule	Biological yield (g)	to	1000 seed weight(g)	Yield / plant (g)	Y teld/	Protein content (%)	Oil Content (%)		
Replication	2	1.36	2.02	215.52	1.02	0.002	23.13	.002	0.24	3.11	.26	0.01	3012.77	0.005	2.00		
Genotype	11	106.33**	80.99**	1789.14**	203.86**	.015*	84.47**	.16**	13.09**	21.20**	4.11**	0.77**	82499.80**	6.21**	7.92		
Error	22	1.17	1.14	60.58	2.20	.005	11.30	.002	0.29	1.08	.12	0.01	4642.68	0.004	0.55		
Total	34																

*, ** = Significant at 5% and 1% levels, respectively

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Table 2: Genetic variability parameters for seed yield and its contributing characters in linseed genotypes

			(
Sr. No.	Characters	Mean	Ra	nge	PCV GCV		H (Bs)	Genetic advance as percent		
		Wiean	Minimum	Maximum	(%)	(%)	(%)	of mean		
1	Days to flowering initiation	53.0	41.0	61.00	11.32	11.14	96	22.57		
2	Days to 50% flowering	60.0	50.0	68.0	8.83	8.65	95	17.44		
3	Plant Stand (Numbers)	390.	340	424.0	6.47	6.16	90	12.07		
4	Plant height (cm)	65.0	51.0	77.0	12.76	12.56	96	25.45		
5	Primary Branches/ plant	2.88	2.7	2.90	3.25	2.06	40	2.70		
6	Capsules/plant	58.8	51.2	68.40	10.15	8.39	68	14.29		
7	Seeds/Capsule	8.50	8.20	8.80	2.81	2.75	96	5.57		
8	Biological yield (g)	17.1	13.4	20.2	12.46	12.06	93	24.04		
9	Days to maturity	114.7	109.3	118.7	2.43	2.25	86	4.31		
10	1000 seed weight (g)	7.20	5.1	8.50	16.80	16.08	91	31.71		
11	Y ield /plant (g)	3.30	2.50	4.20	15.75	15.28	94	30.53		
12	Yield/ha(kg)	1621.3	1174.0	1759	10.78	9.93	84	18.84		
13	Protein content (%)	23.50	21.3	25.7	6.12	6.12	99	12.60		
14	Oil content (%)	38.0	35.5	40.4	4.57	4.13	81	7.69		

Table 3: Genotypic and phenotypic correlation coefficients with seed yield and its contributing characters in linseed genotypes

Sr. No.	Characters	r		Days to 50% Flowering	Plant Stand (Numbers)	Plant height (cm)	Primary Branches/ Plant	Capsules/ Plant	Seeds/ Capsule	Biological yield (g)	Days to maturity	1000 seed weight (g)	Yield/ ha(kg)	Protein Content (%)	Oil Content (%)	seed yield /plant (g)
1	Days to	rg	1.000	0.991	-0.134	0.378	0.184	0.537	-0.412	0.384	0.985	-0.768	0.048	0.103	-0.126	-0.719
	flowering initiation	r _p	1.000	0.976**	-0.148	0.370*	0.186	0.430**	-0.408*	0.376*	0.889**	-0.705**	0.069	0.103	-0.091	-0.681
	Days to	rg		1.000	-0.086	0.413	0.210	0.587	-0.347	0.414	1.006	-0.844	0.084	0.212	-0.153	-0.706
2	50% flowering	r _p		1.000	-0.099	0.386*	0.208	0.458**	-0.340*	0.410	0.904**	-0.786**	0.111	0.206	-0.126	-0.662
	Plant	rg			1.000	-0.086	-0.092	0.340	0.466	-0.073	-0.222	0.016	0.454	-0.126	-0.394	0.159
3	Stand (Numbers)	r _p			1.000	-0.088	-0.092	0.190	0.443**	- 0.097	-0.186	0.036	0.389*	-0.120	-0.378*	0.151
	Plant	rg				1.000	-0.363	-0.032	0.244	1.009	0.368	-0.495	0.427	0.317	-0.216	-0.660
4	height (cm)	r _p				1.000	-0.237	-0.011	0.237	0.974**	0.323	-0.455**	0.368*	0.312	-0.159	-0.624
	Primary	rg					1.000	0.091	0.318	-0.391	0.220	-0.180	-0.414	-0.011	0.286	0.074
5	Branches / plant	r _p					1.000	-0.161	0.122	-0.207	0.207	-0.102	-0.160	-0.000	0.218	0.087
6	Capsules/	rg						1.000	-0.424	-0.021	0.580	-0.542	0.666	0.025	-0.386	0.025
0	plant	r _p						1.000	-0.344	0.005	0.408	- 0.462**	0.452**	0.018	-0.234	0.044
7	seeds/	rg							1.000	0.219	-0.388	0.042	0.209	0.258	-0.176	0.122
'	Capsule	r _p							1.000	0.211	-0.378	0.040	0.177	0.251	-0.167	0.104
8	Biological	rg								1.000	0.384	-0.490	0.427	0.320	-0.224	-0.677
0	yield (g)	r _p								1.000	0.318	-0.468**	0.385*	0.307	-0.167	-0.637
9	Days to	$r_{\rm g}$									1.000	-0.867	0.076	0.274	-0.273	-0.693
_	maturity	r _p									1.000	-0.786**	0.051	0.254	-0.188	-0.579
10	1000 seed	rg										1.000	-0.331	-0.652	0.211	0.605
-	weight (g)	r _p										1.000	-0.267	-0.616	0.199	0.554
11	Yield/	rg											1.000	0.124	-0.527	-0.01
\vdash	ha(kg)	r _p											1.000	0.117	-0.460**	-0.01
12	Protein	rg												1.000	-0.115	-0.360
	Content (%) Oil	r _p												1.000	-0.102	-0.360
13	Content (%)	r _g r _p													1.000	0.096
\vdash	Seed vield /	rp													1.000	0.109
14	plant (g)	rg								D1						1.000

*, ** = Significant at 5% and 1% levels, respectively. rg - Genotypic correlation, rp - Phenotypic correlation

Conclusion

This study was carried out with 12 genotypes of linseed and analysis of variation exhibited a significant and desirable amount of variation for all the traits and this can be exploited for fast improvement through suitable breeding methods. High to moderate magnitude of PCV and GCV were observed for the traits *viz.*, 1000 seed weight, yield per plant, plant height, biological yield per plant, days to flower initiation indicating the presence of significant variability in the existing collection which can be exploited for further improvement by suitable breeding methods. High heritability coupled with high genetic advance as percentage of mean was observed for most of the traits viz., plant height, days to flower initiation, yield per plant, biological yield per plant and 1000 seed weigh which revealed the presence of additive gene effects in these traits. Hence, selection may be effective. In contrary to this, both heritability and genetic advance recorded low for primary branch per plant which indicates the character is highly influenced by environment and selection will be ineffective. In correlation studies seed yield per plant exerted positive phenotypic and genotypic correlation with 1000 seed weight followed by plant stand, seed per capsule, oil content in percent, primary branch per plant,. Hence, indirect selection via contributing traits may be helpful in improving the seed yield in the genotypes studied.

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