Scope
Volume 15 Number 04 December 2025

Genetic Analysis and Factor of Flaxseed

[1] Hasmat Ali, [2] Kiran pal, [3] Shubham Singh, [4] Javad Ahmad Siddhiqui
[1, 2, 3, 4] Department of Botany D.A-V (P.G.) College, Kanpur

Abstract: Flax is an important source of oil rich in omega-3 fatty acid which is proven to have health benefits and utilized as an industrial raw material. An application was observance to estimate the volume of inherited deviation among 33 flaxseed genotype including 3 checks using Mahalanobis D^2 statistics in Randomized block design (RBD) at Agriculture Research Institute Kanpur, Up during Rabi 2022-2023. Examination was record for 11 ethos and based on D^2 statistics, the genotype were classed into 8 apart team using Tocher's method. The outgrowth visible that team I had most number of genotypes followed by team II and team VI while other five team were mono-genotypic. The higher intra-team remoteness was recorded for team VI, followed by team II and team I while the lowest intra-teamremoteness were observed for remaining 5 team. Whereas the most inter-team remoteness was recorded between team IV and VIII, indicating a higher amount of inheritedmulteity available in genotypes of this team and can be harness as parents for inter-breeding schedule.

Key word: inherited, randomized, mono-genotypic and inter-breeding.

Introduction

"Linseed also known as flax is a member of the genus Linum in the family Lunacies. It is one of the chronic yields being ploughed since the start up of gentleness commercially, one or the other or since technology"(Qamar *et.al* 2019). weigh with variantlubeyield, flaxseed inclusive about 36-40% lube is the propertied radix of polyunsaturated fatty acids (PUFA) as alpha-linolenic acid, the majorityampleradix of antioxidants (Andruszczak *et.al* 2015; Goyal *et.al* 2014) and lignin (Kajla *et.al* 2015) which has a finance efficacy on the stopover of the sickness and human well-being. Linseed in a general way called as flax autogamous yield. Its centre of radix is India. It is outrageously self-pollination yield but less than 2% cross-pollination occurred due to pollinator's activity. It is widely grown species with huge pecuniary effect (Wakjira *et.al* 2004). It is soaking and hardening character, which is issued from its sublimate linolenic acid content. About 20% of the total flaxseed lube influence in India is consumed for enjoyment and the comfort about 80% goes to labor for the erection of paints, varnish, oil cloth, linoleum, printing ink and ploymers (Savita *et.al* 2011; Tour and Xueming, 2010). In India it is surmount in 181 thousand ha with a production of 41 thousand tones and producibility of 227 kg/ha" (Annual Project Report, 2020-2021). "The domain under flaxseed cultivation in Rajasthan is 5.7 thousand ha and production is 6.1 thousand tones with an average crop of 1066 kg/ha" (Anonymous 2021). "The genotypes in the prompt action team may be targeted for divers crossing curriculum in order to spring transgressive segregates with superior crop. Exact picking of the parents is fateful to be consumed in carfax to enhance the hereditary recombination for probablecroprise"(Islam *et.al* 2004). Flaxseed is cultivated in majority of the countries in the world. In India flaxseed occupies about 219.86 thousand hectares with a production of 158.64 thousand tones and creativeness of 979 kg/ha (Annual report of AICRP flaxseed, 2022-2023). In Rajasthan, flaxseed is being cultivated in an domain of 22.5 thousand hectares with a production of 24.2 thousand tones and creativeness of 1070 kg/ha (Directorate of financial and statistics, DAC and FW, GOI, 2022-23). To thrive in any yield reformation schedule the pivotal factor is the analysis of the hereditary multeity existent, especially prelude in the primary gene pool. It also plays a vital prelude in effectively managing gene pool thereby conserving it. Among the apart methods for evaluating hereditary multeity, multivariate analysis, such as D^2 statistics, has proven helpful in several breed in praxis, notably in prefer the majority diverse genotypes applicable for cross-breeding. Hence, this checkout was conducted to account the volume of hereditary mule it receivable in 33 flaxseed genotypes (Singh *et.al* 2024). The perusal on hereditary leave analysis manners techniques like Manalanobis D^2 or nonhierarchical were germane to assess hereditary muta preexistent in the 56 genotypes along with four checks (KIRAN, DEEPIKA, PADMINI, INDIRA ALSI)used in this praxis (Payasi, 2000; Diederichsen, 2001). The hereditary mutable more will be the opportunity to hope mend from fit picking process (Muhammad, *et.al* 2003).

Material and Methods

The praxis fixings consisting of 33 genotype of flaxseed inclusive three checks and was estimate in Randomized Block Design 2022-2023 at agriculture Research Institute Kanpur. Each genotype was laid in plot size of 5x1.3 m^2 with a remoteness of 35x15 cm. All recommended agronomic drill and bin aegis measures were betimesconditioned to raise a healthy tiller population. All the inspection were recorded on ten randomly selected bine of each genotype for eleven ethos*viz*., bine height, number of primary branches per bine, number of capsules per bine, number of germ per capsule, biotic crop, crop index, test weight and germ crop per bine in each prototype except for phonological ethos i.e., days to 50% flowering days to maturity and bine stand. These side by side data were used to analyze hereditary diversity using Mahalanobis's D^2calculation and team genotypes were teamed using Tocher's method.

Result and Discussion

The differentiation of genotype into discrete team noticed arrival of high degree of hereditary diversity in the material estimated. Out of all team, team I had most number of genotypes i.e., 15 namely RCRL-21-2, JSL 95, RL 18105, LCK 2109, RL 18114, BRLS 109-2, DLV-24, BRLS 109-5, SLS 142, LMS-2019-I-11, LCK 2037, RLC-190, RL 15580, LSL 93 and Pratap Alsi-2, followed by team II i.e., 8 which comprise genotypes RLC 192, T-397, RL-189, BRLS 109-2-1, RLC-191, LCK 2132, RLC 92 and LMS 9-2K and team VI consists of 5 genotypes *viz*., LCK 2017, LMS-2019-I-4, Kota Alsi-6, RLC 184 and BAU-2021-06. While other five team connected of only one genotype *viz*., team III (BRLS I I I-2), team IV (SLS 133), team V (DLV-23) team VII (RCRL-21-1) and team VIII (SLS 141). The average inters and intra team remoteness based on D^2 values is offered in the Table 2. 1. The intra team remoteness had ranged from 0 to 56.26. The most intra team remoteness was recorded for team VI (56.26), followed by team II (35.92), and team I (35.86) while team III, team IV, team V, team VI and team VIII had least intra team values *viz*., zero as these team include of only one genotype each. The inter team remoteness ranged from 18.06 to 218.51.

The team means value for 11 apart ethos for eight team are offered in Table 3. Team IV consists of genotype (SLS 133) with a higher team mean for test weight, crop index, and bine stand while team VI consists of genotypes (LCK 2017, LMS-2019-1-4, kota Alsi-6, RLC 184 and BAU-2021-06) with highest team mean for seeds per capsule and number of capsules per bine and genotype existent in these team could be spend in cross-breeding curriculum for yield reform. Team III (BRLS 111-2) was cast earliest for days to 50% flowering and days to matureness and the genotype united in it can be used as a giver for early maturing diversity rise schedule.

Table1: List of thirty three flaxseed genotypes grouped in to eight different team by Tocher's method.

Team	No. Of Genotypes	List of Genotypes
Team I	15	RCRL-21-2, JSL 95, RL 18105, LCK 2109, RL 18114, BRLS 109-2, DLV-24, BRLS 109-5, SLS 142, LMS-2019-I-11, LCK 2037, RLC-190, RL 15580, LSL 93 and Pratap Alsi-2
Team II	8	RLC 192, T-397, RL-189, RL 15597, RLC-191, LCK 2132, RLC 92 and LMS 9-2K
Team III	1	BRLS 111-2
Team IV	1	SLS 133
Team V	1	DLV-23
Team VI	5	LCK 2107, LMS-2019-1-4. Kota Alsi-6, RLC 184 and BAU-2021-06
Team VII	1	RCRL-21-1
Team VIII	1	SLS 141

Table 2: Intra and inter team remoteness based on D^2 analysis

Team	Team I	Team II	Team III	Team IV	Team V	Team VI	Team VII	Team VIII
Team I	35.86	74.4	54.12	57.5	61.28	71.76	58.17	109.38
Team II		35.92	93.72	144.24	135.81	116.01	96.28	89.15
Team III			0	79.33	111.38	87.37	97.75	152.42
Team IV				0	18.06	80.78	52.19	218.51
Team V					0	87.78	40.16	204.56
Team VI						**56.26**	129.62	135.29
Team VII							0	167.2
Team VIII								0

Table 3: Team mean values of seed crop and its contributing traits

Team	Days to 50% flowering	Days to maturity	Bine stand	Bine height (cm)	No. of primary branches per bine	No. of capsules per bine	No. of seed per capsule	Biological crop (g)	Crop index (%)	Test weight (g)	Seed crop per bine (g)
Team I	69.02	132.53	133.91	66.70	3.04	47.61	8.12	7.97	47.65	7.50	3.81
Team II	69.21	133.21	129.96	65.37	2.26	50.76	8.15	6.89	49.75	5.68	3.43
Team III	57.33	124.67	141.67	60.60	2.33	47.27	8.60	9.19	55.03	7.88	5.07
Team IV	66.33	128.33	143.33	59.87	4.73	52.25	8.70	9.54	56.91	8.15	5.43
Team V	68.33	128.33	135.33	64.35	4.89	61.87	7.46	9.39	45.30	7.70	4.25
Team VI	74.00	139.73	141.93	71.32	3.58	73.77	9.13	11.25	50.09	7.30	5.65
Team VII	64.00	130.33	125.67	66.85	4.20	45.04	6.90	6.35	38.56	6.91	2.45
Team VIII	75.33	143.00	133.00	95.45	2.32	43.85	8.73	8.57	36.72	5.82	3.14

Conclusion

The extant checkout apparent that ample of hereditary motile was observed among 33 flaxseed genotype. The earliest days to 50% flowering and days to matureness were observed for team III. Team VI had genotypes with rentteam means for bioticcrop, number of germs per capsule, number of capsules per bine and germcrop per bine whereas team IV had genotype highestteam means for bine stand, crop index and teat weight and under team mean for bine height. While a genotype having the majority number of precursive offshoot per bine was put into team V.

References

1. Annual Report of AICRP Linseed, 2022-2023. 1-372.
2. Andruszczak, S., Gawlik-Dziki, U., Kraska, p., Kwiecinska-poppe, E., Rozylo, K and Palys, E (2015), yield anf quality traits of two linseed cultivers as affected by some agronomic factors. Plant Soil and Environment 61:247-252.
3. Annual Project Report. ICAR- All India Coodinated Research Project on Linseed; 2020-2021.
4. Akbar, M., Mahmood, T., Anwar, M., Ali, M.,Shafiq, M and Salim, J(2003), linseed improvement through genetic variability, correlation and path coefficient Analysis. International Journal of Agriculture and Biology 5(3).
5. Directorate of Economics and Statistics, DAC and FW, GOI. 2022-23.
6. Diederichsen, A (2001), comparison of genetic diversity of flax between Canadian cultivars and a world collection. Plant Breeding 120(4):360-362.
7. Goyal, A., Sharma, V., Upadhyay, N., Gill, S., and Sihag, M (2014), flax and flaxseed: An ancient medicine and modern functional food. Journal of Food Science and Technology 51(9):1633-53.
8. Islam, M.R., Faruquei, M.A.B., Bhuivan, M.A.R., Biswas, P.S and Salam, M.A (2004), genetic diversity in irrigated rice. Pakistan Journal of Biological Sciences 7(2):226-29.
9. Kajla, P., Sharma, A and Sood, D.R (2015), flaxseed- A potential functional food source. Journal of Food Science and Technology-Mysore 52:1857-1871.
10. Payasi, S.K (2004), genetic divergence in linseed. Crop Research (Hisar) 19(1):158-161.
11. Qamar, H.,IIyas, M., Shabbir, G., Irshad, G., Nisar, F., Abbas, S.M., Ghias, M and Arshad, A (2019), flax: ancient to modern food. Pure and Applied Biology 8:2269-2276.
12. Savita, S., Kenchanagoudar, P.V and Rudranaik, V (2011), correlation and path coefficient analysis for yield and yield components in linseed. Agriculture and Food Sciences 24(3):382-386.
13. Wakjira, A *et.al* (2004), variability in oil content and fatty acid composition of Ethiopian and introduced cultivars of linseed Journal of the Science of Food and Agriculture 8(4):1-8.