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GENETIC VARIABILITY, TRAIT ASSOCIATION AND PATH ANALYSIS OF SESAME GENOTYPES FOR YIELD AND ITS ATTRIBUTING TRAITS

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ABSTRACT

Sesame is an important oldest oilseed crop widely recognized for its high oil content, nutritional quality and economic value. In the present study, 40 sesame genotypes including four standard checks, namely RT 372, RT 54, TKG 22, and GT 10 were evaluated in a randomized block design (RBD) to assess variability parameters, trait association and path analysis based on yield and its attributing traits. In this study the results indicated that seed yield exhibited highest variability (GCV & PCV) followed by primary branches per plant, capsules per plant, plant height and oil content. High heritability was observed for plant height (92.29%) and seed yield (73.51%), whereas primary branches per plant (59.17%), oil content (47.50%) and capsules per plant (31.63%) showed moderate to low heritability. High genetic advance as percent of mean for seed yield (39.71%) and primary branches per plant (27.07%) suggest good scope for improvement through selection. The correlation analysis revealed that seed yield had a strong and significant positive association with capsules per plant (0.630**), plant height (0.570**) and primary branches per plant (0.562**). The path analysis indicated that capsules per plant had the highest positive direct effect on seed yield, followed by oil content, highlighting their key role in productivity. Overall, the study helps to identify promising genotypes that can be used as potential parents in future sesame breeding programmes to improve yield and adaptability.

***Keywords* :** Sesame, GeneticVariability, Correlation, Path Analysis, Seed Yield

Introduction

Sesame or Gingelly (*Sesamum indicum* L., 2n=26) is a globally significant oilseed crop and is widely recognized for its high oil content (40-55%) and rich natural antioxidant profile, including sesamin, sesamol, sesamolin and sesamolinol (Pathak *et al*., 2014; Biswas *et al*., 2018). It is predominantly grown in semi-arid tropical and sub-tropical to temperate regions, where it contributes significantly to nutritional security and rural livelihoods (Weiss, 2000). Despite its adaptability, sesame productivity remains low in arid and semi-arid regions due to multiple abiotic stresses, particularly drought, high temperature and erratic rainfall distribution (Dossa *et al*., 2016). Western Rajasthan represents a typical arid ecosystem where crop performance is largely influenced by climatic variability and soil constraints, necessitating the identification of genotypes with enhanced adaptability and yield stability.

The assessment of genetic variability, traits correlation and path analysisare crucial for effective crop improvement. Parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as percent of mean help in assessing the extent of variation present in a population. High heritability coupled with high genetic advance indicates the predominance of additive gene action, which is useful for selection in breeding programmes (Mahla*et al*., 2024).Yield in sesame is a complex quantitative trait influenced by several component traits, including plant architecture, capsule number, and branching pattern (Bharathi *et al*., 2015). Therefore, understanding the association among these traits through correlation analysis is essential for effective selection strategies. In this context, path coefficient analysis provides a more precise understanding by partitioning correlation coefficients into direct and indirect effects. This approach helps to plant breeders for identifying key traits that directly affect yield and can be used to select promising genotypes for future breeding programmes.

Material and Methods

Experimental Material: The experimental material consisted of forty sesame genotypes along with four standard checks, including RT 372 and RT 54 as local checks, TKG 22 as a zonal check, and GT 10 as a national check (Table 1).

Experimental Site: The experiment was conducted at the Research Farm, Dr. B. R. Choudhary Agricultural Research Station, Mandor, is located at 26°15′–26°45′ N latitude and 73°00′–73°29′ E longitude, with an altitude of 242.6 m above mean sea level. The soil of the experimental site was classified as loamy sand, which is typical of the arid plains of Rajasthan.

Experimental Design and Management: The experiment was carried out in a Randomized Block Design (RBD) with three replications during the *Kharif*-2024. Standard agronomic practices were followed to ensure proper crop establishment and growth.

Observations Recorded: Observations were recorded on important yield and its attributing traits, including seed yield (kg/ha), plant stand (000/ha), days to 50 % flowering and maturity, plant height (cm), number of primary branches per plant, number of capsules per plant, 1000seed weight (g) and oil content (%). These parameters were measured to comprehensively assess the genotype performance (Table 1).

Statistical Analysis: The recorded data were subjected to analysis of variance to determine the significance of differences among genotypes. GCV, PCV, heritability and genetic advance as percent of mean were calculated using standard methods. Correlation analysis was used to study trait association and path analysis were performed to understand direct and indirect effects on seed yield.

Results and Discussion

The evaluation of sesame genotypes revealed considerable variability for yield andits contributing traits, indicating the presence of substantial genetic variability among the tested genotypes. The experiment was significant with CD of 104 kg/ha. Four genotypes, RMT 695 (833 kg/ha), RMT 705 (817 kg/ha), RMT 708 (703 kg/ha) and RMT 711 (683 kg/ha) recorded significantly higher seed yield over the best check RT 372 (550 kg/ha). The graphical representation (Fig. 1) visually depicts the superior seed yield and oil content of these four promising genotypes compared to the best local check RT 372, highlighting their potential as breeding material. The coefficient of variation (CV) for seed yield was 13.5%, indicating a moderate level of variation and good reliability of the experiment (Table 1).

The estimates of GCV and PCV showed that PCV values were higher than GCV for most characters, indicating that environmental factors had some influence on the expression of these traits (Table 2). The results showed clear variation among the traits, with seed yield (GCV 22.49%, PCV 26.23%) and primary branches per plant (GCV 17.08%, PCV 22.20%) showing higher variability. Similar result for seed yield was reported by Valarmathi *et al*. (2004), Mandal *et al*. (2010), Gidey *et al*. (2013), and Mahla *et al*. (2024). High heritability was observed for plant height (92.29%) and seed yield (73.51%), indicating strong genetic control, whereas primary branches per plant (59.17%), oil content (47.50%) and capsules per plant (31.63%) showed moderate to low heritability. The higher genetic advance as percent of mean was carried out for seed yield (39.71%) and primary branches per plant (27.07%) suggest good scope for improvement through selection. High heritability coupled with high genetic advance as percent of mean for seed yield also reported by Mahla *et al*. (2024).

The correlation analysis (Table 3) showed that seed yield had a strong and significant positive association with capsules per plant (0.630**) followed by plant height (0.570**) and primary branches per plant (0.562**), indicating their important role in yield improvement. Similar findings were reported by Shekhawat *et al*. (2013) for plant height and capsules per plant. These findings underscore the importance of these traits in breeding strategies aimed at yield improvement.

Path coefficient analysis showed that the capsules per plant had the strongest positive direct effect on seed yield followed by oil content, indicating their major role in improving productivity (Table 4 and Fig.

2). Similar findings were reported by Shekhawat *et al*. (2013), where traits oil content, capsules per plant and plant height showed strong positive direct effects on seed yield per plant. In contrast, plant height and primary branches per plant had negative direct effects, but they contributed indirectly to yield through their association with capsules per plant. This suggests that their influence on yield is mainly indirect. The low residual value (0.05620) indicates that these traits together explain most of the variation in seed yield.Overall, the results clearly demonstrate that the identified superior genotypes possess desirable attributes and can serve as valuable genetic resources for future sesame improvement programmes.

Conclusion

This study identified genetic variability parameters for yield and its associated traits among the evaluated sesame genotypes, indicating good scope for improvement through selection. High heritability coupled with high genetic advance observed for seed yield and key traits indicates the effectiveness of selection in breeding programmes. Strong positive correlation of seed yield with capsules per plant, plant heightand primary branches per plant highlight their importance in yield improvement. Path analysis revealed that capsules per plant and oil content had strong direct effects on seed yield. Overall, the findings highlight promising genotypes that can be effectively utilized in future sesame improvement programmes to achieve higher yield and better adaptability.

Table 1: Mean performance of sesame genotypes for yield and associated traits.

S. No.	Genotypes	Seed yield (kg/ha)	Plant stand (000/ha)	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches /plant	Capsules /plant	1000 seed wt.(g)	Oil Content (%)
1.	RMT-637	444	273	47	87	126	2.9	41	3.1	46
2.	RMT-685	411	284	45	82	113	2.7	42	3.1	45
3.	RMT-680	456	273	47	87	116	2.7	44	3.1	45
4.	RMT-681	400	288	49	87	115	2.6	45	3.0	46
5.	RMT-682	417	284	48	87	127	2.8	42	3.0	45
6.	RMT-684	403	281	48	87	118	3.1	48	2.9	46
7.	RMT-686	611	288	44	85	144	3.5	56	3.2	47
8.	RMT-687	500	283	48	86	142	3.0	59	3.0	46
9.	RMT-688	450	277	49	87	115	2.6	43	3.1	47
10.	RMT-689	406	253	46	87	109	1.5	42	3.1	46
11.	RMT-690	483	285	47	87	125	2.5	47	3.0	48
12.	RMT-691	578	271	48	88	133	3.0	51	3.0	46
13.	RMT-692	428	287	48	87	112	2.5	47	3.0	47
14.	RMT-693	394	267	46	87	125	2.5	41	3.1	47
15.	RMT-694	389	259	48	88	123	3.0	58	3.0	46
16.	RMT-695	833	281	46	86	146	3.7	59	3.0	48
17.	RMT-696	447	286	49	88	133	2.9	44	3.0	45
18.	RMT-697	469	281	47	87	129	3.4	49	3.2	47
19.	RMT-698	381	262	46	85	122	2.8	45	3.1	46
20.	RMT-699	419	282	46	87	122	2.6	44	3.0	47
21.	RMT-700	406	283	48	88	114	2.7	45	3.1	47
22.	RMT-701	319	287	48	87	131	2.7	46	3.0	47
23.	RMT-702	500	266	48	87	126	2.5	48	3.1	47
24.	RMT-703	433	283	48	91	128	2.6	38	3.0	45
25.	RMT-704	494	272	47	86	131	2.3	42	2.9	49
26.	RMT-705	817	281	45	87	123	3.5	59	3.0	49
27.	RMT-706	511	273	47	88	123	2.7	46	3.0	47
28.	RMT-707	472	272	48	87	120	2.7	42	3.1	47
29.	RMT-708	703	278	46	86	148	3.5	61	3.1	48
30.	RMT-709	367	283	49	87	127	2.6	42	3.0	47
31.	RMT-710	472	281	49	89	122	1.9	45	3.1	47
32.	RMT-711	683	279	46	86	132	3.1	57	3.1	48
33.	RMT-712	428	291	48	88	129	3.3	48	2.9	48
34.	RMT-713	436	276	46	87	122	2.5	43	3.0	47
35.	RMT-714	406	258	48	88	108	2.1	40	3.0	48

36.	RMT-715	372	269	48	87	119	2.1	41	3.0	46
37.	RT 372 (C)	550	286	46	86	125	3.1	57	3.1	46
38.	RT 54 (C)	417	284	39	80	110	3.3	60	2.7	40
39.	TKG22 (C)	461	286	47	89	118	2.7	53	3.0	46
40.	GT 10 (C)	436	278	48	87	121	3.3	57	2.8	45
G. Mean		475	278	47	87	124	2.8	48	3.0	47
SEm±		37.1	12.6	0.5	0.5	1.5	0.2	4.4	0.05	0.6
CD at 5%		104	NS	1.4	1.5	4.3	0.4	12.3	0.13	5.4
CV (%)		13.5	7.9	1.8	1.1	2.1	9.5	15.7	2.7	6.3

Table 2: Variability parameters for yield and its key associated traits in Sesame.

Particular	**Plant Height**	**Primary Branches/plant**	**Capsules/Plant**	**Oil Content**	**Seed Yield**
GCV (%)	7.616	17.080	10.722	2.621	22.485
PCV (%)	7.928	22.203	19.067	3.803	26.226
Heritability(%)	92.286	59.173	31.625	47.501	73.505
GA (% means)	15.071	27.065	12.422	3.721	39.711

Table 3: PearsonCorrelation coefficients among key traits in sesame genotypes.

Trait	**Plant Height**	**Primary Branches/plant**	**Capsules/Plant**	**Oil Content**	**Seed Yield**
Plant Height	1	0.555**	0.437**	0.330*	0.570**
Pri. Branches/plant		1	0.725**	-0.050^{NS}	0.562**
Capsules/Plant			1	-0.054^{NS}	0.630**
Oil Content				1	0.401*
Seed Yield					1

*Significant at $p < 0.05$, ** Significant at $p < 0.01$ and NS- Non-significant

Table 4: Genotypic path coefficient showing direct and indirect effects for yield and its key attributing traits in sesame.

Trait	**Plant Height**	**Primary Branches/Plant**	**Capsules/Plant**	**Oil Content**	**Seed Yield (r)**
Plant Height	**-0.097**	-0.19032	0.69153	0.20239	0.607
Pri. Branches/Plant	-0.05258	**-0.351**	1.09076	-0.04070	0.647
Capsules/Plant	-0.05408	-0.30874	**1.239**	-0.06644	0.810
Oil Content	-0.03503	0.02550	-0.14707	**0.560**	0.403

Residual Effect = 0.05620

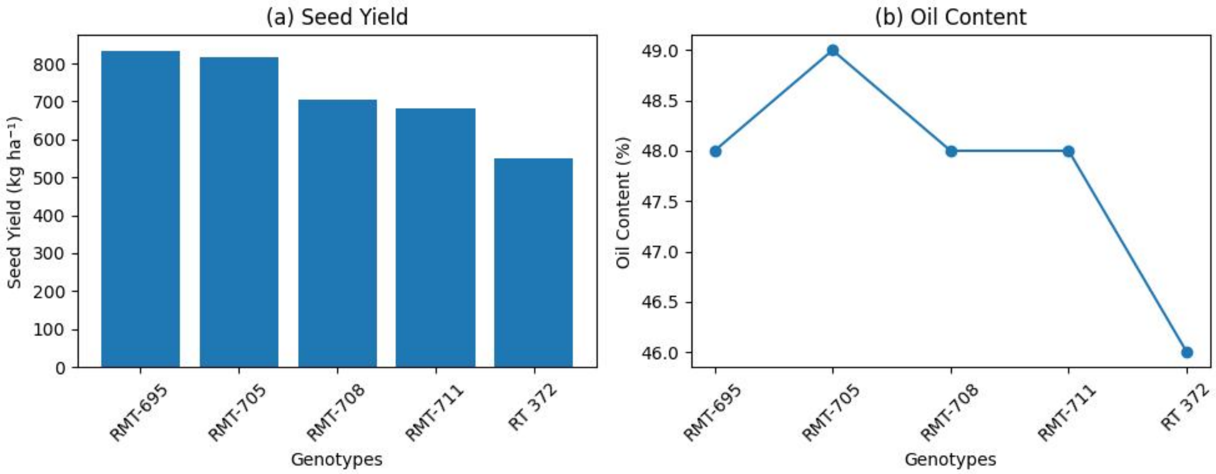

Fig. 1:(a) Seed yield (kg ha^{-1}) and (b) oil content (%) of promising sesame genotypes over best check RT 372.

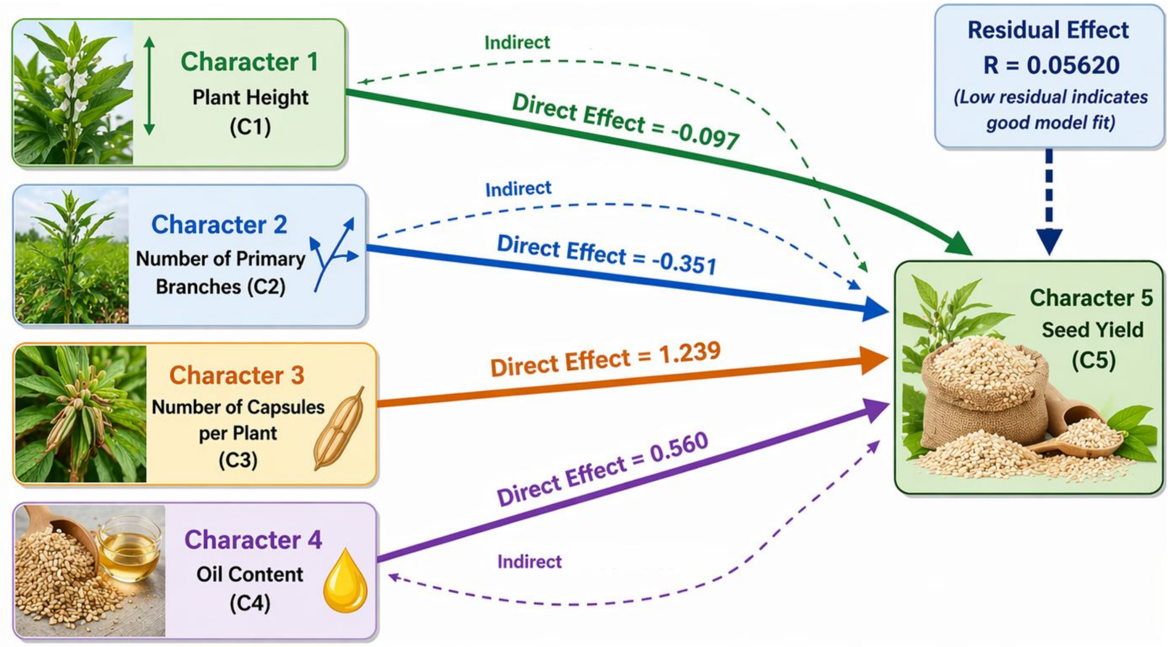

Fig. 2: Genotypic path diagram showing direct and indirect effects for yield and its key attributing traits in sesame

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