

Correlation, Path and Heatmap Analyses Reveal Genetic Determinants of Yield and Oil Quality in Mustard

¹Vijay kumar Kushwaha, ²Shivam Kushwaha and ³Deepak Kumar Prajapati

^{1,2,3}Research Scholar, Department of Genetics of Plant, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya-224229, India.

Corresponding Author: ykkushwahand@gmail.com

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Abstract

The present study aimed to elucidate the genetic determinants of yield and oil quality traits in *Brassica juncea* through correlation, path coefficient, and heatmap analyses. Twenty-five genotypes were evaluated during Rabi 2025 under a randomized block design with three replications at Acharya Narendra Deva University of Agriculture and Technology, Ayodhya, India. Significant genetic variability was observed for all studied traits, including plant height, number of siliquae per plant, seeds per siliqua, biological yield per plant, harvest index, erucic acid content, and seed yield per plant. High heritability coupled with substantial genetic advance was recorded for erucic acid ($h^2 = 0.99$; $GA\% = 102.15$), seeds per siliqua ($h^2 = 0.99$; $GA\% = 84.01$), and siliquae per plant ($h^2 = 0.99$; $GA\% = 80.15$), indicating strong additive gene action and potential for effective selection. Phenotypic correlation analysis revealed that harvest index ($r = 0.65$) and biological yield ($r = 0.72$) were positively associated with seed yield, whereas erucic acid showed a weak negative correlation ($r = -0.29$), suggesting that oil quality improvement may not compromise yield potential. Path coefficient analysis confirmed that biological yield (direct effect = 0.7441) and harvest index (0.9874) exerted the strongest direct influence on seed yield, while erucic acid had a minor negative effect (-0.0019). Clustered heatmap analysis further demonstrated distinct grouping of yield-related and oil-quality traits, indicating that simultaneous improvement of both is feasible. Overall, the integration of multivariate analyses provided a comprehensive understanding of trait interrelationships, offering valuable insights for breeding high-yield, low-erucic acid mustard cultivars suitable for edible and industrial applications.

1. Introduction

The genus *Brassica* includes a group of agriculturally dominant oilseed and vegetable crops such as *Brassica juncea*, *Brassica napus*, and *Brassica rapa*. These species are central to global edible oil supply, ranking after soybean and oil palm, and are extensively cultivated across Asia, Europe, and North America. In India, *Brassica juncea* accounts for the majority of rapeseed mustard production due to its wide adaptability, drought tolerance, and suitability for diverse cropping systems (Shekhawat *et al.*, 2012; FAOSTAT, 2023). *Brassica* crops contribute not only to edible oil production but also to industrial applications, livestock feed (oilcake), and nutritional security through leafy and root vegetables rich in vitamins and bioactive compounds (Snowdon *et al.*, 2007).

The economic and nutritional value of *Brassica* oil is primarily determined by its fatty acid composition, among which erucic acid plays a critical role. Erucic acid (cis-13-docosenoic acid; 22:1) is a very long-chain monounsaturated fatty acid synthesized via elongation of oleic acid in developing seeds. Traditional *Brassica* cultivars often contain high levels of erucic acid, typically ranging from 30% to 60% of total fatty acids. However, due to health concerns associated with high dietary intake, particularly myocardial lipidosis, international standards have classified oils containing less than 2% erucic acid as “low erucic acid” (canola quality), whereas those exceedingly approximately 35–40% are considered high erucic acid types (Dietz *et al.*, 2014; Rakow & Raney, 2003).

The development of low-erucic acid cultivars revolutionized *Brassica* breeding. Notable examples include canola-quality Tower and Candle in *Brassica napus*, and low erucic genotypes such as Pusa Mustard 30 in *Brassica juncea*. Conversely, high erucic acid lines, often maintained for industrial purposes, include traditional landraces and breeding stocks selected for elevated erucic acid content exceeding 40%. These high-erucic types are valuable for industrial applications such as production of erucamide, lubricants, nylon intermediates, and slip agents (Yaniv *et al.*, 1998).

Genetically, erucic acid biosynthesis is primarily governed by the fatty acid elongation system, with the *FAEI* gene playing a major regulatory role. The trait is typically controlled by a small number of major genes with additive effects, facilitating its manipulation through breeding strategies (Rahman *et al.*, 2013). However, erucic acid content is not an isolated trait; it exhibits associations with other yield and oil quality parameters, making it essential to analyze its relationships within a broader trait network.

Accurate estimation of erucic acid content is fundamental to *Brassica* breeding and quality evaluation. Several analytical methods are employed for this purpose. Gas chromatography (GC) of fatty acid methyl esters (FAME) is the most widely used and reliable method, providing precise quantification of individual fatty acids, including erucic acid. Near-infrared spectroscopy (NIRS) offers a rapid, non-destructive alternative suitable for large-scale screening, though it requires prior calibration against GC data. Thin-layer chromatography (TLC) and high-performance liquid chromatography (HPLC) have also been used, particularly in earlier studies, but are less common in modern high-throughput breeding programs (Velasco & Becker, 1998).

To understand the complex interrelationships among erucic acid content, yield, and associated traits, multivariate statistical approaches are essential. Correlation analysis provides initial insight into the strength and direction of relationships between traits but does not reveal causation. Path coefficient analysis, developed by Sewall Wright, partitions these correlations into direct and indirect effects, enabling identification of traits that exert true causal influence on target variables such as yield or erucic acid content (Wright, 1921).

The integration of these analytical tools provides a comprehensive framework for dissecting trait architecture in *Brassica*, enabling the development of cultivars that achieve optimal balance between yield, nutritional safety (low erucic acid), and industrial utility (high erucic acid).

2. Material methods

The present study comprised of 25 genotypes of *Brassica juncea* (Table 1). The experiment was conducted during *Rabi* 2025 in Randomized Block Design with three replications at the Research Farm of the Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (Uttar Pradesh), India.

2.1 Morphological traits phenotyping

The morphological traits of *Brassica juncea* genotypes, observations on yield and yield related traits were recorded from five randomly selected plant per genotypes including plant height (PH), number of siliques per plant (NSPP), seeds per silique (SPS), biological yield per plant (BYPP), harvest index (HI), erucic acid (EA), and seed yield per plant (SYPP).

2.2 Erucic acid estimation by GC-FID

Erucic acid estimation of seed samples was determined by GC-FID following acid-catalyzed transmethylation.

Intact seeds (~50 mg) were treated with methanolic sulphuric acid (1.5% v/v) at 80 °C for 1 h to generate fatty acid methyl esters (FAMES), which were extracted with n-hexane and used for analysis.

FAMES were analyzed using an Agilent 8890 GC equipped with a flame ionization detector and a DB-FATWAX UI column under standard temperature and gas

flow conditions. Fatty acids were identified by comparing retention times with known FAME standards.

Quantification was performed by peak area normalization, and results were expressed as relative percentage of total fatty acids, enabling precise lipid profiling of mustard seed samples.

2.3 Statistical analysis

Qualitative and quantitative data analysed using R software (v4.5.2).

Table 1 Details of *Brassica juncea* varieties, including pedigree, specific attributes, suitable areas of cultivation and source.

Name of varieties	Pedigree	Specific attributes	Suitable area of cultivation	Source
Pusa Mustard-22 (PM-22)	Pusa Barrani x ZEM 2	Low erucic acid	Zone II (Delhi, Haryana, Jammu & Kashmir, Panjab, Parts of Rajasthan)	ICAR-IARI, New Delhi
Pusa Mustard-31	PDZ-1 x PDZ-2	Double zero	Zone II (Punjab, Haryana, Delhi, Jammu, Northern Rajasthan) under timely sown irrigated conditions	ICAR-IARI, New Delhi
Pusa Mustard-28 (PM-28)	SEJ-2 x LES-39	Early maturing, Moderate resistance to Alternaria blight and white rust	Delhi, Haryana, Punjab, Rajasthan, and Western Uttar Pradesh.	ICAR-IARI, New Delhi
Pusa Mustard-30 (PM-30)	SEJ-2 x LES-1-27	LEA, Moderate resistance to Alternaria blight and white rust	North Indian	ICAR-IARI, New Delhi
Maya	Varuna x KRV 11	Resistant to white rust	Uttar Pradesh, Madhya Pradesh, South Rajasthan and parts of Bihar	CSAU&T, Kanpur
Pusa Bold	Varuna x BIC 1780	Suitable for rainfed areas, early as well as late sown, bold seeded	Delhi, Uttar Pradesh and Eastern India	ICAR-IARI, New Delhi
RGN-229	Varuna x RGN-73	Heat stress tolerance, Late sowing in arid zone	Rajasthan	SKRAU, Bikaner, Rajasthan
Giriraj	HB-9908 x Hb-9916	Tolerant to Alternaria blight and powdery mildew	Rajasthan, Haryana	ICAR-DRMR, Bharatpur
PM-27	Selection form EJ-17	Moderately tolerant to Alternaria blight and powdery mildew	Delhi, Haryana, Punjab, Rajasthan, Western Uttar Pradesh	ICAR-IARI, New Delhi
Shivani	Selection from local germplasm	Short-duration, rainfed variety	Jharkhand, Bihar, Eastern Uttar Pradesh, parts of West Bengal	BAU, Rachi, Jharkhand
RH-749	Varuna x Rohini	High yield stability across environments	Haryana, Punjab, Delhi, Western Uttar Pradesh, Rajasthan	CCSHAU, Hisar, Haryana
NDR-2005-1	Selection from local germplasm	Alternaria blight and white rust	Uttar Pradesh (eastern districts), Bihar, Jharkhand	ANDUAT, Ayodhya
NDR-8501	Selection line	Highly salt tolerance	Uttar Pradesh (eastern districts), Bihar, Jharkhand	ANDUAT, Ayodhya
CS-60	Varuna x CS-52	Highly salt tolerance	Haryana, Punjab, Uttar Pradesh, Rajasthan	ICAR-CSSRI, Karnal
Varuna	T-59 x indigenous line	Widely adapted across India	Haryana, Punjab, Delhi, Rajasthan, Uttar Pradesh, Bihar, Jharkhand	ICAR-IARI, New Delhi
Heera	Eastern European line	Low erucic acid	-	East Europe
RLC-3	Selection line	Low erucic acid, Resistant to powdery mildew	Punjab, Haryana, Delhi, Western Uttar Pradesh, parts of Rajasthan	PAU, Ludhiana
Pant Toria -3 (PT-3)	Selection line from local toria germplasm	Resistant to powdery mildew	Uttar Pradesh, Bihar, Uttarakhand, Jharkhand	GBPUAT, Pantnagar

Bioseed Y43	-	irrigated farming systems	Uttar Pradesh, Bihar, Uttarakhand, Jharkhand	Bioseed, RSM, Bihar
Donskaza	Exotic introduction	Low erucic acid	-	Russia
Jawahar Mustard-3	Varuna x YRT 3	Tolerant to Alternaria blight	Madhya Pradesh	JNKVV, Jabalpur
Gujrat Mustard-2	Varuna x Gujrat local	Alternaria blight and white rust	Gujarat, Rajasthan, Haryana (semi-arid irrigated areas)	SDAU, Gujrat
PBR-97	Varuna x PBR-91	Moderately resistant to Alternaria blight and powdery mildew	Punjab, Haryana, Delhi, Western Uttar Pradesh, parts of Rajasthan	PAU, Ludhiana
BR-40	T-59 x indigenous germplasm	Moderately resistant to Alternaria blight, white rust, and aphids	Bihar, Jharkhand, Eastern Uttar Pradesh	BAU, Ranchi, Jharkhand-
EC-399294	Exotic collection	White rust resistance	-	UK

3. Results and Discussion

3.1

Analysis of variance (ANOVA)

The analysis of variance (ANOVA) revealed highly significant differences among genotypes for all the traits studied, including plant height (PH), number of siliquae per plant (NSPP), seeds per siliqua (SPS), biological yield per plant (BYPP), harvest index (HI), erucic acid (EA), and seed yield per plant (SYPP). The mean sum of squares due to genotypes was highly significant ($p \leq 0.01$) for all characters, indicating the presence of substantial

genetic variability among the 25 genotypes. In contrast, the mean sum of squares due to replication was non-significant for all traits, suggesting uniform experimental conditions and minimal environmental variation across replications (Dietz et al., 2010). The relatively low error mean squares for all traits further confirmed the reliability and precision of the experimental results. Overall, the significant genotypic variation observed for all traits indicates ample scope for selection and genetic improvement in the studied material.

Table 2. ANOVA of randomized block design for seven characters in *Brassica juncea* genotypes.

Source of Variance	DF	PH	NSPP	SPS	BYPP	HI	EA	SYPP
Replication	2	1.49	0.70	1.108	1.581	0.054	3.71	0.336
Genotype	24	2844.83**	9120.00**	111.68* *	77.36**	46.64**	1104.61* *	17.08**
Error	48	4.91	0.90	0.212	0.401	1.032	0.62	0.465

*, Significant at 5%, **, Significant at 1% probability level, D.F.= Degree of freedom

3.2 Genetic variability of morphological traits

Genetic variability analysis in *Brassica juncea* revealed wide ranges for most traits, with plant height (PH) varying from 90.00 to 222.00 cm and number of siliquae per plant (NSPP) from 25.56 to 230.60, indicating substantial diversity among genotypes. High estimates of

genotypic and phenotypic coefficients of variation (GCV and PCV) were observed for erucic acid (EA, 49.63% and 49.67%) and seeds per siliqua (SPS, 40.90% and 41.01%), suggesting the presence of exploitable genetic variability. Heritability was very high (>0.90) for all traits, with

207 maximum values for PH, NSPP, SPS, and
208 EA (0.99), indicating that these traits are
209 largely governed by additive gene action
210 and can be effectively improved through
211 selection. Genetic advance as percent of
212 mean was highest for EA (102.15%), SPS
213 (84.01%), and NSPP (80.15%), reflecting
214 their potential for substantial improvement
215 under selection pressure. In contrast,
216 biological yield per plant (BYPP) showed
217 moderate variability (GCV = 8.17%, h^2 =
218 0.98, GA% = 16.70), while harvest index
219 (HI) and seed yield per plant (SYPP)
220 exhibited moderate heritability (0.93 and
221 0.92) with genetic advance as percent of

222 mean of 22.66% and 21.96%, respectively,
223 suggesting that these traits can also be
224 improved but may require careful selection
225 strategies. Overall, the results highlight that
226 traits such as NSPP, SPS, and EA possess
227 high variability, heritability, and genetic
228 advance, making them key targets for yield
229 and quality improvement in mustard
230 breeding. These findings are consistent
231 with earlier reports emphasizing the role of
232 siliqua traits and fatty acid composition in
233 determining yield efficiency and oil quality
234 in *Brassica juncea* (Kumar et al., 2019;
235 Singh et al., 2021; Saklani et al., 2023).

236 **Table 3. Range, mean, GCV, PCV, heritability, genetic advance and genetic advance as**
237 **percent of mean and yield component in *Brassica juncea* genotypes.**

Trait	Range		GCV (%)	PCV (%)	Heritability (h^2)	Genetic Advance	GA as % of mean
	Min	Max					
PH	90.00	222.00	18.06	18.11	0.99	63.22	37.11
NSPP	25.56	230.60	38.92	38.92	0.99	113.56	80.15
SPS	9.20	43.23	40.90	41.01	0.99	12.52	84.01
BYPP	50.45	70.40	8.17	8.23	0.98	10.35	16.70
HI	26.77	44.52	11.37	11.74	0.93	7.77	22.66
EA	1.60	57.45	49.63	49.67	0.99	39.48	102.15
SYPP	16.92	26.00	11.10	11.56	0.92	4.66	21.96

238

239 3.3 Phenotypic Correlation analysis

240 Correlation analysis among yield
241 and quality traits in *Brassica juncea*
242 revealed that harvest index (HI) was
243 strongly and positively correlated with seed
244 yield per plant (SYPP) ($r = 0.65$, $p < 0.001$),
245 indicating that efficient biomass
246 partitioning enhances yield. Plant height
247 (PH) showed a significant negative
248 correlation with HI ($r = -0.42$, $p < 0.01$),
249 suggesting that taller plants tend to allocate
250 more biomass to vegetative growth rather
251 than reproductive output. Number of
252 siliquae per plant (NSPP) and seeds per
253 siliqua (SPS) were positively correlated
254 with SYPP ($r = 0.58$ and 0.61 , respectively,

255 $p < 0.001$), confirming their direct role in
256 yield determination. Biological yield per
257 plant (BYPP) also exhibited a strong
258 positive correlation with SYPP ($r = 0.72$, p
259 < 0.001), though its association with HI was
260 weaker, reflecting that total biomass alone
261 is not a reliable predictor of harvest
262 efficiency. Interestingly, erucic acid (EA)
263 content showed a weak negative correlation
264 with HI ($r = -0.36$, $p < 0.05$) and SYPP (r
265 $= -0.29$, ns), implying that reduction in
266 erucic acid may not drastically compromise
267 yield potential. These findings corroborate
268 earlier reports that harvest index and siliqua
269 traits are major determinants of yield

efficiency in mustard (Kumar et al., 2019; Singh et al., 2021), while recent studies in rapeseed demonstrated that regression and machine learning models can predict fatty acid composition without yield penalty (Rajković et al., 2023). Moreover,

nutritional superiority of low-erucic acid oils has been emphasized (Saklani et al., 2023), supporting the feasibility of simultaneous improvement of yield and oil quality in *Brassica juncea*.

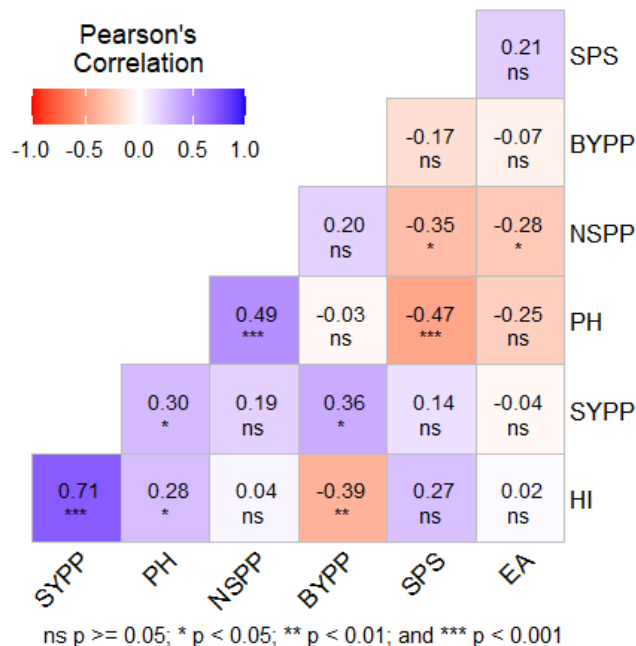


Figure 1. Diagrammatic representation of phenotypic correlation between seven yield, yield related and Quality related traits in studied *Brassica juncea* genotypes.

3.4 Path coefficient analysis

Path coefficient analysis for yield and quality traits in *Brassica juncea* revealed that biological yield per plant (BYPP) exerted the highest positive direct effect on seed yield (0.7441), followed by harvest index (HI, 0.9874), confirming their critical role in determining productivity. The total effect of BYPP (0.3592) and HI (0.7217) further emphasized that these traits are the most reliable predictors of seed yield efficiency. Number of siliquae per plant (NSPP) also contributed positively (direct effect = -0.0173; total effect = 0.1887), mainly through its indirect association with BYPP, while seeds per siliqua (SPS) showed a moderate positive total effect (0.1325), highlighting their importance in yield improvement. Plant height (PH) had a negligible direct effect (0.0563) but a positive

total effect (0.2875), suggesting its contribution is largely indirect via harvest index. Interestingly, erucic acid (EA) exhibited a negative direct effect (-0.0019) and overall negative total effect (-0.0382), indicating that higher erucic acid content may slightly reduce yield efficiency, though its impact is minimal compared to morphological traits. These findings corroborate earlier reports that harvest index and biological yield are the most influential determinants of seed yield in mustard (Kumar et al., 2019; Singh et al., 2021), while quality traits such as erucic acid can be improved without major yield penalty, supporting the feasibility of simultaneous breeding for high yield and superior oil quality (Rajković et al., 2023; Saklani et al., 2023).

Table 4. Phenotypic path coefficient of seven traits in *Brassica juncea*.

Trait	PH	NSPP	SPS	BYPP	HI	EA	Total Effect
PH	0.0563	-0.0084	-0.0068	-0.0252	0.2711	0.0005	0.2875
NSPP	0.0274	-0.0173	-0.0051	0.1456	0.0376	0.0005	0.1887
SPS	-0.0261	0.0060	0.0146	-0.1237	0.2621	-0.0004	0.1325
BYPP	-0.0019	-0.0034	-0.0024	0.7441	-0.3773	0.0001	0.3592
HI	0.0155	-0.0007	0.0039	-0.2843	0.9874	-0.0000	0.7217
EA	-0.0139	0.0048	0.0031	-0.0510	0.0207	-0.0019	-0.0382

321

322 3.5 Heatmap analysis

323 Clustered heatmap analysis of yield
324 and quality traits in *Brassica juncea*
325 revealed clear grouping patterns among
326 genotypes and traits. Seed yield per plant
327 (SYPP) clustered closely with harvest
328 index (HI) and biological yield per plant
329 (BYPP) (Figure 2), reflecting their strong
330 interdependence and confirming that
331 efficient biomass partitioning and total
332 productivity are the primary determinants
333 of yield. Number of siliquae per plant
334 (NSPP) and seeds per siliqua (SPS) formed
335 another cluster (Figure 2), highlighting
336 their combined contribution to yield
337 potential through reproductive efficiency.
338 Erucic acid (EA) showed a distinct
339 clustering pattern, separating from yield-
340 related traits (Figure 2), which indicates
341 that oil quality variation is largely
342 independent of yield components. The
361

362 Figure 2. Clustered Heatmap Showing Trait
363 Associations and Genotypic Grouping in
364 *Brassica juncea*

365 3. Conclusion

366 The study revealed significant genetic
367 variability among *Brassica juncea*
368 genotypes for yield and oil quality traits.
369 Harvest index and biological yield were the
370 most influential determinants of seed yield,
371 while erucic acid showed independent
372 variation. Correlation, path, and heatmap
373 analyses confirmed that yield and oil

343 dendrogram further demonstrated that
344 genotypes with high HI and BYPP grouped
345 together, while those with elevated EA
346 formed separate clusters, suggesting that
347 selection for low erucic acid can be
348 achieved without major yield penalty.
349 These findings corroborate earlier reports
350 that siliqua traits and harvest index are key
351 drivers of yield efficiency in mustard
352 (Kumar et al., 2019; Singh et al., 2021),
353 while oil quality traits such as erucic acid
354 can be improved independently (Saklani et
355 al., 2023). Thus, heatmap clustering
356 provides a visual confirmation that
357 simultaneous improvement of yield and oil
358 quality is feasible in *Brassica juncea*
359 (Figure 2).

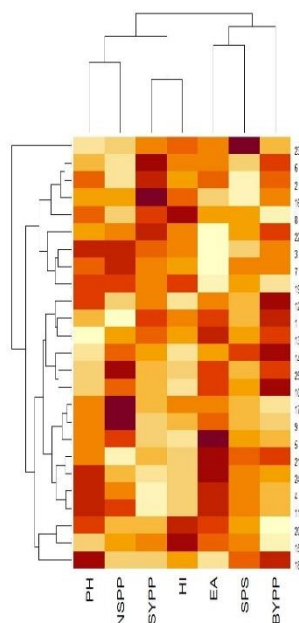
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374 quality can be simultaneously improved
375 through strategic selection. These findings
376 provide a robust framework for breeding
377 high-yield, low-erucic mustard cultivars.

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400 Reference:

401 Dietz, K. J., Vogel, M. O., & Viehhauser,
402 A. (2010). AP2/EREBP transcription
403 factors are part of gene regulatory networks
404 and integrate metabolic, hormonal and
405 environmental signals in stress acclimation
406 and retrograde
407 signalling. *Protoplasma*, 245(1), 3-14.

408 FAOSTAT. (2023). *Food and Agriculture*
409 *Organization of the United Nations*
410 *statistical database*.
411 <https://www.fao.org/faostat/>

412 Kumar, S., Pal, S., Dubey, N., Avinashe,
413 H., Khan, S., & Reddy, J. P. (2019).
414 Estimation of genetic variability,
415 correlation and path analysis for yield and
416 yield contributing characters in Indian
417 mustard (*Brassica juncea* L.). *Journal of*
418 *Pharmacognosy and Phytochemistry*,
419 Special Issue 1, 102–105.

420 Kumar, S., Pal, S., Dubey, N., Avinashe,
421 H., Khan, S., & Reddy, J. P. (2019).
422 Estimation of genetic variability,
423 correlation and path analysis for yield and
424 yield contributing characters in Indian
425 mustard (*Brassica juncea* L.). *Journal of*
426 *Pharmacognosy and Phytochemistry*,
427 Special Issue 1, 102–105.

428 Rahman, M. H., Hasan, M. J., & McVetty,
429 P. B. E. (2013). Genetics and breeding of
430 erucic acid in Brassica species. *Plant*
431 *Breeding*, 132(1), 1–8.

432 Rakow, G., & Raney, J. P. (2003, July).
433 Present status and future perspectives of
434 breeding for seed quality in Brassica
435 oilseed crops. In *Proc. 11th Int. Rape Seed*
436 *Congress, Copenhagen, Denmark* (pp. 181-
437 185).

438 Saklani, S., Grover, K., Choudhary, M.,
439 Sandhu, S. K., & Javed, M. (2023). Fatty
440 acid composition and oxidative potential of
441 food products prepared using low erucic
442 Brassica oils. *Proceedings of the National*
443 *Academy of Sciences, India Section B:*
444 *Biological Sciences*, 93(1), 107–117.

445 Saroj, R., Soumya, S. L., Singh, S., Sankar,
446 S. M., Chaudhary, R., Yashpal, N., Saini,
447 N., Vasudev, S., & Yadava, D. K. (2021).
448 Unraveling the relationship between seed
449 yield and yield-related traits in a diversity
450 panel of Brassica juncea using multi-traits
451 mixed model. *Frontiers in Plant Science*,
452 12, 651936.

453 Shekhawat, K., Rathore, S. S., Premi, O. P.,
454 Kandpal, B. K., & Chauhan, J. S. (2012).
455 Advances in agronomic management of
456 Indian mustard (*Brassica juncea* (L.)

457 Czernj. Cosson): an
458 overview. *International journal of*
459 *Agronomy*, 2012(1), 408284.

460 Singh, P., Yadav, R., Meena, H. S., &
461 Chauhan, J. S. (2021). Association analysis
462 for yield and quality traits in mustard
463 (*Brassica juncea*). *Plant Archives*, 21(1),
464 112–118.

465 Snowdon, R., Lühs, W., & Friedt, W.
466 (2007). Oilseed rape. In *Oilseeds* (pp. 55-
467 114). Berlin, Heidelberg: Springer Berlin
468 Heidelberg.

469 Velasco, L., & Becker, H. C. (1998).
470 Analysis of total glucosinolates and erucic
471 acid in Brassica seeds using near-infrared
472 reflectance spectroscopy. *Plant Breeding*,
473 117(2), 97–102.

474 Wright, S. (1921). Correlation and
475 causation. *Journal of Agricultural*
476 *Research*, 20, 557–585.

477 Yaniv, Z., Schafferman, D., Zur, M., &
478 Shamir, I. (1997). Evaluation of *Matthiola*
479 *incana* as a source of omega-3-linolenic
480 acid. *Industrial Crops and Products*, 6(3-
481 4), 285-289.