AATCC Review

12 October 2024: Received
07 January 2024: Revised
05 February 2025: Accepted
09 February 2025: Available Online

https://aatcc.peerjournals.net/

Original Research Article

Open Access

Genetic Analysis of Traits in Indian Mustard Using Additive-Dominance Model

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ABSTRACT

The study investigates the genetic basis of key traits in Indian mustard (Brassica juncea) using the additive-dominance model, with a focus on genotype × environment interactions. Conducted over two Rabi seasons (2021-22 and 2022-23) at Sri Karan Narendra College of Agriculture, Rajasthan, the research involved ten genetically diverse mustard genotypes crossed in a 10 × 10 half-diallel mating design. The parents and F_1 hybrids were evaluated under three sowing conditions to simulate different environmental scenarios. Significant genotypic, environmental, and genotype × environment interactions were observed for various traits, including days to flowering, plant height, siliquae per plant, and seed yield per plant. Diallel analysis revealed the suitability of the additive-dominance model for several traits, with both additive and dominant genetic effects playing substantial roles. Dominance gene action predominated for most traits, with overdominance observed for plant height, seed yield, and siliqua length. Genetic diversity among parents was evident, with specific genotypes showing dominance for traits like early flowering, plant height, and seed yield. These findings provide valuable insights into the genetic architecture of mustard traits and offer strategies for improving yield, stress tolerance, and adaptability in mustard breeding programs, ensuring better productivity in varying environmental conditions.

Keywords: *Additive, environment, additive-dominance model, half diallel, seed yield, partial dominance and overdominance*

Introduction

The additive-dominance model is a crucial tool for studying the genetic basis of quantitative traits in crops like Indian mustard (*Brassica juncea*). This model divides phenotypic variance into two components. Additive effects reflect the combined influence of individual alleles. Dominance effects result from allele interactions at the same locus [1,8]. Indian mustard is an important crop in India, with multiple applications in soap and lubricant manufacturing and as cattle feed and manure [13,14].

Genetic variability in mustard provides immense potential for improving yield, stress tolerance, and adaptability [4,18]. The additive-dominance model is instrumental in dissecting this variability, helping breeders calculate genetic parameters such as additive (D) and dominance (H_1 and H_2) variances. These insights guide selection processes, enabling the development of high-yielding and stress-tolerant cultivars [3,8]. This is particularly vital as climate change increasingly affects mustard cultivation through altered temperatures and rainfall patterns [10, 15].

The model also evaluates genotype x environment interactions, which are critical for identifying cultivars with stable performance under varying environmental conditions [9, 16]. Mustard's predominantly autogamous nature, combined with 5–15% cross-pollination facilitated by insects, enhances its genetic study potential [17].

The application of the additive-dominance model has advanced mustard breeding programs by identifying superior genotypes and elucidating the genetic basis of key traits [1,4]. By integrating this model into breeding strategies, researchers can enhance mustard's productivity and resilience, ensuring sustainable production and meeting future agricultural demands.

Materials and Methods

The study was conducted at Sri Karan Narendra College of Agriculture in Jobner Rajasthan during the Rabi seasons of 2021-22 and 2022-23. The experimental material included ten genetically diverse mustard genotypes namely, BPR 543-2, BPR 349-9, DRMR 2017-15, PM 25, NRCHB 101, PM 28, IC 122449, EC 766136, RAJAT, and LAXMI. These genotypes were crossed using a 10 × 10 half-diallel mating design during Rabi 2021-22 to produce 45 F_1 crosses while excluding reciprocal crosses. In the subsequent Rabi season (2022-23) the parents and F_1 hybrids were evaluated under three sowing conditions to create different environments including normal sowing (October 15, 2022), late sowing (October 30, 2022), and very late sowing (November 15, 2022). The experimental design followed a randomized block layout with three replications for each environment. Each genotype was grown in paired rows of 2-meter length with a spacing of 45 cm between rows and 20 cm between plants within rows. All recommended agronomic practices were followed to ensure optimal crop growth.

Data collection included phenological traits such as days to flowering and days to maturity as well as morphological and yield traits like plant height, primary branches per plant, siliquae per plant, siliqua length, seeds per siliqua, 1000-seed weight, biological yield per plant and seed yield per plant.

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DOI: https://doi.org/10.21276/AATCCReview.2025.13.01.266

Observations were recorded on five randomly selected competitive plants per genotype in each replication except days to flowering and days to maturity.

Diallel analysis was conducted following the methodology of Mather and Jinks [11] and genetic parameters were estimated using R software. Graphical analysis was carried out based on the Hayman approach [6] by plotting the covariance Wr of each array against its variance Vr. The position of the regression line in the Wr-Vr graph provided information about dominance relationships. Dominance was indicated if the line passed through the origin while partial dominance was indicated if the line cut the Wr-axis above the origin. No dominance was suggested if the line touched the limiting parabola and overdominance was indicated if the line cut the Vr-axis below the origin. Genetic parameters included the average degree of dominance the proportion of positive and negative genes in the parents the proportion of dominant and recessive genes and the number of gene groups exhibiting dominance.

Results and Discussion

The analysis of variance revealed the significant genotype × environment interactions for all traits indicating that the genotypes responded differentially to environmental variations. These interactions highlighted that the variation observed in all traits was heritable but not fixable, as the environmental components significantly influenced the expression of the traits [8, 12].

The differential analysis was conducted separately for each environment, and the additive-dominance model was deemed suitable for several traits. These included days to maturity, plant height, biological yield per plant, and seed yield per plant across all environments, as well as primary branches per plant and the number of siliquae per plant in E_1 and E_2. Additionally, the model was appropriate for traits like siliqua length in E_1, 1000-seed weight in E_3, and days to 50% flowering in E_2 and E_3. However, for certain traits such as siliqua length in E_2 and E_3, days to 50% flowering and 1000-seed weight in E_1, primary branches per plant, siliquae per plant, and seeds per siliqua in E_3, the additive-dominance model was inadequate. In these cases, graphical analysis was employed to gain insights into the genetic composition of the parents. This analysis revealed the existence of epistatic interactions, indicating deviations from the additive-dominance assumptions. These findings align with previous research [1,5], which similarly highlighted both the applicability and limitations of the additive-dominance model for various traits across different environmental conditions.

The genetic variance components analysis indicated that both additive (D) and dominance (H_1 and H_2) components were significant for traits that fit the additive-dominance model. Traits such as plant height, siliqua length, and seeds per siliqua in E_1, and seed yield per plant in E_3, showed a significant influence of both components (D, H_1, and H_2), emphasizing the importance of both additive and non-additive genetic effects in their inheritance [8, 15]. The dominance components (H_1 and H_2) were of greater magnitude than the additive component (D) for most traits, suggesting the predominance of dominance gene action [1, 3]. The asymmetric distribution of positive and negative alleles among parents, as evidenced by significant H_1 and H_2 values, further emphasizes the potential for hybridization and heterosis exploitation in breeding programs [1]. Estimates of H_1 were higher than H_2 for all traits, suggesting an unequal distribution of alleles in the population. These results align with previous studies [15, 12], which similarly found that the dominance components played a more significant role in trait variation in mustard. The estimates of 'F' were significant for certain traits, such as days to maturity in E_1, indicating that dominant alleles were more frequent than recessive ones. However, non-significant values of 'F' for other traits suggested an equal frequency of dominant and recessive alleles. These findings corroborate previous observations [2, 7], which also noted the presence of both dominant and recessive alleles in mustard populations.

The environmental component E was significant in days to maturity and plant height in all the environments, biological yield per plant in E_1 and E_3, seeds per siliqua in E_1 and days to 50% flowering in E_3. This suggests that these traits were highly influenced by environmental fluctuations, as similar environmental influences were reported for mustard in previous studies [8, 12].

The analysis of genetic variation revealed that the ratio $(H_1/D)^{1/2}$, which signifies the degree of dominance, exceeded unity for all the traits, indicating the presence of overdominance. This finding aligns with previous studies [1,8,3,12], which also reported overdominance in mustard. Additionally, the $H_2/4H_1$ ratio was found to be less than 0.25 for all traits, suggesting an unequal distribution of positive and negative alleles among the parents. This result corroborates earlier reports [8, 15], further supporting the existence of overdominance and epistatic interactions in mustard. Furthermore, the ratio of dominant and recessive alleles, calculated as $[(4DH_1)½ + F] / [(4DH_1)½ - F]$, was less than unity for most traits, indicating an accumulation of recessive alleles, except for days to 50% flowering, primary branches per plant, seeds per siliqua, and 1000-seed weight in E3, where the ratio was greater than unity, signifying the predominance of dominant alleles [15, 12].

The present study revealed varying degrees of genetic dominance for different traits across three environments, indicating the influence of environmental interactions and partial failure of diallel assumptions. For primary branches per plant, partial dominance was observed in E_3, while over-dominance was exhibited in E_1 and E_2, with similar patterns noted for siliqua per plant, seed yield per plant, and harvest index. Complete and over-dominance were recorded for siliqua length and seeds per siliqua, whereas traits such as days to 50% flowering, days to maturity, plant height, 1000-seed weight, and biological yield per plant consistently showed over-dominance. These findings align with previous studies [1, 3], emphasizing the significant role of non-additive gene action and environmental interactions in trait expression.

The analysis of the scattering of array points demonstrated substantial genetic diversity among the parents for the traits studied, with their relative positions from the origin indicating the relative proportions of dominant and recessive alleles. Parents such as PM 28 in E_1, and IC 122449 in E_1 and E_3 for days to 50% flowering exhibited a high frequency of dominant alleles, making them potential candidates for early flowering in breeding programs. RAJAT in E_2 for days to maturity displayed dominance, indicating its potential for contributing to maturity regulation in hybrid combinations. For plant height, LAXMI in E_3 showed a dominance pattern favorable for improving this trait under specific environmental conditions. PM 28 consistently appeared across all three environments for primary branches per plant, along with BPR 543-2 and RAJAT in E_1 and IC 122449 in E_3, suggesting their potential to improve plant architecture.

For siliqua per plant, dominant alleles were most evident in BPR 543-2, DRMR 2017-15, PM 28, and IC 122449 in E_3, indicating their utility in increasing reproductive output. Regarding siliqua length, PM 28 and IC 122449 in E2, along with BPR 349-9 in E_3, demonstrated strong dominance, offering the potential for siliqua trait enhancement.

In the case of seeds per siliqua, PM 28 and RAJAT exhibited dominance across all three environments, while LAXMI in E_1 and E_3, and other parents like DRMR 2017-15, PM 25, NRCHB 101, and EC 766136, showed environment-specific dominance. For 1000-seed weight, parents such as RAJAT in E_1 and E_3, PM 28 in E_2 and E_3, and PM 25 in E_1 consistently exhibited dominance, highlighting their importance in breeding for seed quality traits. For biological yield per plant, PM 25 and RAJAT in E_1, and NRCHB 101 and EC 766136 in E_2, emerged as promising parents. For seed yield per plant, PM 28 in E_1 and E_3, RAJAT in E_1, NRCHB 101, IC 122449, and LAXMI in E_2, and BPR 349-9 in E_2, showed high dominance. Similarly, for harvest index, PM 28 in E_2 and E_3, EC 766136 in E_1 and E_2, and RAJAT in E_2 demonstrated dominance. These findings emphasize the importance of these parents as genetic resources for breeding programs[1]. By utilizing parents with dominant alleles in strategic hybrid combinations, significant improvements in seed yield and related traits can be achieved, contributing to the advancement of mustard crop breeding.

The narrow sense heritability (h^2) estimates were notably high for biological yield per plant in environments E_1 and E_2, as well as for days to 50% flowering, primary branches per plant, and seed yield per plant in E_2. This indicates that these traits are minimally affected by environmental factors and possess a robust genetic foundation, making them highly amenable to selection in breeding programs [8, 12]. In contrast, traits such as plant height, days to maturity, and siliqua length displayed lower heritability estimates, suggesting a stronger influence of non-additive genetic effects and environmental variability. This highlights the potential of utilizing heterosis breeding strategies to enhance these traits effectively.

The future scope of this study, based solely on traditional breeding approaches, involves expanding the exploration of genotype × environment interactions across a wider range of mustard genotypes and environments. Further work could focus on utilizing specific parents with desirable traits for hybridization to improve yield and stress tolerance. Emphasis on the development of stable and high-yielding varieties through recurrent selection and crossing of superior genotypes will be valuable. Additionally, conducting long-term field trials under varying environmental conditions could help identify genotypes with consistent performance, thereby contributing to more reliable mustard breeding programs.

Conclusion

In conclusion, this study highlights the significant influence of genotype × environment interactions on mustard traits. Environmental factors affected all traits while genotypic differences contributed to the observed variation. Traits with high heritability such as biological yield and seed yield have strong genetic bases making them ideal for selection. Traits like plant height and siliqua length showed lower heritability indicating a stronger environmental and non-additive genetic effect. This suggests that heterosis breeding could be effective for these traits. The differential analysis revealed both additive and non-additive gene actions supporting hybridization and heterosis for trait improvement. The dominance patterns in parent lines offer insights for breeding high-yielding mustard varieties. Overall the study provides useful information for mustard breeding under varying environmental conditions.

Compliance with Ethical Standards

Conflict of Interest

The authors declare that there is no conflict of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish, or preparation of the manuscript.

Acknowledgment

The author would like to thank the Department of Genetics and Plant Breeding, SKN College of Agriculture, Jobner, Jaipur, for providing materials and all the necessary resources required for conducting the research.

Table 1: Estimates of regression coefficients, standard errors, deviation from zero and unity for different characters in individual environments

Characters	Env.	Source of variation			
		b	SE(b)	(b-0)/SE(b)	(1-b)/SE(b)
Days to 50% flowering	E_1	0.35	0.12	2.82*	5.27**
	E_2	0.65	0.26	2.53*	1.34
	E_3	0.64	0.16	4.02**	2.30
Days to maturity	E_1	0.61	0.18	3.50**	2.21
	E_2	0.52	0.21	2.44*	2.26
	E_3	0.63	0.21	2.95*	1.71
Plant height (cm)	E_1	0.56	0.20	2.78*	2.22
	E_2	0.60	0.24	2.49*	1.65
	E_3	0.60	0.23	2.65*	1.77
Primary branches per plant	E_1	0.76	0.13	6.00**	1.87
	E_2	0.53	0.21	2.54*	2.27
	E_3	-0.07	0.17	-0.42	6.19**
Siliqua per plant	E_1	0.52	0.21	2.49*	2.26
	E_2	0.52	0.21	2.48*	2.27
	E_3	0.25	0.07	3.81**	11.47**
Siliqua length (cm)	E_1	0.55	0.22	2.48*	2.02
	E_2	0.20	0.16	1.24	4.87**
	E_3	0.36	0.14	2.66*	4.66**
Seeds per siliqua	E_1	0.68	0.14	4.84**	2.23
	E_2	0.62	0.17	3.65**	2.27
	E_3	0.54	0.10	5.43**	4.66**
1000-seed weight (g)	E_1	0.45	0.19	2.39*	2.88*
	E_2	0.45	0.31	1.46	1.81
	E_3	0.57	0.19	3.04*	2.26
Biological yield per plant (g)	E_1	0.82	0.14	5.78**	1.31
	E_2	0.74	0.21	3.47**	1.24
	E_3	0.65	0.24	2.70*	1.44
Seed yield per plant (g)	E_1	0.60	0.17	3.46**	2.28
	E_2	0.61	0.18	3.33*	2.17
	E_3	0.60	0.18	3.35*	2.26
Harvest index (%)	E_1	4.18**	1.99**	0.31	0.19
	E_2	7.55**	1.41**	0.46	0.62
	E_3	5.65**	3.42**	0.23	0.14
	E_2	-0.03	0.20	-0.14	5.13**
	E_3	-0.01	0.14	-0.09	7.00**

**, **Significant at 5 per cent and 1 per cent levels, respectively*

Table 2(a): Estimates of components of genetic variances for yield and its contributing attributes in three environments

Characters	Days to 50% flowering		Days to maturity			Plant height (cm)			Primary branches per plant		Siliqua per plant	
Environment	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_1	E_2
Component												
D	3.37*	8.87**	4.66*	6.14*	16.52**	30.20	47.22	30.05	0.10**	0.03*	485.07**	168.29*
SE±	1.52	1.17	2.19	2.88	5.41	25.80	30.54	19.59	0.02	0.01	136.84	72.01
H_1	32.67**	21.38**	70.93**	49.11**	84.28**	583.85**	606.55**	279.57**	0.24**	0.20**	2465.09**	1113.25**
SE±	3.23	2.50	4.67	6.13	11.52	54.93	65.00	41.71	0.04	0.03	291.28	153.28
H_2	22.86**	15.38**	65.31**	40.28**	70.69**	497.38**	570.66**	237.84**	0.22**	0.17**	1956.26**	1009.61**
SE±	2.75	2.12	3.97	5.21	9.79	46.68	55.24	35.45	0.04	0.02	247.55	130.27
h^2	0.81	3.54*	23.30**	64.23**	24.43**	140.75**	151.70**	161.50**	0.41**	0.13**	890.23**	859.38**
SE±	1.84	1.42	2.66	3.49	6.55	31.25	36.98	23.73	0.02	0.01	165.70	87.20
F	1.70	-0.99	-14.83**	-9.54	-8.81	-62.18	-112.59	-70.88	-0.08	0.00	-303.71	-236.86
SE±	3.50	2.71	5.06	6.64	12.49	-59.54	70.46	45.21	0.05	0.03	315.73	166.15
E	0.63	0.70*	3.79**	2.63**	3.82*	28.15**	26.92**	14.59*	0.02**	0.02**	36.94	40.25
SE±	0.46	0.35	0.66	0.87	1.63	7.78	9.21	5.91	0.01	0.00	41.26	21.71
$(H_1/D)^{1/2}$	3.11	1.55	3.90	2.83	2.26	4.40	3.58	3.05	1.55	2.58	2.25	2.57
$H_2/ 4 H_1$	0.17	0.18	0.23	0.21	0.21	0.21	0.24	0.21	0.23	0.21	0.20	0.23
$[(4DH_1)^{½} +F / (4DH_1)^{½}-F]$	1.18	0.93	0.42	0.57	0.79	0.62	0.50	0.44	0.59	1.00	0.76	0.57
h^2/ H_2	0.04	0.23	0.36	1.59	0.35	0.28	0.27	0.68	1.86	0.76	0.46	0.85
h2 (NS)	0.48	0.64	0.38	0.49	0.48	0.37	0.37	0.49	0.57	0.32	0.55	0.47

Table 2(b): Estimates of components of genetic variances for yield and its contributing attributes in three environments

Characters	Siliqua length (cm)	Seeds per siliqua		1000-seed weight (g)	Biological yield per plant (g)			Seed yield per plant (g)		
Environment	E_1	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3
Component										
D	0.02	0.20	1.19**	0.09**	21.59**	25.04**	3.20*	1.02**	1.89**	0.33
SE±	0.02	0.11	0.18	0.02	2.00	5.68	1.34	0.28	0.48	0.18
H_1	0.36**	1.43**	2.18**	0.31**	43.67**	79.71**	42.83**	4.43**	4.13**	3.21**
SE±	0.04	0.23	0.39	0.05	4.25	12.09	2.86	0.60	1.02	0.39
H_2	0.34**	1.32**	1.98**	0.20**	40.80**	64.84**	37.87**	4.18**	3.79**	2.97**
SE±	0.03	0.19	0.33	0.04	3.61	10.28	2.43	0.51	0.87	0.33
h^2	0.05*	2.83**	0.81**	0.05	57.24**	12.60	7.30**	1.96**	0.97	0.12
SE±	0.02	0.13	0.22	0.03	2.42	6.88	1.63	0.34	0.58	0.22
F	-0.02	-0.22	0.55	0.07	-1.80	-14.09	-3.78	-0.43	-1.07	-0.27
SE±	0.04	0.25	0.42	0.05	4.61	13.11	3.10	0.65	1.11	0.42
E	0.02**	0.12**	0.09	0.01	1.50*	1.65	1.12**	0.07	0.06	0.03
SE±	0.01	0.03	0.05	0.01	0.60	1.71	0.40	0.08	0.14	0.06
$(H_1/D)^{1/2}$	4.24	2.67	1.35	1.86	1.42	1.78	3.66	2.08	1.48	3.12
$H_2/ 4 H_1$	0.24	0.23	0.23	0.16	0.23	0.20	0.22	0.24	0.23	0.23
$[(4DH_1)^{½} +F / (4DH_1)^{½}-F]$	0.79	0.66	1.41	1.53	0.94	0.73	0.72	0.82	0.68	0.77
h^2/ H_2	0.15	2.14	0.41	0.25	1.40	0.19	0.19	0.47	0.26	0.04
h2 (NS)	0.22	0.37	0.42	0.52	0.53	0.60	0.36	0.43	0.62	0.35

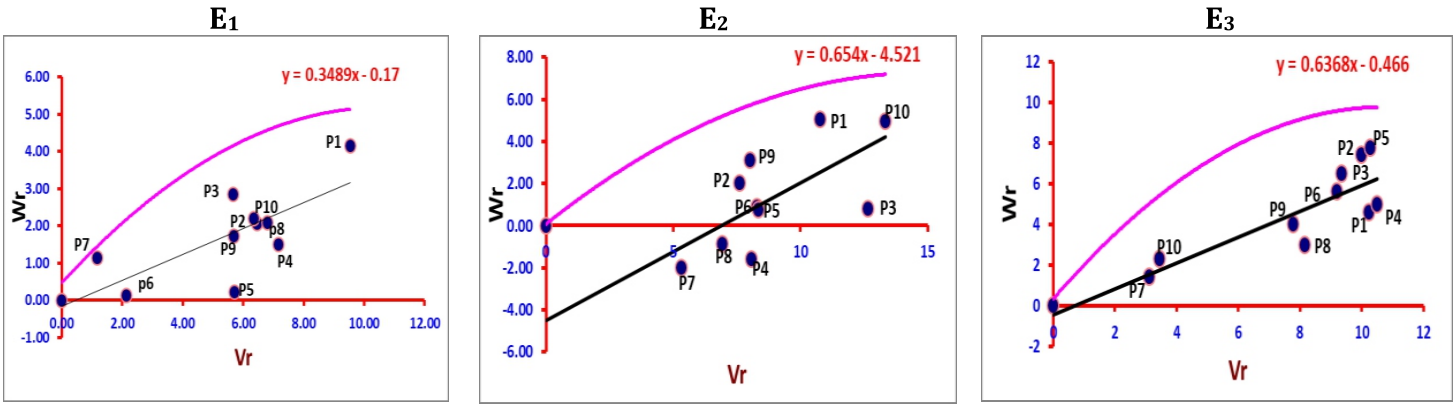

Fig 1: W_r-V_r graph for days to 50% flowering in the three environments

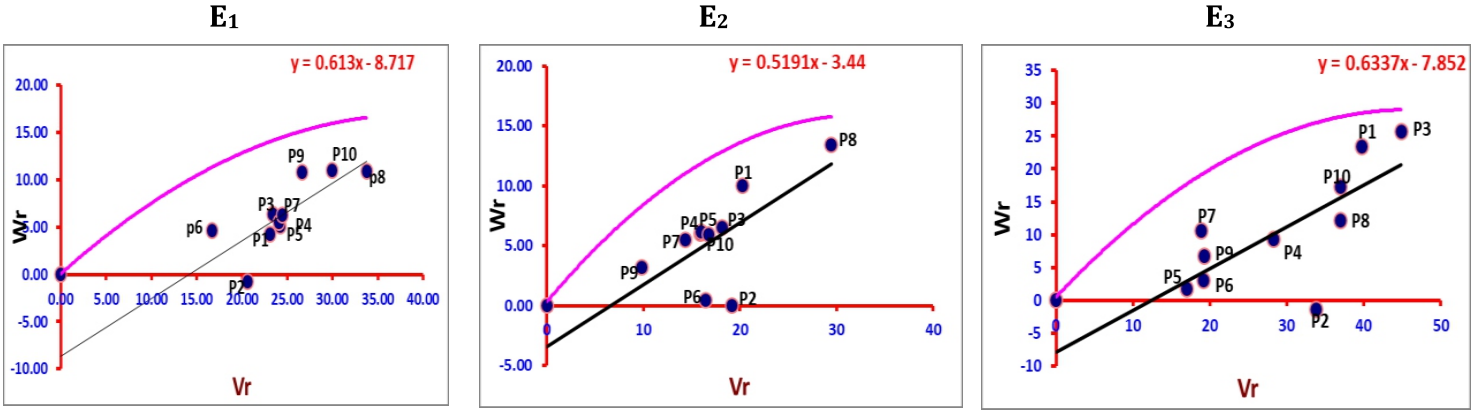

Fig 2: W_r-V_r graph for days to maturity in the three environments

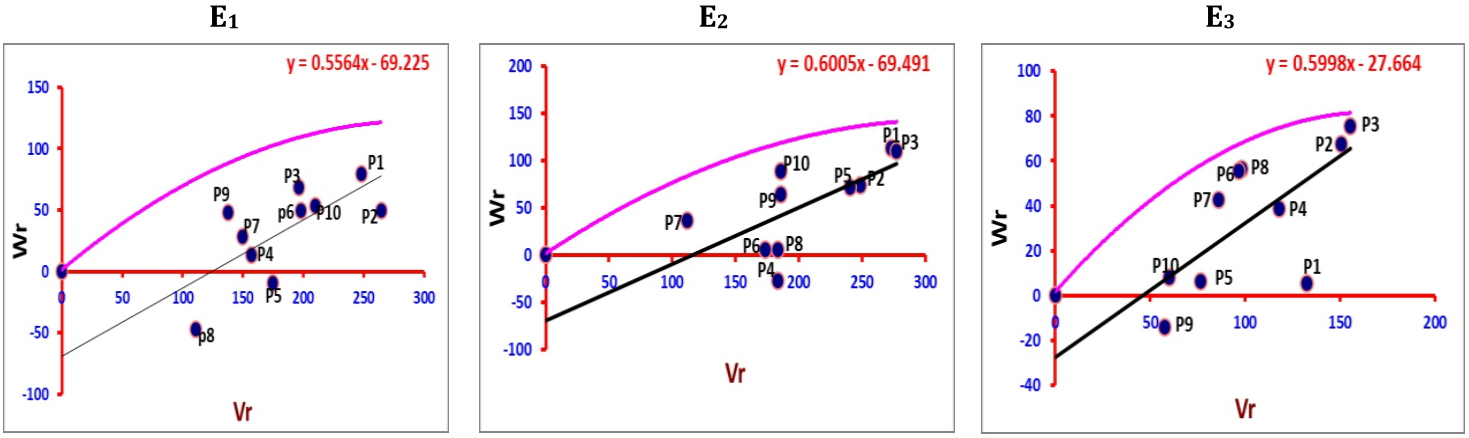

Fig 3: W_r-V_r graph for plant height (cm) in the three environments

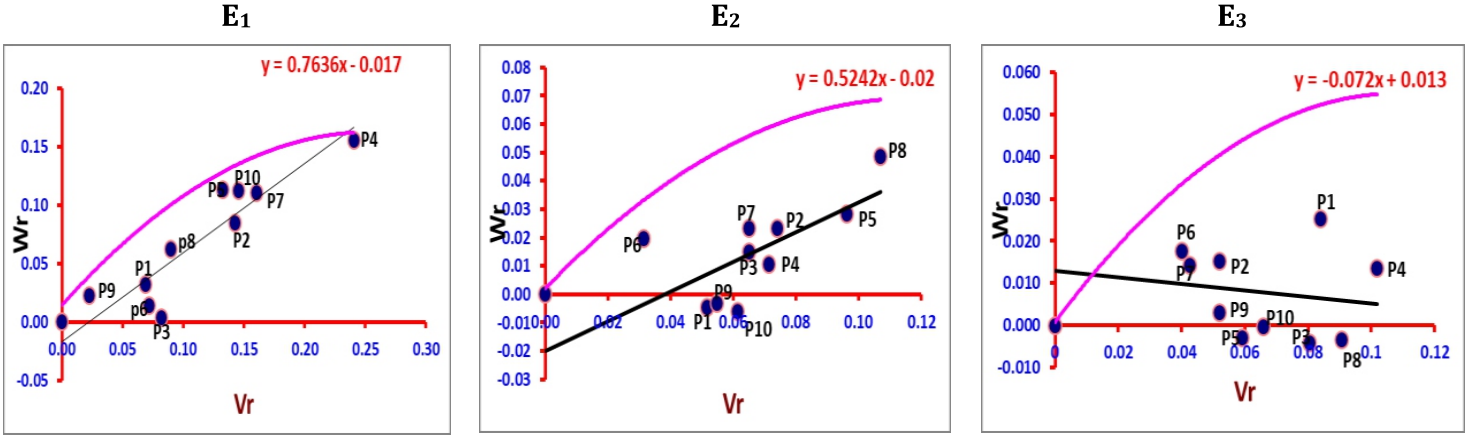

Fig 4: W_r-V_r graph for primary branches per plant in the three environments

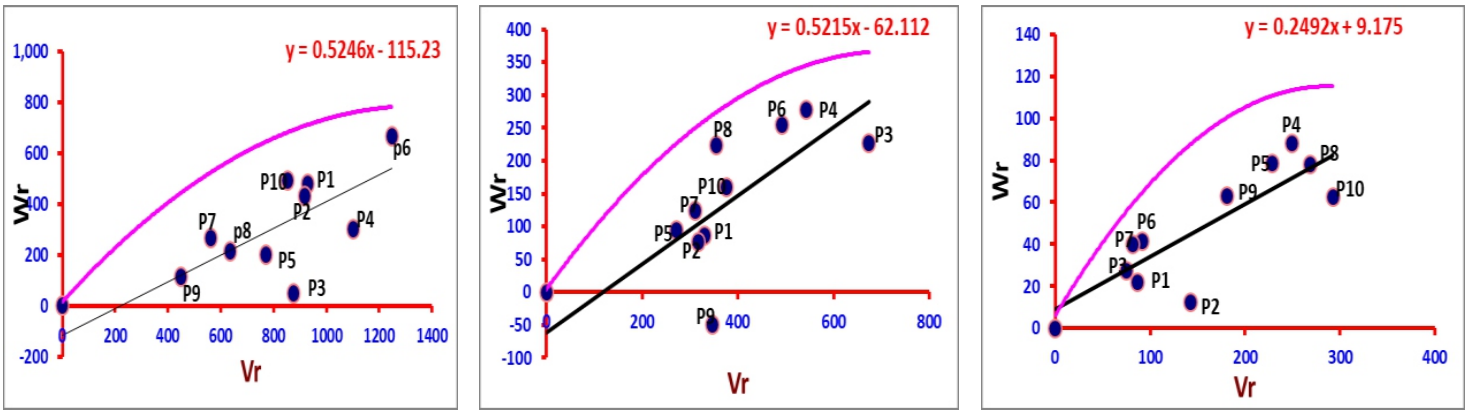

Fig 5: W_r-V_r graph for siliqua per plant in the three environments

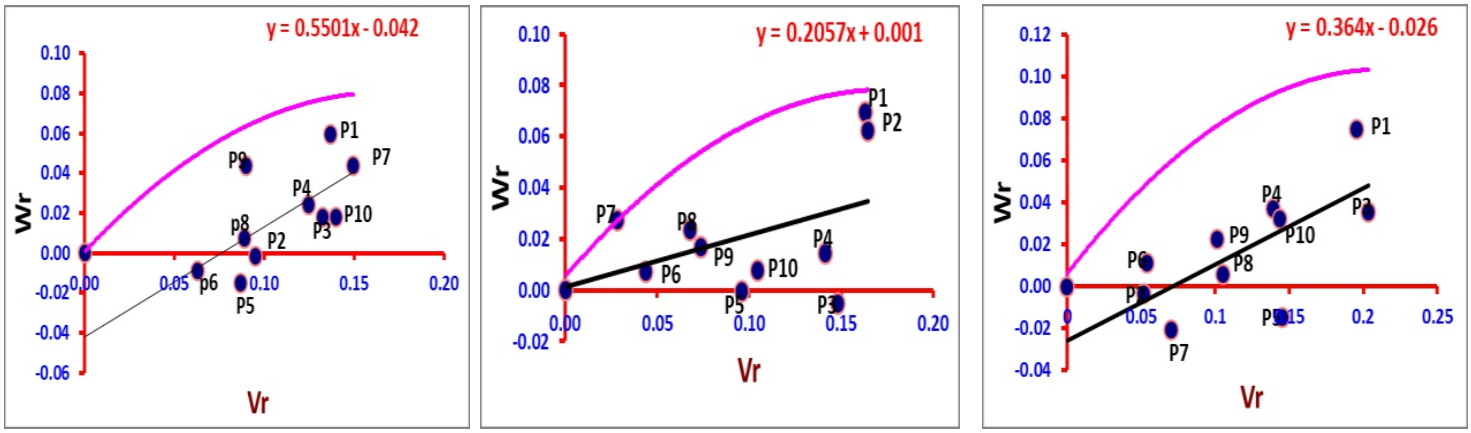

Fig 6: W_r-V_r graph for siliqua length (cm) in the three environments

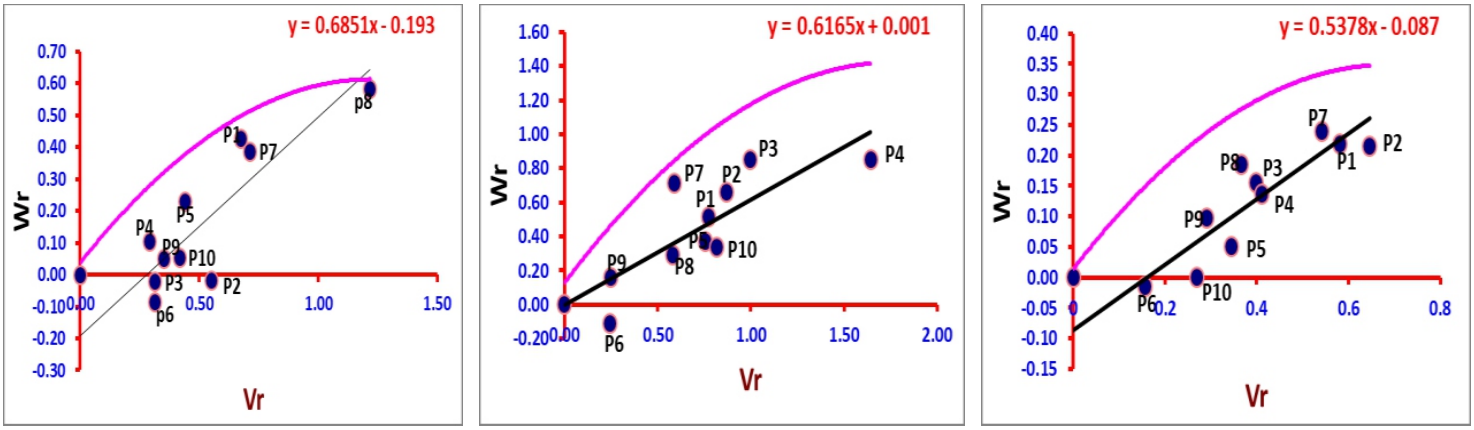

Fig 7: W_r-V_r graph for seeds per siliqua in the three environments

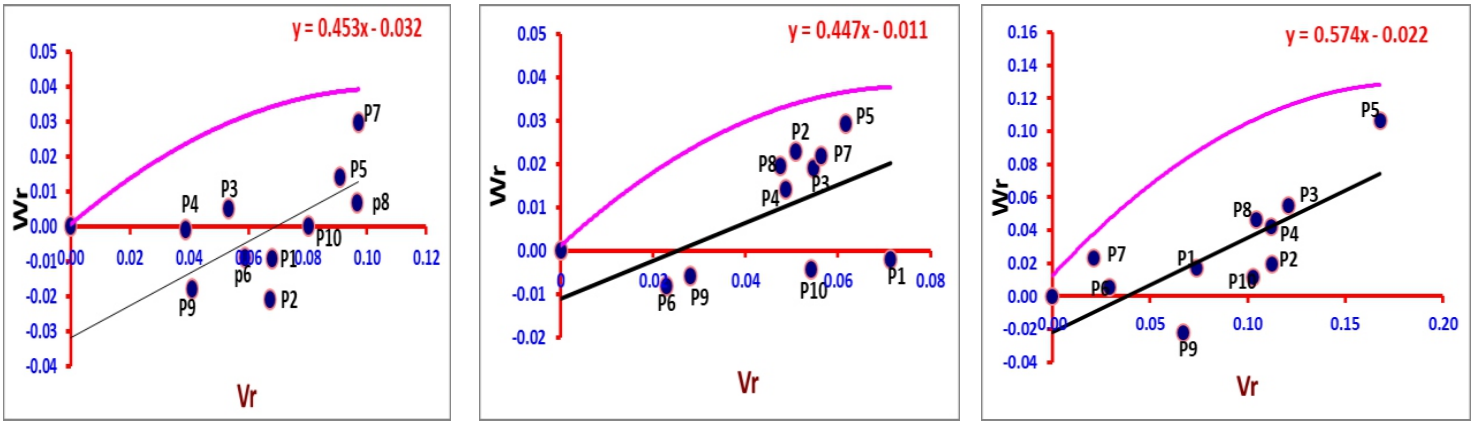

Fig 8: W_r-V_r graph for 1000-seed weight (g) in the three environments

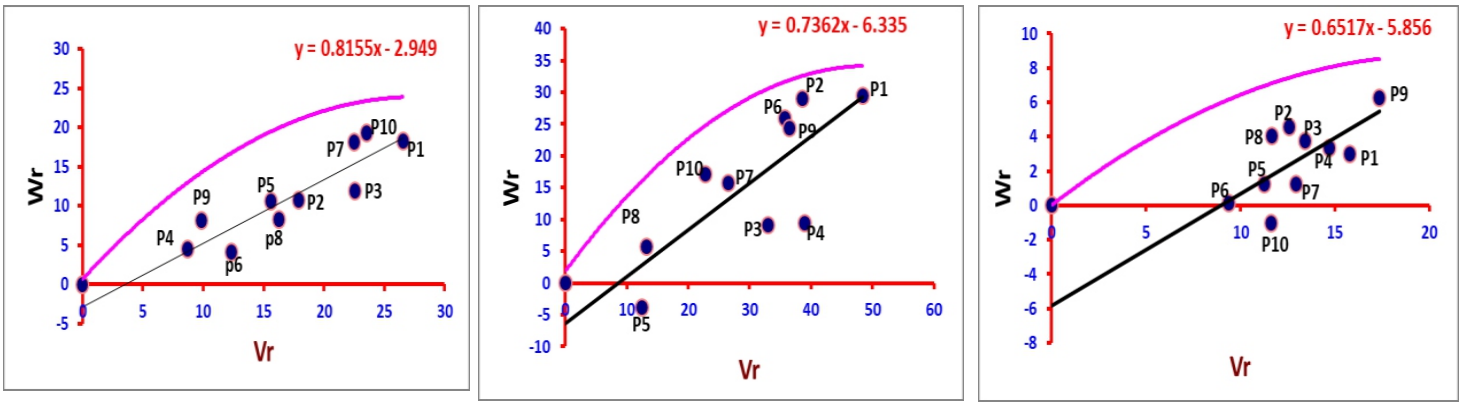

Fig 9: W_r-V_r graph for biological yield per plant (g) in the three environments

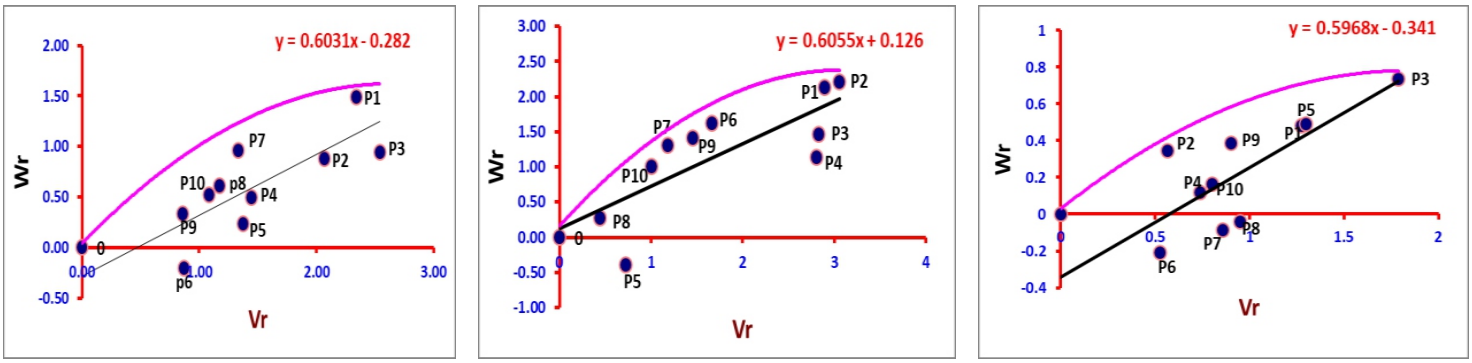

Fig 10: W_r-V_r graph for seed yield per plant (g) in the three environments

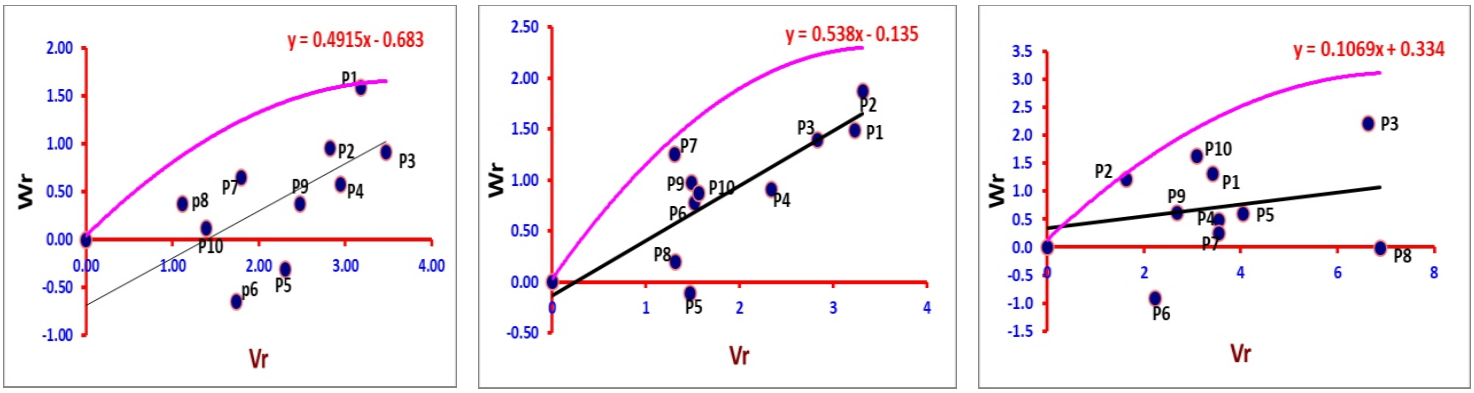

Fig 11: W_r-V_r graph for harvest index in the three environments

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