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STABILITY PERFORMANCE OF INDIAN MUSTARD (*Brassica juncea* L. CZERN. & COSS.) UNDER MULTI-ENVIRONMENT CONDITIONS

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ABSTRACT

Genotype × environment (G×E) interaction plays a crucial role in determining the stability and adaptability of yield and associated traits in Indian mustard. The present study evaluated the phenotypic stability of parents and hybrids using joint regression analysis across multiple environments, employing the environmental index (bi) and deviation from regression (S^2d_i) as stability parameters. Analysis of variance indicated that environmental effects were significant for all traits except glucosinolate content, while genotypic effects were significant for all characters, demonstrating substantial genetic variability. Significant G×E interactions further justified the application of stability analysis. Stable performance across environments for plant height was observed in PM-31 and PM-25 × GDM-4. Several parents GM-1, PM-25 and Pusa Bold and hybrids PM-25 × GM-1, Kranti × JD-60, PM-25 × CS-58, Kranti × CS-60, PM-31 × GM-1 and Kranti × CS-58 showed high mean performance and stability for total branches per plant. The seed yield per plant, parents PM-32, PM-33, CS-58, Pusa Bold, PM-31 and hybrids PM-31 × CS-58, PM- 32 × GM-1, CS-60 × PM-31, PM-32 × GDM-4, PM-25 × GDM-4, PM-31 × GDM-4 and PM-32 × PM-31. For test weight, parents PM-33, PM-32, GDM-4, GM-1 hybrids PM-32 × GM-1, JD-60 × CS-58, CS-60 × Pusa Bold, PM-32 × Pusa Bold, CS-60 × GM-1, PM-31 × GM-1, GM-1 × Pusa Bold, CS-60 × GDM-4, JD-60 × GDM-4 and PM-32 × CS-58 demonstrated superior mean performance with regression coefficients close to unity and negligible deviation from regression. These genotypes were identified as stable and widely adapted across environments, supporting their potential use in mustard improvement programmes.

Keywords : Genotype × environment interaction, Indian mustard, Joint regression analysis, Phenotypic stability, Seed yield and Wide adaptability.

Introduction

Rapeseed–mustard is one of the most important oilseed crops in India and play a vital role in the country’s edible oil economy. Indian mustard (*Brassica juncea* (L.) Czern & Coss.) is an amphidiploid species belonging to the family *Brassicaceae*, which also includes other economically important rapeseed–mustard crops such as *B. napus*, *B. carinata* and *B. rapa* var. *toria*. India ranks as the third largest producer of rapeseed–mustard globally, after Canada and China, contributing approximately 14% of the world’s total production (ICAR-IIRMR, 2023-24).

Although rapeseed–mustard is grown across most states of India, a major share of production is concentrated in Rajasthan (45.40%), followed by Uttar Pradesh (14.24%), Madhya Pradesh (13.28%), Haryana (10.78%) and West Bengal (6.0%) (ICAR-IIRMR, 2023–24). This uneven productivity is largely attributed to cultivation under marginal environments with suboptimal agronomic practices, including limited irrigation facilities and inadequate pest and disease management. A major constraint is delayed sowing, often caused by the late harvesting of preceding rice crops, which exposes mustard to terminal heat stress during the flowering and pod-filling stages. Despite these challenges, mustard is considered a hardy crop with inherent tolerance to abiotic stresses, making it suitable for cultivation under rainfed and resource-limited conditions (Yadav *et al*., 2010).

Rapeseed–mustard, owing to its wide adaptability across diverse agroclimatic conditions and inherent tolerance to abiotic stresses, occupies a premier position as one of the major oilseed crops in India. Despite this adaptability, the performance of existing mustard varieties in Rajasthan remains highly sensitive to environmental variations, resulting in considerable fluctuations in yield. Such variability is largely attributed to genotype × environment (G × E) interactions, which pose a major challenge to achieving stable and consistent performance of genotypes across diverse growing conditions. Identification of germplasm with broad adaptability and yield stability is therefore essential for the development of improved cultivars. In this context, the present investigation was undertaken to assess G × E interactions for seed yield, yield-contributing traits, to identify promising and stable genotypes using appropriate stability parameters.

Genotype × environment interaction was assessed using the linear regression model proposed by Eberhart and Russell (1966), which is widely employed for stability analysis. In this model, the regression coefficient (b_i) provides an estimate of genotype adaptability, while the deviation from regression (S^2d_i) serves as an indicator of stability. Genotypes exhibiting high mean performance, regression coefficients close to unity, and minimal deviation from regression are considered widely adapted and stable. Exploitation of G × E interaction thus facilitates enhanced genetic gain by enabling targeted selection of genotypes suited to specific or broad environments. Therefore, it is essential to identify genotypes, including released varieties and promising hybrids, that can maintain stable performance across environments created by variations in sowing dates.

Materials and Methods

The present investigation comprised ten parental genotypes, 45 F_1 crosses and two standard checks *viz.,* NRCHB-101 and PM-33. The experimental material was evaluated across three locations E_1- MPUAT, Udaipur, E_2- KVK, Chittorgarh, E_3-KVK, Badgaon and under three sowing dates, *viz.*, timely, late, and very late, during the *rabi* seasons of 2021–22 and 2022–23. These combinations resulted in six distinct environments. A row to row spacing of 30 cm was maintained between rows of the same genotype, while a spacing of 60 cm was kept between rows of different genotypes; plant-to-plant spacing was maintained at 10 cm. All recommended agronomic practices were followed to ensure optimal crop growth.

Observations were recorded on five randomly selected plants per genotype, and mean values were used for statistical analysis. Data were collected for eighteen yield and yield-related traits, *viz.*, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, total branches per plant, length of main raceme, number of siliquae on the main raceme, number of siliquae per plant, number of seeds per siliqua, siliqua length (cm), 1000-seed weight (g), harvest index (%), biological yield per plant (g), seed yield per plant (g), oil content (%), protein content (%) and glucosinolate content (μmol g^{-1}).

Stability analysis was performed using the model proposed by Eberhart and Russell (1966). According to this model, a genotype is considered stable when it exhibits high mean performance, a regression coefficient (b_i) close to unity and a non-significant deviation from regression (S^2d_i).

Result and Discussion

The analysis of variance for joint regression involving yield and its component traits is presented in Table 1. The mean sum of squares due to environments was significant for all traits, except glucosinolate content, indicating differential environmental influence. In contrast, the mean sum of squares attributable to genotypes (varieties) was significant for all the characters studied except oil content, reflecting the presence of substantial genetic variability among the genotypes. In support of the above finding of significant environment + (genotypes x environment), environment (liner) and genotypes x environment (liner) by Chaudhary *et al.* (2004) and Brar *et al.* (2007).

Table 1 : Analysis of variance for stability performance of quantitative traits in Indian Mustard

Source of Variation	Variety	Environment	Var. X En.	En + Var X En	En (Linear)	En X Var (Lin)	Pooled Deviation	Pooled Error
df	**56**	**2**	**112**	**114**	**1**	**56**	**57**	**336**
Days to 50% flowering	14.29*	185.98**	7.58**	10.71**	371.96*	4.56	10.43**	1.14
Days to maturity	10.21*	829.17**	5.42**	19.88	1658.35**	5.15	5.61**	1.94

Plant height	212.20**	8381.17**	48.15	194.34	16762.35**	23.11	71.90*	117.93
Primary branches per plant	0.57*	12.75**	0.34	0.56	25.51**	0.34	0.33**	0.14
Secondary branches per plant	11.08**	381.90**	0.97	7.66	763.80**	0.78	1.15**	0.67
Total branches per plant	14.86**	478.84**	1.61*	9.99**	957.68**	0.92	2.28**	0.85
Main raceme length	124.86**	2356.18**	11.32	52.46	4712.36**	16.61**	5.93	22.19
Siliqua main raceme	35.39**	125.78**	2.21	4.38	251.56**	1.10	3.26	7.46
Siliqua per plant	6995.81**	44681.37**	431.40	1,207.71	89362.74**	332.33	521.16**	357.41
Siliqua length	0.63**	1.31**	0.04	0.07	2.61**	0.04	0.05	0.12
Seeds per siliqua	2.26**	58.05**	0.90	1.90	116.11**	1.04	0.75**	0.83
Seed yield per plant	13.28**	37.80**	1.64*	2.28**	75.61**	1.71	1.56**	0.97
Biological Yield per plant	149.11**	1042.48**	32.21	49.93	2084.96**	36.35	27.58**	23.69
Harvest index	26.92**	351.35**	9.13*	15.14*	702.70**	9.42	8.68**	4.57
Test weight	0.43**	0.85*	0.14*	0.16*	1.71*	0.10	0.20**	0.07
Oil content	6.74	206.33**	4.32*	7.87*	412.66**	6.57**	2.04**	2.52
Protein Content	8.18**	12.37*	2.14*	2.32*	24.74**	2.51	1.74**	1.07
Glucosin (umole/g)	168.05**	2.345	2.78**	2.77**	4.69	2.26	3.24**	0.89

*P = 0.05, **P = 0.01

Significant G×E interaction effects were observed for days to maturity. The parents Pusa Bold and PM-25, along with the crosses CS-60 × PM-31, PM-32 × JD-60, Kranti × CS-60 and Kranti × JD-60, exhibited mean values lower than the overall mean, coupled with a regression coefficient close to unity (bi ≈ 1) and negligible deviation from regression (S^2di ≈ 0), indicating high stability across environments. For plant height, the parent PM-31 and the cross PM-25 × GDM-4 also recorded mean values lower than the general mean with bi ≈ 1 and S^2di ≈ 0, suggesting wide adaptability and phenotypic stability. Similar findings regarding stability under diverse environments have been reported by Kumari *et al.* (2019).

The primary branches per plant, the parents CS-58, PM-25, CS-60, GM-1, PM-31 and the hybrids Kranti × CS-58, PM-25 × GDM-4, Kranti × GM-1, PM-32 × JD-60, Kranti × CS-60 and Kranti × PM-25 exhibited high mean performance, regression coefficients close to unity (bi ≈ 1) and negligible deviations from regression (S^2di ≈ 0), indicating wide adaptability and stability across environments. For secondary branches per plant, the parents GM-1, PM-25 and Pusa Bold, along with the hybrids Kranti × Pusa Bold, Kranti × CS-58, PM-31 × Pusa Bold, Kranti × JD-60, PM-25 × CS-58, CS-60 × GM-1 and PM-32 × GM-1, showed superior mean values with bi ≈ 1 and S^2di ≈ 0, suggesting phenotypic stability over environments. Similarly, for total branches per plant, the parents GM-1, PM-25, Pusa Bold and the hybrids PM-25 × GM-1, Kranti × JD-60, PM-25 × CS-58, Kranti × CS-60, PM-31 × GM-1, and Kranti × CS-58 recorded high mean performance with regression coefficients close to unity and minimal deviation from regression and were therefore identified as stable and desirable genotypes. Comparable stability responses across environments have also been reported by Rezaizad (2018).

The seed yield per plant, the parental lines PM-32, PM-33, CS-58, Pusa Bold and PM-31, along with the hybrids PM-31 × CS-58, PM-32 × GM-1, CS-60 × PM-31, PM-32 × GDM-4, PM-25 × GDM-4, PM-31 × GDM-4 and PM-32 × PM-31, exhibited high mean performance with regression coefficients close to unity (bi ≈ 1) and negligible deviation from regression (S^2di ≈ 0), indicating wide adaptability across environments. Similarly, for biological yield per plant, the parent GM-1 and the hybrids PM-25 × GDM-4, PM-25 × GM-1, Kranti × CS-58 and PM-31 × GDM-4 showed stable performance with desirable stability parameters. For harvest index, the parents PM-25 and NRCHB-101, together with the hybrids PM-31 × CS-58, GM-1 × CS-58, JD-60 × CS-58 and JD-60 × PM-31, recorded high mean values with bi ≈ 1 and S^2di ≈ 0. Likewise, for test weight, the parents PM-33, PM-32, GDM-4, GM-1, and the hybrids PM-32 × GM-1, JD-60 × CS-58, CS-60 × Pusa Bold, PM-32 × Pusa Bold, CS-60 × GM-1, PM-31 × GM-1, GM-1 × Pusa Bold, CS-60 × GDM-4, JD-60 × GDM-4 and PM-32 × CS-58 exhibited superior mean performance with regression coefficients close to unity and minimal deviation from regression, therefore identified as stable and desirable across environments. Most stable crosses for seed yield per plant in different environments *viz.*, PM-31 × CS-58, PM-32 × GM-1, CS-60 × PM-31, PM- 32 × GDM-4, PM-25 × GDM-4, PM-31 × GDM-4 and PM-32 × PM-31 Table 3. These findings corroborate earlier reports on phenotypic stability under diverse environments (Sagolsem *et al.,* 2013, Tadesse *et al.,* 2018, Dube *et al.,* 2021, Shekhawat *et al.,* 2020, Srivastava and Srivastava, 2020).

Table 2 : Character wise summary of stable genotypes for nine characters

S.N.	Name of traits	Name of genotypes
1	Days to maturity	Pusa Bold, PM-25, CS-60 × PM-31, PM-32 × JD-60, Kranti × CS-60 and Kranti × JD-60
2	Plant height	PM-31, PM-25 × GDM-4
3	Primary branches per plant	CS-58, PM-25, CS-60, GM-1, PM-31, Kranti × CS-58, PM-25 × GDM-4, Kranti × GM-1, PM-32 × JD-60, Kranti × CS-60 and Kranti × PM-25
4	Secondary branches per plant	GM-1, PM-25,Pusa Bold, Kranti × Pusa Bold, Kranti × CS-58, PM-31 × Pusa Bold, Kranti × JD-60, PM-25 × CS-58, CS-60 × GM-1 and PM-32 × GM-1
5	Total branches per plant	GM-1, PM-25, Pusa Bold, PM-25 × GM-1, Kranti × JD-60, PM-25 × CS-58, Kranti × CS-60, PM-31 × GM-1 and Kranti × CS-58
6	Seed yield per plant	PM-32, PM-33, CS-58, Pusa Bold, PM-31, PM-31 × CS-58, PM- 32 × GM-1, CS-60 × PM-31, PM-32 × GDM-4, PM-25 × GDM-4, PM-31 × GDM-4 and PM-32 × PM-31
7	Biological yield per plant	GM-1, PM-25 × GDM-4, PM-25 × GM-1, Kranti × CS-58 and PM-31 × GDM-4
8	Harvest index	PM-25, NRCHB-101, PM-31 × CS-58, GM-1 × CS-58, JD-60 × CS-58 and JD-60 × PM-31
9	Test weight	PM-33, PM-32, GDM-4, GM-1, PM-32 × GM-1, JD-60 × CS-58, CS-60 × Pusa Bold, PM-32 × Pusa Bold, CS-60 × GM-1, PM-31 × GM-1, GM-1 × Pusa Bold, CS-60 × GDM-4, JD-60 × GDM-4 and PM-32 × CS-58

Table 3 : List of crosses found stable for seed yield and yield contributing traits

Traits	b_i <1	b_i = 1
Primary branches per plant	Kranti X PM-25, Kranti X PM-31, Kranti X GM-1, Kranti X Pusa Bold, PM-25 X GM-1, PM-25 X CS-58, CS-60 X PM-31 and JD-60 X PM-31	Kranti × CS-58, PM-25 × GDM-4, Kranti × GM-1, PM-32 × JD-60, Kranti × CS-60, Kranti × PM-25, Kranti × Pusa Bold, PM-31 × Pusa Bold, PM-25 × CS-58, CS-60 × GM-1 and PM-32 × GM-1
Secondary branches per plant	PM-32 X GM-1, Kranti X CS-60, Kranti X JD-60, CS-60 X PM-31 and GDM-4 X Pusa Bold	Kranti × CS-58, PM-25 × GDM-4, Kranti × GM-1, PM-32 × JD-60, Kranti × CS-60, Kranti × PM-25, Kranti × Pusa Bold, PM-31 × Pusa Bold, PM-25 × CS-58, CS-60 × GM-1 and PM-32 × GM-1
Siliqua per plant	PM-32 X JD-60, PM-32 X CS-58 and PM-31 X Pusa Bold	JD-60 × CS-58
Seeds per siliqua	Kranti X CS-60, PM-32 X GM-1, PM-32 X PM-31 and GM-1 X Pusa Bold,	Kranti × JD-60, PM-31 × Pusa Bold, CS-60 × JD-60, CS-60 × GDM-4, Kranti × CS-60 and GM-1 × GDM-4
Seed yield per plant	–	PM-31 × CS-58, PM-32 × GM-1, CS-60 × PM-31, PM- 32 × GDM-4, PM-25 × GDM-4, PM-31 × GDM-4 and PM-32 × PM-31

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