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INVESTIGATING THE EFFECTS OF GENOTYPE AND ENVIRONMENT INTERACTION (GEI) AND STABILITY ANALYSIS ON SHORT-DURATION RAPESEED YIELD AND OIL CONTENT UNDER DIFFERENT ENVIRONMENTAL CONDITIONS

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Abstract

The yield and oil content of rapeseed (*Brassica rapa*), one of the most important sources of edible oil in the world, have been significantly impacted by environmental factors. The primary objective of this research is to identify the most optimal genotype(s) with a high yield and oil content that can adapt to various environments in Bangladesh. The GE interaction was estimated using the analysis of variance (ANOVA) and the AMMI model. An environment-wise ANOVA demonstrated significant variations in all traits across all environments. Heritability, genetic advance as a percentage of mean, GCV, and PCV were estimated. High GCV and PCV for seed yield and total dry matter were observed in all environments. Heritability and genetic advance as a percentage of the mean were found to be high for yield plant^{-1} across all environments. The AMMI analysis utilized the IPCA1 (First Interaction Principal Component Axis) scores of genotypes to predict environmental stability or adaptation. Higher IPCA1 scores indicated that a genotype was more suited to a given environment. Based on IPCA1 scores, BARI Sharisha-14 was a high-yielding, stable genotype. Under favourable conditions, BARI Sharisha-9 (G2), BARI Sharisha-15 (G4), and Sompod (G5) produced a higher yield. All genotypes in the Mymensing environment had high oil content (%). Sompod had the lowest mean seed yield across environments and was extremely environment sensitive. It was discovered that Ishwardi was better for rapeseed production than Cumilla.

Key words: Yield stability, Genotype, Different environments; Genotype environment interaction; AMMI model.

Introduction

Rapeseed (*Brassica rapa* L.) is the most significant oil crop in Bangladesh, having a significant impact on the economy (Joya *et al*., 2017; Chauhan *et al.,* 2022). It has the top position among oilseed crops in Bangladesh and is the second most significant oilseed crop globally, behind soybean. (Helal *et al*., 2022). In Bangladesh, the average amount of edible oils each person will need in 2023 is estimated to be 1.53 kg. In 2023, the edible oils market will be worth $1.39 billion, and the market is expected to grow by 11.47% per year (CAGR 2023-2027).

However, rapeseed cultivation is severely neglected in Bangladesh due to its low seed yield in comparison to other growing nations around the world. Conventional rapeseed production is also very low due to the use of genotypes with low yield potential, the lack of availability of seeds of high yielding genotypes, the competition of rapeseed with more lucrative alternative crops, and the length of time required to fit the rice-rice cropping pattern. T. Aman-Fallow-Boro rice occupies over 45% of the land area in Bangladesh, while T. Aman-Rapeseed-Boro occupies less than 6% (Nasim *et al*., 2021). Between T. Aman and Boro rice, this fallow time must be used to grow short-duration, high-yielding genotypes of rapeseed (Rafat-Al-Foysal & Biswas, 2017). Because it will primarily aid in increasing cropping intensity by expanding rapeseed production and area, thereby accelerating Bangladesh's efforts to reduce its edible oil shortage (Rafat-Al-Foysal & Biswas, 2017).

The main factors contributing to genotype x environmental interaction (GEI) in crop yield uncertainty and the low average rapeseed yield in various regions in Bangladesh are pests and diseases (biotic) and non-living factors such as soil, water, rainfall, sunshine, moisture, and

temperature (abiotic) (Teshome *et al*., 2020). It is evident that various genotypes differ in their growth response to various environments and in their relative ranking, and that no single genotype exhibits the same phenotypic performance in all conditions (Islam *et al*., 2020). Genotype and environment interaction (GEI) simulates the different responses of the genotypes to distinct environmental conditions, i.e., the best genotype for one set of conditions is not necessarily the best genotype for another (Islam *et al*., 2020). Crop phenotypes are always affected by environmental conditions (Gregorius & Namkoong, 1986) because this can lead to variation in genotypic responses among testing environments, leading to differences in GEI (Bakare *et al*., 2022). The lack of consistent response of genotypes to changing environmental conditions is attributed to genotype-environment interaction (GEI) (Pham & Kang, 1988). As the knowledge of GEI increases the efficacy of a breeding programme and the selection of the best genotypes (Fikere *et al*., 2008; Yan *et al*., 2001), it is beneficial to possess a genotype that is capable of producing a high yield in a consistent manner over broad environmental conditions.

Stability is an important genetic trait to examine when breeding new variety, as it determines the level of yield performance that can be achieved by that genotype in a specific set of environmental conditions (Islam *et al*., 2021; Bazzaz *et al*., 2020). According to Piepho (1998), the inherent genetic capacity for producing a crop and its ability to maintain stability throughout diverse environmental conditions are both key factors in the adaptation of a genotype and the spread of the genotype among the growers. Important in selecting stable genotypes is relying on crop performance evaluation to select better plant types, whether they come from local or exotic sources (Fikere *et al*., 2008; Yan *et al*., 2001; Islam *et al.*, 2019). Stability parameters can be employed in the assessment of varieties to mitigate risk, enhance profitability for the growers, allow for differences in yield across locations, and allow the transfer of technologies to various environments without the need for vast experimentation at each locations (Piepho, 1998). Stable genotypes are identified using a variety of techniques on a global scale (Piepho, 1998; Becker & Leon, 1988; Lin *et al*., 1986; Westcott, 1986). The joint regression (Eberhart & Russell, 1966) and Additive Main Effect and Multiplicative Interaction (AMMI) (Gauch, 1992) models have been effectively employed in a various crops to analyze the stability parameters. Reducing the negative impact of GEI and increasing rapeseed productivity can be accomplished through the clustering of testing environments, identifying the degree of genotype-environment interaction and recommending stable or adaptive genotypes for each environment (Crossa, 1990). This strategy will aid in the development of a short-duration rapeseed genotype, which is essential in order to confront the impending food, health, and oil content issues in Bangladesh. Consequently, the present study was carried out with the following objectives: (1) To determine a rapeseed genotype characterized by a brief growth period, high oil content and an excellent yield potential; and (2) to identify genotypes that exhibit exemplary adaptability to the different environmental conditions prevalent in Bangladesh.

Material and Methods

The experiment was carried out at five different locations, namely Mymensingh (E1), Jamalpur (E2), Ishwardi (E3), Rangpur (E4), and Cumilla (E5), from November 2022 to February 2023, with five various rapeseed genotypes, to estimate yield stability at five different locations in a single year. Five rapeseed genotypes were collected as experimental materials from the Regional Agricultural Research Station (RARS) in Jamalpur, Bangladesh, which is part of the Bangladesh Agricultural Research Institute (BARI). During the final step of land preparation, urea, cow dung, triple super phosphate (TSP), muriate of potash (MoP), gypsum, zinc oxide, and boron were utilized as fertilizers. The experimental field was fertilized with 10 tonnes of cow dung, 250 kg of urea, 170 kg of TSP, 85 kg of MoP, 150 kg of gypsum and 10 kg of boric acid per hectare, following the recommendations of the Bangladesh fertilizer recommendation guide 2018. After a period of 25 days, the remaining urea was administered as a top dressing. The experiment employed a randomized complete block design (RCBD) with three replications. Each plot had an area of 10 square metres, measuring 4 metres in length and 2.5 metres in width, with a 1 metre gap between each replication. The distance between lines in a row was 30 cm. The seeds were sown in rows with a spacing of 10 cm on November 14, 2022. To make sure there were no clods on the seeds, the soil was carefully spread over the seeds after they had been sown. After sowing, the seeds were carefully covered with soil to ensure that no clods were on the seeds. Weeding, thinning, irrigation, pest management, and other intercultural operations were carried out uniformly in all plots. Following sowing, the soil was irrigated with a cane to maintain optimal moisture levels and consistent seed germination. A good drainage system was maintained throughout the growth season to enable for the prompt release of precipitation from the experimental plot. The first and second weedings were done respectively, 15 and 35 days after sowing. To maintain a spacing of 10 cm between seedlings in rows that were 30 cm apart, concurrent thinning was conducted. The insecticide Malataf 57 EC was applied @ 2 ml/liter of water to inhibit aphids during the siliqua development stage.

Data collection: Depending on its maturity, the crop was harvested at different times and in various locations. Harvesting commenced when 80% of the crop exhibited indications of maturation, including straw-colored siliqua, mature leaves, stem, and appropriate seed pigmentation in mature siliqua. A total of ten plants were randomly selected from each plot in each environment for harvesting. In order to examine various genetic parameters, associations, and genetic diversity 12 yield-contributing traits were taken into account. The traits measured were days to 50% flowering (DF), days to maturity (DM), plant height (PH), number of branches per plant (BNPP), number of siliquae per plant (SPP), length of siliqua (SL), number of seeds per siliqua (SPS), yield per plant (YPP), straw yield (SY), oil content (%), total dry matter (TDM), and crop growth rate (CGR).

Oil content (%): The percentage of seed oil was determined using ISO procedures (ISO, 2009). The collected data was utilized to compute the oil content, which was defined as the proportion of oil extracted by every process calculated as a percentage (%), this refers to the proportion of extractable oil in relation to the total amount available.

Total dry matter (TDM): To ascertain the dry weight of five plants at 20, 40, and 60 DAS, a random selection of five plants was made from each plot in the experimental area. After extracting the roots of each plant, they were subsequently cleansed with tap water. After dividing the plant stems, the plant samples were sealed in brown paper bags with labels and dried at 45°C for 72 hours in order to achieve a constant weight. Samples of oven-dried stem and leaf were weighed in order to ascertain the dry weight of the plant.

Crop growth rate: The growth rate of the crop was determined using the following formula:

$$\text{CGR} = \frac{W2-W1}{T2-T1} \times \frac{1}{GA}\ gm^{-2}d^{-1}$$

W_1 denotes dry weight at first harvest (gm^{-2}); W_2 denotes dry weight at second harvest (gm^{-2}); GA denotes ground area; and T_1 and T_2 denote time intervals.

Statistical analysis

Analysis of variance: Initially, the data was subjected to a pooled analysis of variance. The ANOVA structure is illustrated in (Table 1).

The following formula was used to calculate different types of variances:

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{MS1}-\text{MS2}}{\text{r}}$$

$$\text{Phenotypic variance } (\sigma_P^2) = \sigma_g^2 + \sigma_e^2$$

Table 1. ANOVA for genotypes grown in various environments.

Source	df	MSS	Expected MSS
Env (Sowing dates)	s-1		
Rep / Env	s (r-1)		
Gen	v – 1	MS_1	$\sigma_e^2 + r\sigma_{e+}^2 rs\sigma_g^2$
Gen x Env	(v-1) (s-1)	MS_2	$\sigma_e^2 + r\sigma_{ge}^2$
Error	s(r-1) (v-1)	MS_3	σ_e^2
Total	**svr-1**		

Whereas r is the number of replications, s denotes the number of sowing dates (environment), v denotes the number of genotypes, σ_g^2 denotes the genotypic variance and σ_P^2 denotes the phenotypic variance. Based on the criteria defined by Sivasubramanium and Madhavamenon (1973), the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were classified as low, moderate, and high.

Heritability in broad sense [h^2 (bs)]: Heritability was estimated by dividing the amount of genetic variance by the total variance or phenotypic variance. After having been calculated by Johnson *et al*., (1955) and Hanson *et al*., (1956), it was converted into a percentage by multiplying the number by 100, as proposed by Lush (1940). It is stated as follows:

$$h^2 \text{ (bs) } \% = \frac{\sigma_g^2}{\sigma_P^2} \times 100$$

Here, the genotypic and phenotypic variance of a character are denoted by the symbols σ_g^2 and σ_P^2 respectively.

Estimation of genetic advance (GA): The genetic advance for each trait was calculated using the formula described by Lush (1940) and Johnson *et al*., (1955), and the results were expressed as a percentage of the mean value.

$$\text{Genetic advance} = k \times \sigma_P \times h^2 \quad \text{and}$$

$$\text{GA (\% of mean)} = \frac{\text{Genetic advance}}{\bar{X}} \times 100$$

The parameter h^2 indicates heritability in a broad sense, while σ_P denotes the phenotypic standard deviation. The standardized selection differential is represented by k, which has a value of 2.06. $\bar{X}$ represents the overall mean of the character being considered. According to (Johnson *et al*., 1955), genetic advance was classified as low (10%), moderate (10-20%), or high (>20%).

Stability analysis

The stability analysis was carried out in accordance with Eberhart and Russell (1966). The basic model employed is as follows:

$$Y_{ij} = \mu_i + \beta_i I_j + \sigma_{ij}$$

Where, Y_{ij} = Mean of the i^{th} genotype at j^{th} environment,
μ_i = Mean of the i^{th} genotype across environments
β_i = Regression coefficient of i^{th} genotype to various environmental indices
I_j = Environmental index, which is the mean of all genotype in the j^{th} environment minus the grand mean
σ_{ij} = Deviation from regression of i^{th} genotype in j^{th} environment

Joint regression analysis: Joint regression analysis is included in (Table 2) along with the formula for calculating the sum of squares for each source. An analysis was conducted using pooled error to determine the significance of the variation generated by genotypes, environments, genotypes × environments interaction, environment +

(genotypes x environments) interaction, environment (linear), and genotypes x environment (linear). The following formula was used to calculate the pooled deviation: The following formula was used to calculate the pooled deviation:

$$MS = \frac{\text{Pooled error}}{r}$$

where r is the number of replications.

Stability parameters: Regression coefficient (bi) and deviation from regression (S^2d), which were first proposed by Eberhart and Russell in 1966, are used to evaluate the stability of a genotype.

$$\text{Regression coefficient (bi)} = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

Y_{ij} and I_i indicate, as previously explained, the performance of the i^{th} genotype in the j^{th} environment and index, respectively. The mean square deviation obtained using linear regression. S^2d denotes pooled errors as estimated in Table 2.

$$S^2d = \frac{E_j \sigma ij^2}{s-2} - \frac{Se^2}{r}$$

Where,

$$\sum_j \sigma^2 ij = (\sum j Y_{ij}^2 - \frac{Yi^2}{S}) - \frac{\sum_j Y_{ij} Ij^2}{\sum j Ij^2}$$

$(\sum j Y_{ij}^2 - \frac{Yi^2}{S})$ = is variance due to dependent variable and

$\frac{\sum_j Y_{ij} Ij^2}{\sum j Ij^2}$ =is variance due to regression

Regression coefficient (bi) equal to one (bi=1.0) and a deviation (S^2d) not substantially different from zero (S^2d=0) are characteristics of a stable genotype, according to Eberhart and Russell (1966). Based on these stability parameters as well as the average characteristic value, a genotype's adaptability is assessed. The following formula is used to calculate the regression coefficient (bi):

Standard error of regression coefficient, $(bi) = (\frac{\text{MS due to pooled deviation due to } i^{th} \text{ genotype}}{\sum j I_j^2})^{1/2}$

Table 2. Joint regression analysis of variance (Eberhart & Russell, 1966).

Source	df	SS	MSS
Gen (v)	(v-1)	$1/s \sum_i, y^2 i - C.F.$	MS_1
Env (s)	(s-1)	$1/v \sum_i, y^2 j - C.F.$	
Gen X Env	(v-1)(s-1)	$\sum_i \sum_j Y_i j^2 - \frac{\sum Y_i^2}{s} - \frac{\sum y^2 j^2}{v} + CF$	
Env+ (Gen + Env)	v (s-1)	$\sum_i \sum_j Y_i j^2$-$(\sum_i Y_i^2/s)$	
Env (Linear)	1	$1/v \sum_i (Y_j I_j)^2 / \sum_j I_j^2$	
Gen × Env (Linear)	v-1	$\sum_i / (\sum_i Yi_j)^2 / \sum; I_j^2$ Env. (linear)ss.	MS_2
Pooled deviation	s(s-2)	$\sum_i \sum_j \sigma_{ij}^2$	MS_3
Pooled deviation (Due to genotype)	v (s-2)	$[\sum_j Y_j^2$ -$(Y_i)^2/s]$-$(\sum_j Y_{ij} ij)^2 / \sum_j 1_j^2 = \sum_j \sigma_{ij}^2$	
Pooled Error	s (r -1) (v-1)		MS_4

Results and Discussion

Estimation of analysis variance: Analysis of variance was performed on pooled data (Table 3) and revealed highly significant differences between genotypes for all traits. The most desirable traits were as follows: plant height (683.88 cm), number of siliquae per plant^{-1} (62.29), days to maturity (126.78 days), and oil content (32.58%). The days to 50% flowering (130.35), oil content (5754.53), and crop growth rate (306.97) were found to be highly significant in different environments. For days to maturity (16.06), plant height (14.61), number of siliquae plant^{-1} (17.21), straw yield (17.30), oil content (13.50), total dry matter (14.28), and crop growth rate (13.53) the mean square resulting from the genotype x environment was also highly significant. Comparable results were documented in rapeseed by Mahla *et al*., (2003), Upadhyay & Kumar (2008), Kumar *et al*., (2011), and Singh *et al*., (2010). A pooled analysis of variance was conducted to evaluate the measure of genetic variation in the genetic material being studied, revealing significant differences between the environmental conditions (resulting from sowing in different locations) for all of the traits. With the exception of the days of emergence and plant height, there were no significant relationships observed among the three environments. The genotype x environment interaction has a highly significant effect on all of the parameters, except for days to 50% flowering. The significance of the variance attributed to genotype x environment interaction indicated that genotypes exhibit distinct performance across different environments for various traits. Therefore, it was essential to determine the source or cause of the variability in genotype performance across different environments. Khan *et al*., (2008), Badiger *et al*., (2009), Dar *et al*., (2011), Patel & Arha (2012), Kumar *et al*., (2012), and Waraich *et al.,* (2020) revealed significant interactions between genotypes (G) x environments (E).

Estimation mean performance of yield plant^{-1} over various environments: The average yield performance of five genotypes of *Brassica rapa* across all environments is shown in Table 4. Jamalpur (E2) had the greatest yield performance for Tori-7 (1.00 tha^{-1}) while Cumilla (E5) had the lowest yield performance (0.93 tha^{-1}). The highest yield performance of genotype BARI Sarisha-9 was observed in Rangpur (E4) with (1.23 tha^{-1}) and the lowest in Mymensing (E1) with ((0.95 tha^{-1}). The highest yield performance of genotype BARI Sarisha-14 was observed in Jamalpur (E2) with (1.43 tha^{-1}) and the lowest in Mymensing (E1) with (1.06 tha^{-1}). The yield performance of BARI Sarisha-15 and Sompod was maximum in Rangpur (E4) with (1.34 tha^{-1} and 1.02 tha^{-1}) and lowest in Mymensing (E1) with (1.23 tha-1 and 0.87 tha^{-1}). (BARI sharisha-14) genotypes provided the highest seed yield compared to the mean value of 1.33 tha^{-1}, while (Sompod) genotypes performed lowest with a mean value of 0.95 tha^{-1} (Table 4).

Estimation of range, mean yield, and yield contributing traits in different environments: The five environments were compared to the range of several yield-contributing characteristics, and it was found that Mymensing (E1) had the widest ranges for days to 50% flowering (39–42 days), plant height (68–96.33 cm), number of seeds siliqua-1 (15.60–27.00), and oil content (37.10–44.20%). Jamalpur (E2) had the greatest variation for number of siliquae plant^{-1} (68.00-99.00 number) and seed yield plant^{-1} (0.91-1.50 tha-1). Ishwardi (E3) had the greatest variation in terms of number of siliquae plant^{-1} (68.00-99.00 no.) and embryo siliqua^{-1} (14.40-22.10 no.). Rangpur (E4) had the greatest variation in days to maturation (80.00 to 91.00) and siliqua length (3.50 to 6.52 cm). Rangpur (E4) had the highest mean performance of days to maturity (86.80 days), while Cumilla (E5) had the lowest (84.40 days). Mymensingh (E1) had the greatest mean plant height (80.51 cm), while Jamalpur (E2) had the lowest (79.46 cm). Cumilla (E5) had the longest average siliqua length (5.46 cm), while Mymensingh (E1) had the shortest (4.01 cm). The average number of siliqua plant^{-1} was highest in Jamalpur (E2) and Ishwardi (E3) with 85.46, and lowest in Mymensingh (E1) with 83. Mymensingh (E1) had the highest average number of seed siliqua^{-1}, with 19.95, followed by Jamalpur (E2), with 15.74. The E4 region had the highest average seed plant^{-1}, measuring 1.19 tha^{-1}, while the Mymensingh region (E1) had the lowest, measuring 1.01 tha^{-1}. Mymensingh (E1) had the highest average oil content at 39.71%, followed by Ishwardi (E3), Rangpur (E4), and Cumilla (E5). Kumari *et al*., (2018) and Rout *et al*., (2019) revealed the mean and standard deviation of the performance of various rapeseed genotypes.

Table 3. Pooled analysis of variance for various phenological traits in rapeseed genotypes.

Sources	df	Mean sum of squares					
		DF	DM	PH	BNPP	SL	SPP
Environment	4	130.35*	11.58**	2.49^{ns}	3.12**	5.61**	14.16**
Rep /Env	10	60.89**	0.03^{ns}	14.81^{ns}	0.25^{ns}	0.14**	15.08**
Gen	4	29.65^{ns}	126.78**	683.88**	5.64**	5.14*	1059.03**
Env x Gen	16	3.30^{ns}	16.06**	14.61^{ns}	`13.64**	0.25**	17.21**
Pooled error	40	5.79	0.03	34.19	0.52	0.04	11.57
Sources	**df**	**Mean sum of squares**					
		SPS	**YPP**	**SY**	**OC**	**TDM**	**CGR**
Env	4	39.06**	0.07**	0.73**	5754.53**	1.924**	306.97**
Rep /Env	10	3.34**	0.01^{ns}	0.05*	0.224*	0.22^{ns}	0.032^{ns}
Gen	4	62.29**	0.47**	2.43^{ns}	32.58**	13.28**	0.69**
Env x Gen	16	5.16**	0.01**	17.30**	13.50**	14.28**	13.53**
Pooled error	40	1.131	0.003	0.02	0.112	0.56	0.15

Here, DF = Days 50% flowering, DM = Days to maturity, PH = Plant height (cm), BNPP = Branch number per plant, SL = Length of siliqua (cm), SPP = Siliquae per plant, SPS = Seed per siliqua, YPP = Yield per plant, SY = Straw yield (tha^{-1}), OC= Oil content (%), TDM = Total dry matter, CGR = Crop growth rate. * = Significant at P = 0.05, ** = Significant at P = 0.01

Table 4. Seed yield of five rapeseed genotypes among different environments.

Sl. No.	Genotypes	Yield (t ha^{-1})					
		Mymensing (E_1)	Jamalpur (E_2)	Ishwardi (E_3)	Rangpur (E_4)	Cumilla (E_5)	Mean
1	Tori-7	0.95	1.00	0.95	0.97	0.93	0.96
2	BARI Sarisha-9	0.94	1.08	1.10	1.23	1.08	1.09
3	BARI Sarisha 14	1.06	1.43	1.40	1.41	1.33	1.33
4	BARI Sarisha-15	1.23	1.24	1.30	1.34	1.25	1.27
5	Sompod	0.87	0.93	0.95	1.02	0.96	0.95
	Mean	1.01	1.14	1.15	1.19	1.11	1.12
	LSD (5%)	0.10	0.08	0.11	0.09	0.07	
	CV (%)	5.36	4.20	5.40	4.03	3.62	

Estimation of genotypic and phenotypic coefficient of variation (GCV and PCV): According to the findings of the current study (Table 6), E1 (Mymensingh) exhibited a high genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) for number of seeds siliqua^{-1} (17.71% and 18.96%), total dry matter (31.82% and 31.99%), and crop growth rate (34.19% and 34.19%). Similar results have been reported by Arpna *et al*. (2018) for CGR, Uddin *et al*., (1995) for yield plant^{-1}, Pradhan *et al*. (2021) for seed siliqua^{-1}, siliqua length, and Kumari *et al*. (2018) for oil content. The plant height, number of siliqua plant^{-1}, and yield plant^{-1} exhibit moderate GCV and PCV. The GCV values for plant height are 10.66% and 13.56%, for number of siliqua plant^{-1} are 10.85% and 11.75%, and for yield plant^{-1} are 14.06% and 15.06%. For days to maturity (3.68% and 13.56%), siliqua length (8.04% and 9.44%), oil content (6.77% and 6.83%), and straw yield (8.10% and 8.32%), E1 (Mymensingh) exhibited low GCV and PCV values. For seed yield plant^{-1} (17.43% and 17.94%) and total dry matter (26.79% and 27.10%), E2 (Jamalpur) demonstrated significant GCV and PCV values. GCV and PCV values for siliqua length (10.90% and 11.60%), siliqua plant^{-1} (10.62% and 11.40%), straw yield (14.64% and 15.20%), and number of seeds siliqua^{-1} (10.83% and 14.83%) were moderate. Low GCV and PCV values for days to maturity (4.40% and 11.41%); plant height (6.66% and 11.41%); oil content (6.15% and 6.28%); total dry matter (8.24% and 11.84%); and crop growth rate (7.99% and 11.72%). E3 (Ishwardi) had high GCV and PCV values for total dry matter (24.65% and 24.98%), crop growth rate (19.39% and 24.19%), oil content (15.67% and 16.6%), and plant^{-1} yield (18.09% and 18.88%). Rout *et al*. (2019) discovered similar findings for siliqua length, number of siliquae plant^{-1}, and number of seeds siliqua^{-1}. In earlier studies, Arpna *et al*. (2018) measured plant^{-1} yield, while Kumar *et al*. (2015) measured straw yield for the same traits. Moderate GCV and PCV values were found for siliqua length (13.84% and 14.2%); number of siliquae plant^{-1} (10.62% and 11.40%), number of seeds siliqua^{-1} (10.85% and 12.29%), and straw yield (14.97% and 15.96%). Days to maturity (3.61% and 9.20%), plant height (7.90% and 9.20%), and total dry matter (7.5% and 11.74%) all had low GCV and PCV values. For siliqua length (17.17% and 17.46%) and seed yield plant^{-1} (16.19% and 16.68%), E4 (Rangpur) showed high GCV and PCV values. For the number of seeds siliqua^{-1} (11.31% and 11.63%), straw yield (13.55% and 1.17%), oil content (14.11% and 14.70%), and crop growth rate (13.51% and 15.10%), moderate GCV and PCV values were recorded. Low GCV and PCV values were found for days to maturity (5.11% and 7.66%); plant height (6.86% and 7.66%); number of siliqua plant^{-1} (9.99% and 11.40%); total dry matter (9.82% and 10.40%). E5 (Cumilla) demonstrated significant GCV and PCV values for seed yield plant^{-1} (15.76% and 16.17%). GCV and PCV values are moderate for straw yield (12.63% and 13.16%), siliqua length (11.77% and 12.59%), number of seeds siliqua^{-1} (10.20% and 10.91%), oil content (13.33% and 13.82%), and crop growth rate (12.71% and 14.21%). Days to maturity (3.79% and 10.79%), plant height (5.47% and 10.39%), number of siliqua plant^{-1} (7.36% and 7.66%), and total dry matter (6.68% and 7.89%) were found to have low GCV and PCV values. Similar findings were reported for oil content by Gupta *at al*., (2019), siliqua length by Kumari *et al*., (2018), and days to maturity and plant height by Tripathi *et al*., (2013).

Estimation of heritability: Heritability estimates provide a more precise representation of the genetic impact on the manifestation of a trait's phenotype. Heritability levels ranged from high (> 80 %) to moderate (60 to 80 %), and low (< 60 %). In five environments all of the traits had high heritability values with some exceptions. Mymensing (E_1) showed the highest heritability for siliqua plant^{-1} (85%), seed siliqua^{-1} (89%), yield plant^{-1}(87%), straw yield (94%), oil content (98%), and CGR (100%) and the lowest for days to maturity (61%). Jamalpur (E_2) demonstrated high heritability performance for siliqua length (88%), siliqua plant^{-1} (86%), yield plant^{-1} (94%), straw yield (92%), oil content (95%) and lowest for days to maturity (34%) and plant height (34%). Ishwardi (E_3) exhibited superior results for siliqua length (95%), siliqua plant^{-1} (86%), yield plant^{-1} (91%), straw yield (88%), and oil content (89%) although lowest for total dry matter (40%). Rangpur (E_4) demonstrated high heritability for the number of days to maturity (80%), plant height (80%), siliqua length (96%), siliqua plant^{-1} (82%), seed siliqua^{-1} (94%), yield plant^{-1} (94%), straw yield (91%), oil content (92%), total dry matter (89%) and crop growth rate (80%) and lowest for days to flowering (29.1%). Cumilla (E_5) demonstrated high heritability for siliqua length (87%), number of siliquae plant^{-1} (92%), number of seedd siliqua^{-1} (87%), yield plant^{-1} (95%), straw yield (92%), and oil content (92%) and lowest for plant height (27%). A more heritability estimate denotes the presence of more fixable variability; Uddin *et al*., 1995; Tripathi *et al*., 2013 Vermai *et al*., 2016 reported high heritability estimates for the majority of the traits under study. Singh *et al*., (2003); Chauhan & Singh (2008); Singh *et al*., (2010); Akabari & Niranjana (2015); Lyngdoh *et al*., (2017)*;* Kumar *et al*., (2018) had previously shown moderate heritability estimates for various traits.

Estimation of genetic advance (GA): The results showed that siliqua plant^{-1} had a high GA at Mymensing (E1) (20.66), Jamalpur (E2) (20.4), and Ishwardi (E3) (20.4) (Table 7). Jamalpur (E2) (21.08), Ishwardi (E3) (27.81), Rangpur (E4) (34.8), and Cumilla (E5) (22.67) had the highest GA for Siliqua length. Mymensing (E1) (27.1), Jamalpur (E2) (34.91), Ishwardi (E3) (35.7), Rangpur (E4) (32.38), and Cumilla (E5) (31.65) had the highest GA of yield plant^{-1}. At Mymensing (E1) (34.59) and Rangpur (E4) (22.65), number of seeds siliqua^{-1} exhibited a high GA. Mymensing (E1) (17.28%), Ishwardi (E3) (13.98%), and Rangpur (E4) (12.66%) all had moderate GA of plant height. When at Mymensing (E1), siliqua length GA was 14.13 %. Mymensing (E1) (7.56%), Jamalpur (E2) (9.05%), Ishwardi (E3) (7.44%), Rangpur (E4) (10.53%), and Cumilla (E5) 7.81% had low GA for days to maturity in this study. Plant height of Jamalpur (E2) (8.01%) and Cumilla (E5) (5.94%). Other traits demonstrated moderate GA. These findings were consistent with the findings of Mahla *et al*., 2003, who found high heritability combined with high genetic advance as a percentage of the mean for siliqua length, number of seeds siliqua^{-1}, number of siliqua plant^{-1}, and yield plant^{-1}. Rout *et al*., (2019) found comparable results. Both this study and Gupta *et al*., (2019) found high heritability and moderate GA for oil content. Anand *et al*. (2020) discovered that siliqua plant-1 had a high heritability and a moderate GA. Neelam *et al*., (2014)

discovered a similar relationship between seed siliqua^{-1} and days to maturity. For some characters, Jarman *et al*., (2020) found low genetic advance and low heritability. Mahla *et al*., (2003), Tripathi *et al*., (2019), Ray *et al*., (2019), and Akabari *et al*., (2015) obtained similar results for siliqua plant-1, yield plant-1, and siliqua length. Rout *et al*., (2019) found similar results. Gadi *et al*., (2020) previously observed the same finding. Selection for qualities with high heritability and GA is likely to accrue additional additive genes, leading to further enhancement of their performance. Routet *et al*. (2019) discovered a similar high GA for number of seeds siliqua^{-1}. Furthermore, Kumari *et al*., (2018) discovered a high GA for CGR.

Regression analysis of variance: A joint regression analysis of yield plant^{-1} and its components was performed in accordance with the model proposed by Eberhart and Russell (1966), and the results are shown in (Table 8). The joint regression analysis findings demonstrated that genotype variance was significant for all characteristics. There was no discernible variation found, with the exception of days to 50% flowering. For every trait, there was a non-significant difference between environment + (genotype environment). For all characteristics, there was no statistically significant difference between environment + (genotype environment). Furthermore, for every attribute, non-significant environmental variance (linear) was observed. There was no statistically significant different found between environment + and the genotype environment across all characters. Furthermore, for all traits, non-significant environmental variance (linear) was observed. Significant genotype x environment (linear) variation was observed for days to maturity (38.5), plant height (39.2 cm), branch number plant^{-1}(0.55), siliqua length (0.71 cm), number of siliquae plant^{-1}(33.2), number of seeds siliqua^{-1} (10.9), yield plant^{-1} (0.04), straw yield (0.92), oil content (13.2), total dry matter (0.52), and crop growth rate (0.04). Only non-significant variation was observed for flowering days (1.88). (1.88). In *Oleiferous brassica*, Chaudhary *et al*., (2004); Brar *et al*., (2007); and Kumar *et al*., (1990) have reported evidence for a significant G E (linear) relationship for various characteristics. Sharma & Ray, (1993) reported the days to 50% flowering and days to maturity for *Brassica napus*. Verma *et al*., (1994) reported the days to maturity of *Brassica juncea* but not its seed yield. Singh *et al*., (1995), on the other hand, documented the days to maturity of Toraia in addition to the number of siliquae plant^{-1}.

Table 5. Range, mean, variation, and yield components of rapeseed genotypes by environment.

Sl. No.	Yield contributing traits	Range					Mean				
		Mymensing (E_1)	Jamalpur (E_2)	Ishwardi (E_3)	Rangpur (E_4)	Cumilla (E_5)	E_1	E_2	E_3	E_4	E_5
1.	DF	39-42	36-38	38-42	37-41	37-40	39-42	40-42	40-42	38-42	40-42
2.	DM	80.00-88.00	79.00-89.00	82-89	80.00-91.00	80.00-88.00	85.33	85.13	86.2	86.8	84.6
3.	PH	68-96.33	68-92	71-90	72.00- 88.00	69-90	80.51	79.46	79.6	79.73	79.73
4.	BNPP	04-Jun	05-Jul	04-Jun	04-Jun	05-Jun	04-May	04-Jun	05-Jun	05-Jun	05-Jun
5.	SL	3.30-4.48	3.44-5.02	3.88-6.02	3.88-6.52	4.33-6.50	4	4.28	4.88	5.18	5.46
6.	SPP	69.60-98.00	68.00-99.00	68.00-99.00	72.00-97.00	72.00-90.00	83.22	85.46	85.46	84.73	84
7.	SPS	15.60-27.00	11.7-19.30	14.40-22.10	13.70-18.80	14.70-21.50	19.95	15.74	17.57	16.39	17.74
8.	YPH	0.83-1.27	0.91-1.52	0.89- 1.47	0.95-1.43	0.89-1.30	1.01	1.13	1.13	1.19	1.1
9.	SY	2.99-3.70	3.04-4.86	2.97-4.70	3.23- 4.58	3.03-4.45	3.31	3.72	3.72	3.91	3.63
10.	OC	37.10-44.20	37.50-44.00	37.70-44.01	37.30-43.90	37.70-44.00	40.61	40.71	4.86	5.11	4.74
11.	TDM	7.26-11.69	7.66-11.7	7.66-11.75	8.86-12.35	9.10-11.86	10.1	10.25	10.52	10.97	10.76
12.	CGR	0.07-0.20	7.66-11.7	0.11-0.24	0.12-0.18	0.13-0.18	0.13	10.26	0.15	0.14	0.15

Here, DF = Days to 50% Flowering, DM = Days to maturity, PH = Plant height (cm), BNPP = Branch number per plant, SL = Siliqua length (cm), SPP = Siliqua per plant, SPS = Seed per siliqua, YPP = Yield per plant, SY = Straw yield (t ha^{-1}), OC= Oil content (%), TDM = Total dry matter, CGR = Crop growth rate

Table 6. Environmental coefficient of variation (ECV), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for yield and yield components in different environments.

Sl. No.	Traits	Environmental coefficient of variance (ECV %)					Genotypic coefficient of variation (GCV %)					Phenotypic coefficient of variation (PCV %)				
		E1	E2	E3	E4	E5	E1	E2	E3	E4	E5	E1	E2	E3	E4	E5
1.	DF	2.11	2.68	2.56	3	2.44	1.65	1.64	1.24	1.23	1.44	8.99	7.67	7.45	7.68	6.45
2.	DM	8.38	9.27	4.71	3.4	8.83	3.68	4.4	3.61	5.11	3.79	13.56	11.41	9.2	7.66	10.79
3.	PH	8.38	9.27	4.71	3.4	8.83	10.66	6.66	7.9	6.86	5.47	13.56	11.41	9.2	7.66	10.39
4.	BNPP	2.2	2.33	2.56	2.45	2.34	3.56	3.45	3.22	3.67	3.1	5.69	5.78	5.88	4.56	7
5.	SL	4.93	3.99	3.16	3.17	4.48	8.04	10.9	13.84	17.17	11.8	9.44	11.6	14.2	17.46	12.59
6.	SPP	4.5	4.13	4.13	4.67	2.11	10.85	10.62	10.62	9.99	7.36	11.75	11.4	11.4	11.03	7.66
7.	SPS	5.95	10.12	5.77	2.71	3.87	17.71	10.83	10.85	11.31	10.2	18.69	14.83	12.29	11.63	10.91
8.	YPP	5.35	4.19	5.39	4.03	3.62	14.06	17.43	18.09	16.19	15.76	15.06	17.94	18.88	16.68	16.17
9.	SY	1.9	4.11	5.52	4.14	3.68	8.1	14.64	14.97	13.55	12.63	8.32	15.2	15.96	14.17	13.16
10.	OC	0.95	1.25	5.49	4.11	3.66	6.77	6.15	15.67	14.11	13.33	6.83	6.28	16.6	14.7	13.82
11.	TDM	3.3	4.11	4.02	4.36	5.38	31.82	26.79	24.65	16.57	16.71	31.99	27.1	24.98	17.13	17.56
12.	CGR	5.09	8.58	14.64	7.03	5.38	34.19	7.99	19.39	13.51	12.71	34.19	11.72	24.19	15.1	14.21

Here, DF = Days to 50% Flowering, DM = Days to maturity, PH = Plant height (cm), BNPP = Branch number per plant, SL = Siliqua length (cm), SPP = Siliqua per plant, SPS = Seed siliqua^{-1}, YPP = Yield plant^{-1}, SY = Straw yield (t ha), OC= Oil content (%), TDM = Total dry matter, CGR = Crop growth rate

Table 7. Heritability and genetic advance for yield and yield components of rapeseed in each environment.

Sl. No.	Characters	Heritability (%)					Genetic Advance					Genetic Advance as a % mean				
		E1	E2	E3	E4	E5	E1	E2	E3	E4	E5	E1	E2	E3	E4	E5
1.	DF	34.12	33	28	29.1	27.34	5.45	5.12	4.88	4.78	4.89	11.2	12.1	12	13	13
2.	DM	61	34	73.74	80	27.76	6.45	7.71	6.42	9.14	6.61	7.56	9.05	7.44	10.53	7.81
3.	PH	61	34	73	80	27	13.91	6.36	11.13	10.09	4.74	17.28	8.01	13.98	12.66	5.94
4.	BNPP	56	58	58	68	63	64	5.78	5.89	5.89	5.67	15.6	16.4	19.5	22.4	22
5.	SL	72	88	95	96	87	0.56	0.9	1.35	1.8	1.24	14.13	21.08	27.81	34.8	22.67
6.	SPP	85	86	86	82	92	17.19	17.43	17.43	15.8	12.25	20.66	20.4	20.4	18.65	14.58
7.	SPS	89	53	77	94	87	6.9	2.56	3.46	3.71	3.48	34.59	16.31	19.73	22.65	19.65
8.	YPH	87	94	91	94	95	0.27	0.39	0.4	0.38	0.35	27.1	34.91	35.7	32.38	31.65
9.	SY	94	92	88	91	92	0.53	1.08	1.07	1.04	0.9	16.25	29.04	28.94	26.69	24.99
10.	OC	98	95	89	92	92	5.6	5.05	1.48	1.42	1.25	13.81	12.42	30.46	27.9	26.47
11.	TDM	49	48	40	89	71	1.3	1.21	1.04	2.09	1.25	12.91	11.82	9.88	19.11	11.66
12.	CGR	100	46	64	80	80	0.09	1.15	0.04	0.03	0.03	70.44	11.22	32.06	24.93	23.45

Here, DF = Days to 50% Flowering, DM = Days to maturity, PH = Plant height (cm), BNPP = Branch number per plant, SL = Siliqua length (cm), SPP = Siliqua per plant, SPS = Seed siliqua^{-1}, YPP = Yield plant^{-1}, SY = Straw yield (t ha^{-1}), OC= Oil content (%), TDM = Total dry matter, CGR = Crop growth rate

Table 8. Joint regression analysis (Eberhart and Russell) for yield and yield component traits of rapeseed genotypes.

Source	GEN	ENV + (GEN x ENV)	ENV (linear)	GEN x ENV (linear)	Pooled deviation	Pooled error
DF	1.25^{ns}	2.51	31.7	1.88^{ns}	0.73	2.35
DM	127**	15.2	46.3	38.5**	6.86	0.03
PH	684**	12.2	9.98	39.2**	5.14	34.2
BNPP	5.64**	1.14	12.5	0.55**	0.54	0.52
SL	5.14**	1.32	22.4	0.71**	0.08	0.04
SPP	1059**	16.6	56.6	33.2**	9.49	11.6
SPS	62.3**	11.9	15.6	10.9*	2.61	1.13
YPP	0.47**	0.024	0.264	0.04**	0.005	0.003
SY	2.43**	0.38	2.92	0.92**	0.076	0.023
OC	32.6**	1154	23018	13.5**	0.13	0.11
TDM	13.3**	0.591	7.69	0.53*	0.13	0.57
CGR	0.023**	0.03	0.43	0.03**	0.001	0.01
df	4	20	1	4	15	40

Here, DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), BNPP = Branch number per plant, SL = Siliqua length (cm), SPP = Siliqua per plant, SPS = Seed siliqua^{-1}, YPP = Yield plant^{-1}, SY = Straw yield (t ha^{-1}), OC= Oil content (%), TDM = Total dry matter, CGR = Crop growth rate. * = Significant at P = 0.05, ** = Significant at P = 0.01

Estimation of stability analysis: Previously, Finlay and Wilkinson (1963) stated that the unit regression coefficient (bi = 1) should be stable on average. If bi > 1, it means below average stability, and if bi<1, it means above average stability. The regression coefficient (bi) for days to 50% flowering ranged from -1.14 for Sompod to 2.95 for Tori-7 (Table 9). The genotypes Tori-7, BARI Sharisha-9, and BARI Sharisha-14 demonstrated considerably higher values than those with below-average stability, suggesting that these genotypes were more desirable in a favourable environment. Furthermore, BARI Sharisha-15 and Sompod had lower values than one to negative value, indicating above-average stability. For plant height, the regression coefficient (bi) ranged from -2.20 for Tori-7 to 8.63 for BARI Sharisha-15. Tori-7, BARI Sharisha-9, BARI Sharisha-14, and Sompod had lower value than one displayed above average stability, whereas Tori-7 and Sompod had negative regression coefficient.

BARI Sharisha-15 had a regression coefficient that was much more than unity and demonstrated below-average stability, indicating that this genotype required better care or a better environment. Branches number plant-1 ranged from 0.408 (Sompod) to 1.64 (BARI Sharisha-15). The S^2di estimations were non-significant for all genotypes, indicating that genotypes were stable and desirable. The genotype BARI Sharisha-9 had bi=1 and S^2di =0, indicating that the genotypes were desirable and stable in the environment. BARI Sharisha-14 and BARI Sharisha-15 had much higher values, indicating that this genotype required better management or a better environment. Tori-7 and Sompod genotypes exhibited above average stability and were desirable for challenging environments.

The regression co-efficient for siliqua length ranged from 0.537 (Sompod) to 1.41 (BARI Sharisha-14). The S^2di estimations for all genotypes were non-significant, indicating that genotypes were stable and desirable. The genotypes BARI Sharisha-9, BARI Sharisha-14, and BARI Sharisha-15 exhibited below average stability despite having higher values, suggesting that they required better environmental conditions or better management. Tori-7 and Sompod were also desirable for the poor environment due to their lower value for stability performance. Number of siliquae plant^{-1} revealed a range of (-0.19 to 2.55) for BARI Sharisha-14 and Tori-7 genotypes, indicating that all genotypes behaved differently to diverse conditions. The calculated S^2di for all genotypes was non-significant, indicating that genotypes were stable and desirable. Regression coefficients significantly lower than one for the genotypes BARI Sharisha-9, BARI Sharisha-14, and Sompod indicated that they were suited for poor environments. Regression coefficients significantly greater than one indicated below-average stability or that the Tori-7 and BARI Sharisha-15 genotypes were appropriate in favourable environments.

Table 9. Stability parameters (bi and S2di) of the five genotypes of rapeseed for yield components.

Code	Genotypes	DF		DM		PH		BNPP		SL		SPP	
	Name	bi	S^2di	bi	S_2di	bi	S^2di	bi	S^2di	bi	S^2di	bi	S^2di
G1	Tori-7	2.95	0.0003	2.67	0.004	-2.2	-10.2	0.76	0.05	0.61	0.01	2.55	3.68
G2	BARI Sharisha-9	1.36	-0.12	0.23	-0.21	0.22	-10.7	0.97	-0.14	1.22	-0.01	0.31	-0.84
G3	BARI Sharisha-14	2.39	-0.11	2.45	-0.33	0.33	-10.4	1.22	0.07	1.41	0.02	-0.19	-2.68
G4	BARI Sharisha-15	-0.57	0.08	-10	0.09	8.63	-10.1	1.64	0.01	1.22	0.02	3.08	-0.32
G5	Sompod	-1.14	-0.08	0.05	-0.09	-1.98	-7.1	0.41	0.05	0.54	0.03	-0.76	-3.31

Code	Genotypes	SPS		YPP		SY		OC		TDM		CGR	
	Name	bi	S_2di	bi	S^2di	bi	S^2di	bi	S^2di	bi	S^2di	bi	S^2di
G1	Tori-7	0.95	-0.34	0.12	-0.0001	-0.57	0.02	0.94	-0.01	0.83	-0.17	1.09	-0.003
G2	BARI Sharisha-9	0.24	1.47	1.53	-0.0002	1.83	-0.003	1.01	0.03	0.82	-0.16	1.14	-0.003
G3	BARI Sharisha-14	1.89	0.02	2.15	0.0036	2.57	0.07	1.05	0.06	1.82	-0.16	1.59	-0.003
G4	BARI Sharisha-15	1.03	-0.16	0.47	0.0004	0.984	-0.002	1.05	-0.04	0.25	-0.15	1.12	-0.0023
G5	Sompod	0.89	1.47	0.73	-0.0001	0.179	0.01	0.95	-0.02	1.27	-0.06	0.06	-0.0021

Table 10. AMMI analysis of variance with GEI partitioning for yield plant^{-1} across different environments.

Sources	DF	SS	MS	TSS explained (%)
Environment (E)	4	0.26	0.07	11.23**
Genotype (G)	4	1.87	0.47	79.60**
Interaction (G x E)	16	0.22	0.01	9.12**
AMMI Component 1	7	0.17	0.02	79.43
AMMI Component 2	5	0.04	0.01	16.67**
AMMI Component 3	3	0.01	0.002	2.69
Residuals	40	0.16		
Total	90	0.03		

* = Significant at P = 0.05, ** = Significant at P = 0.01, *** = Significant at P = 0.001

The regression coefficients for the number of seeds siliqua^{-1} with BARI Sharisha-9 and BARI Sharisha-14 ranged from 0.24 to 1.89, which showed that these two genotypes responded differently to various environments. When examining the bi and S^2di genotypes, it became clear that each genotype displayed a unique response to particular environmental conditions. All estimated S^2di values were non-significant, indicating that genotypes were stable and desirable. The regression coefficient of BARI Sharisha-14 was significantly greater than below-average stability, or this genotype was preferable for a favourable environment. The genotypes Tori-7, BARI Sharisha-15, and Sompod exhibited stability and were suitable for all environmental conditions for this trait with regression coefficient values near to one. The genotype BARI Sharisha-9 displayed a regression coefficient significantly below one and demonstrated above-average stability. Such genotypes were considered favourable for a challenging environment.

For yield plant^{-1}, Tori-7 and BARI Sharisha-14 consistently exhibited regression coefficients between 0.12 and 2.15. The differences in bi values indicated that these genotypes had distinct responses to different environments. In light of the bi and S^2di values, it was evident that each genotype demonstrated unique responses to diverse environmental conditions in terms of adaptability. All estimated S^2di values were non-significant, indicating that genotypes were stable and desirable. BARI Sharisha-15, Tori-7, and Sompod displayed regression coefficients that were significantly lower than one and demonstrated above-average stability. These genotypes were considered favourable for a challenging environment. The regression coefficient for straw yield for Tori-7 and BARI Sharisha-14 varied between -0.57 and 2.57. The variations in bi values suggested that all genotypes exhibited distinct responses to different environmental conditions It was clear from the bi and S^2di that each genotype responded differently to environmental changes in terms of adaptation. All genotypes exhibited non-significant S^2di estimates, indicating that they were stable and desirable. BARI Sharisha-15 exhibited stability with a regression coefficient close to one, making it appropriate for all environmental conditions. The oil content of Tori-7 and BARI Sharisha-15 varied between 0.94% and 1.05%. The variations in bi-values suggest that each genotype responded differently to distinct environmental conditions. When the bi and S^2di genotypes were considered, it was evident that all of the genotypes demonstrated distinct adaptation responses to varied environments. S^2di estimations for all genotypes were non-significant, indicating that they were stable and desirable. All genotypes showed stability with a regression coefficient close to one, indicating that they are suitable for all conditions for this trait. Crop growth rates ranged from 0.06 (Sompod) to 1.59 (BARI Sharisha-14). The variations in bi-values indicated that each genotype had distinct responses to different environmental situations. The S^2di estimates were all non-significant, indicating that the genotypes were stable. A BARI Sharisha-14 genotype with a regression coefficient greater than one indicated below-average stability or was preferable in a favourable environment. The genotypes Tori-7, BARI Sharisha-9, and BARI Sharisha-15 had regression coefficients that were close to unity, suggesting that these genotypes were both desirable and stable across different environmental conditions. Furthermore, Sompod had a regression coefficient that was significantly lower than one and had above-average stability; a genotype with these characteristics would be beneficial in a harsh environment.

AMMI analysis of variance: The results of the combined analysis of variance and AMMI are shown in (Table 10). Environmental effects accounted for 11.23% of the total variation, while genotypes accounted for 79.60 % and the GEI accounted for 9.12% of the total sum squares that significantly affected yield plant^{-1} in various environments. First principal component interaction analysis (IPCA1) explained 79.43% of the variation due to the interaction. Second principal component interaction analysis (IPCA2), on the other hand, only explained 16.67% of the variation due to the GEI interaction. The fact that the two principal components accounted for 96.09% of the GEI variation in yield per plant and were substantially affected indicates that the model is suitable to describe stability. The accuracy of the model in predicting the total treatment variation in GEI data, as measured by yield plant^{-1}, accounts for 96.09% of the variance predicted by the AMMI biplot.

Interaction biplot of AMMI model: As shown in Figure 1, the AMMI biplot depicts the correlation between the First Interaction Principal Component Axis (IPCA1) or AMMI component 1, the genotype, and the environment. Breeders can therefore provide a comprehensive overview of genotypic behaviour, environments, and G x E interactions by constructing biplots using genotypic and environmental scores of AMMI 1 components (Tarakanovas & Ruzgas, 2006). (Tarakanovas and Ruzgas, 2006). In comparison to other interaction axes, the first principal component axis of interaction (AMMI component 1) demonstrated exceptional significance and offered a more comprehensive elucidation of the interaction pattern. According to Balestre *et al*., (2009), the GGE biplot technique facilitates the analysis of genotype-environment (GE) and genotype + environment (G+GE) interactions better than the AMMI 1 graph.

The "0" in this case is a perpendicular line. The graph indicates that the genotypes with the highest mean values of grain yield are invariably those with environments on the right side, both upper and lower. In comparison to the lower right quadrant, which has lower mean grain yield values, the upper right quadrant has greater mean grain yield values. By plotting genotypes and environments against the mean yield plant^{-1}, respectively, the IPCA1 scores have been obtained and displayed in (Fig. 1). BARI Sharisha-14 (G3) was a high-yielding and stable genotype at E2 (Jamalpur) and E4 (Rangpur) when only the IPCA 1 scores were considered. The second genotype with a large yield was BARI Sharisha-15 (G4). BARI Sharisha-9 (G2) was a genotype with a low production that was stable at E2 (Jamalpur), E3 (Ishwardi), E4 (Rangpur), and E5 (Cumilla). (Mymensingh) Tori-7 (G1) was discovered to be a low-yielding, stable genotype at E1 level. Sompod (G5) was determined to be a medium-yielding and unstable cultivar in all environments. Therefore, among the five genotypes, genotypes G3, G4, G2, G1, and G5 are generally high yielding and have the highest males values (1.33, 1.27, 1.09, 0.96, and 0.95 t ha-1, respectively). BARI Sharisha-14 (G3) was a high-yielding and stable genotype at E2 (Jamalpur) and E4 (Rangpur) when only the IPCA 1 scores were considered. The second genotype with a large yield was BARI Sharisha-15 (G4). BARI Sharisha-9 (G2) was a genotype with a low production that was stable at E2 (Jamalpur), E3 (Ishwardi), E4 (Rangpur), and E5 (Cumilla). (Mymensingh) Tori-7 (G1) was discovered to be a low-yielding, stable genotype at E1 level. Sompod (G5) was determined to be a medium-yielding and unstable cultivar in all environments. Therefore, among the five genotypes, genotypes G3, G4, G2, G1, and G5 are generally high yielding and have the highest mean values (1.33, 1.27, 1.09, 0.96, and 0.95 t ha^{-1}, respectively).

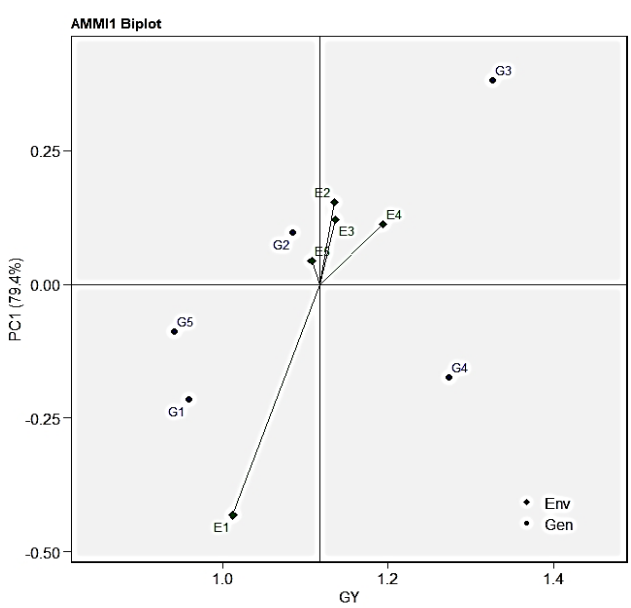

Fig. 1. Interaction biplot of AMMI1 in which IPCA1 score (y-axis) is plotted against mean yield (x-axis) for five genotypes of rapeseed across various environments.

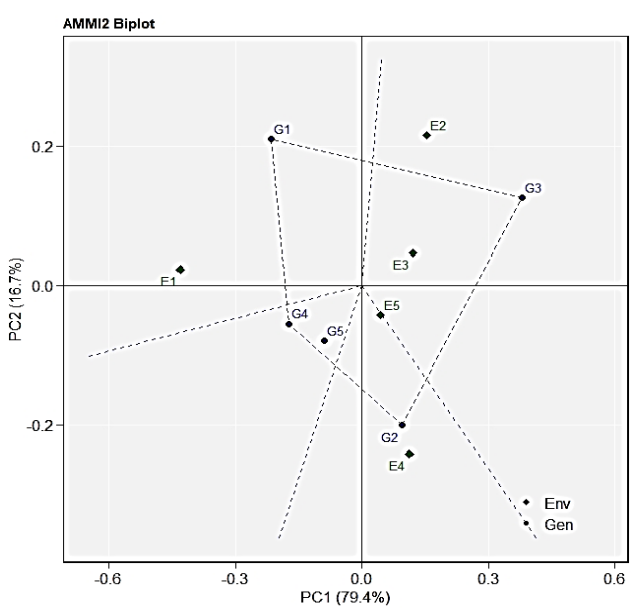

Fig. 2. AMMI2 interaction biplot with IPCA2 score (Y-axis) plotted against IPCA1 score (X-axis) for five genotypes in different environments.

Using both IPCA scores, the biplot in (Fig. 2) was constructed. i.e., since IPCA2 scores are important in explaining the GEI. According to Figure 2, BARI Sarisha-9 (G2) and BARI Sharisha-14 (G3) were more stable for yield plant^{-1} when tested in various environments. Therefore, BARI Sarisha-9 (G2) was the highest performing genotype for environments E4 (Rangpur) and E5 (Cumille). The BARI Sharisha-14 (G3) performed best in E2 (Jamalpur) and E3 (Ishwardi) environments. The most unstable and discriminatory genotypes for yield plant-1 were G4, and G5, which were also less responsive to all environmental factors. Tori-7(G1) was extremely stable and performed best with E1 (Mymensingh). However, among the genotypes that shown stability and maximum performance, BARI Sharisha-14 (G3) demonstrated a high mean yield plant^{-1} at E2, and BARI Sharisha-9 (G2) demonstrated a high mean yield plant^{-1} at E4.

Conclusions

The AMMI statistical model could be a valuable tool for selecting the best suitable and stable high yielding genotype for specific as well as different environments. Consequently, the GEI effects impacted almost all of the genotypes evaluated, hence no genotype performed better in all environments. Based on the stability values obtained in the current investigation, it was apparent that each genotype demonstrated distinct responses to adaptability when exposed to diverse environmental conditions. Consequently, the environmental stability of the Tori-7, BARI Sharisha-9, and BARI Sharisha-14 genotypes was comparatively high. The GEI indicated that BARI Sharisha-14 (G3) had a high mean yield value (1.33 tha-1) and performed the best across all five environments. It was also found that BARI Sharisha-9(G2) was a low-yielding genotype, but its performance could be better under different environmental conditions. In conclusion, E3 (Ishwardi) was the best environment for rapeseed cultivation, while E5 (Cumilla) was also beneficial. High heritability and genetic advance were observed for yield plant^{-1} across all environments, suggesting that additive gene action regulates the trait and that trait selection could potentially facilitate the development of high yielding genotypes.

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