Short Communication

Genotype x environment interaction in Indian mustard (*Brassica juncea* L. Czern and coss) under Manipur valley conditions

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Abstract

An investigation was conducted during rabi season of 2009-10 and 2010-11 to assess the stability on yield and its attributes along with oil content of twelve genotypes of Indian mustard (Brassica juncea L. Czern and Coss) at two locations with two different dates of sowing creating eight artificial environments. Variance due to G x E interaction was significant for all the characters except for days to 50% flowering, while G x E (linear) was found to be significant for number of secondary branches per plant, number of siliquae per plant, siliqua length, seed yield per plot and 1000 seed weight. Genotypes, GM-2, JD-6 and Pusa Bold could be recommended for general cultivation and their utilization in future breeding programme. Under favourable environments, genotypes Kranti, NDRE-7, NDRE-22 and Sej-2 are suitable for general cultivation. On the contrary, Urvashi could be recommended for poor/unfavourable environmental conditions.

Key words: *Brassica juncea*, Stability, Yield and its attributes, Indian mustard, G x E interaction

Morphological characters are limited in number and often do not reliably portray genetic relationships since genotype by environment (G x E) interaction reduces the rate of genetic improvement [1]. This makes it necessary to test selections over several seasons and sites. Testing over the seasons and locations change the genotypic composition of selected or rejected cultivars in a given environment. On the other hand, G x E interaction may offer opportunities especially in the selection and adoption of genotypes showing positive interactions with location and its prevailing environmental conditions (exploitation of specific adaptation) or of genotypes with low frequency of poor yield or crop failure (exploitation of yield stability) [2]. In nutshell, G x E interaction plays the decisive role in allowing a population to persist and adapt in a changing environment [3].

Rapeseed and mustard, because of its resilience to diverse agro climatic conditions and sustainability towards abiotic stresses, occupies the premier position as the largest oil producing crop in India. However, the sensitive behaviour of the existing varieties of mustard to different growing environments in Manipur leads to fluctuations in its yield, which is mainly attributable to the occurrence of G x E interaction posing a major challenge for the genotypes to perform uniformly under diverse environments. The identification of germplasm with broad adaptation would be helpful in development of improved cultivars. Hence, the present investigation was carried out to evaluate the G x E interaction on vield and important vield contributing attributes and to isolate the promising and stable genotypes based on their stability parameters.

Twelve promising genotypes of Indian mustard

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were planted at two different locations viz., Langthabal Kunja Mayai Leikai and Andro Research Farm grown for two consecutive years (2009-10; 2010-11) during rabi season at two different dates of sowing (15th November and 25th November) creating eight artificial environments. Each experiment was laid out in randomized block design with three replications consisting of 5 rows with a plot size of 4 x 1.5 cm and a spacing of 30 x 10 cm. Standard cultural practices were followed throughout the crop season. The characters namely, number of primary branches per plant, number of siliquae per plant, number of seeds per siligua, 1000 seeds weight were recorded from 10 sampled plants /plot/ replication chosen at random excluding the border rows. The average yield of the 10 sampled plants was considered as seed yield per plant. Stability analysis was done as per the model proposed by Eberhart and Russell [4].

The ANOVA demonstrated highly significant differences among genotypes (G) and environments indicating that the genotypes were distinct in their attributes and the environments were different from one another. Significant genotype x environment interaction for all the characters indicates differential expression of genotypes for the traits studied over the eight environments. Similar results for various traits were also reported earlier [5, 6] with different materials and soil conditions. G x E (linear) component was significant for number of siliquae per plant and 1000 seed weight suggesting predictable nature of the

performance of genotypes taken over the environment. Number of primary branches per plant, number of seeds per siliqua and seed yield per plant have significant value both for $G \times E$ (linear) and pooled deviation confirming the presence of predictable and non-predictable components. Even for the unpredictable factors, prediction can be made if one considers the stability performance of individual genotypes [5].

A desired variety is defined as a variety with a high mean (x_i) , unit regression coefficient (bi = 1.0) and the deviations from the regression as small as possible ($S^2di = 0$) [4]. If bi is (a) equal to unity, a genotype was considered to have average stability (same performance in all the environments) (b) more than unity, it is suggested to have less than average stability (good performance in favourable environments) and (c) less than unity, it is reported to have more than average stability (uniform performance even under poor environments).

Analysing the individual stability parameters (Table 1), for the character primary branches per plant, Sej-2 and GM-2 can be recommended for wide adaptation (bi = 1), NDRE-22 for the favourable environment (bi > 1) whereas JD-6 and NDRE-7 for the unfavourable environment (bi < 1). Genotypes NDRE-7, Urvashi, RH-0447and Pusa Bold had non-significant S²di for number of seeds per siliqua and 1000 seed weight enabling it to predict the stability.

| Genotype (G) | No. of primary branches per plant | | | No. of siliquae per plant | | | No. of s | No. of seeds per siliqua | | |
|--------------|-----------------------------------|--------|-------------------|-----------------------------|----------------------|-------------------|-----------------------------|--------------------------|-------------------|--|
| | x i | bi | S ² di | $\overline{\mathbf{x}_{i}}$ | bi | S ² di | $\overline{\mathbf{x}_{i}}$ | bi | S ² di | |
| JD-6 | 4.07 | 0.56* | 0.07 | 162.05 | 0.94** | 6.86 | 11.17 | 0.91** | 0.22 | |
| SEJ-2 | 4.01 | 1.04** | 0.05 | 179.52 | 1.44** | 17.43 | 11.44 | 0.62** | 0.17 | |
| GM-1 | 3.87 | 1.69** | 0.53** | 129.81 | 3.86** ⁺⁺ | 76.83** | 10.83 | 0.80 | 1.48** | |
| GM-2 | 4.00 | 1.04** | 0.06 | 159.63 | 0.68*** | -9.13 | 10.92 | 1.03** ⁺⁺ | 0.25 | |
| NDRE-22 | 4.40 | 1.30** | 0.01 | 168.66 | 0.82** | -2.75 | 11.55 | 1.29** | 0.51* | |
| NDRE-74.14 | 0.87** | 0.05 | 143.83 | 0.58* | 9.34 | 11.31 | 1.12** | 0.23 | | |
| URVASHI | 3.97 | 0.81* | 0.21* | 155.50 | 0.80** | -4.45 | 11.65 | 0.89** | -0.08 | |
| KRANTI | 4.52 | 0.55 | 0.36** | 160.07 | 0.13 | 28.95* | 12.32 | 1.51** ⁺⁺ | -0.28 | |
| RH-0447 | 4.33 | 1.06* | 0.34** | 164.48 | 1.12** | 32.26** | 11.37 | 0.82** | 0.04 | |
| PUSA BOLD | 3.82 | 0.91* | 0.28** | 125.37 | 0.53*** | -2.92 | 11.02 | 0.83** | 0.42 | |
| LOCAL YELLA | 4.90 | 1.20** | 0.32** | 174.73 | 0.53*+ | 5.68 | 11.36 | 1.00 | 1.38** | |
| BIO-902 3.75 | 1.91* | 0.24* | 119.90 | 0.51*** | -1.59 | 10.50 | 1.12** | 0.56* | | |
| Mean | 4.15 | | | 153.63 | | | 11.29 | | | |
| SEm (±) | 0.18 | | | 2.03 | | | 0.30 | | | |
| CD (G) at 5% | 0.37 | | | 4.02 | | | 0.60 | | | |

Table 1. Estimates of stability parameters for yield and its contributing attributes in Indian mustard

| Genotype (G) | 100 | 0 seeds weigh | Seed yield per plant (g) | | | |
|--------------|-----------------------------|----------------------|--------------------------|-----------------------------|---------|-------------------|
| | $\overline{\mathbf{x}}_{i}$ | bi | S ² di | $\overline{\mathbf{x}}_{i}$ | bi | S ² di |
| JD-6 | 3.19 | 0.62* | 0.00 | 4.75 | 0.93** | -0.06 |
| SEJ-2 | 3.05 | 1.42*** | -0.00 | 4.22 | 1.15** | 0.22 |
| GM-1 | 3.70 | 2.63*** | 0.06** | 4.95 | 1.68*** | 0.50** |
| GM-2 | 5.21 | 0.76 | 0.05** | 6.57 | 1.14** | 0.03 |
| NDRE-22 | 3.12 | 1.12* | 0.01* | 4.39 | 1.33** | 0.30* |
| NDRE-7 | 3.22 | 0.29** ⁺⁺ | -0.00 | 4.08 | 0.42 | 0.06 |
| URVASHI | 3.28 | 0.69** | -0.00 | 5.35 | 1.12** | 0.24 |
| KRANTI | 3.19 | 1.25** | -0.00 | 5.83 | 0.31 | 1.57** |
| RH-0447 | 3.16 | 0.93** | 0.00 | 5.23 | 1.39** | 0.23 |
| PUSA BOLD | 5.36 | 1.25** | 0.01 | 5.77 | 1.08** | 0.56** |
| LOCAL YELLA | 2.57 | -0.32 | 0.000 | 3.83 | 0.63** | 0.01 |
| BIO-902 | 5.22 | 1.32** | -0.00 | 5.05 | 0.77** | 0.30* |
| Mean | 3.69 | | | 5.00 | | |
| SEm (±) | 0.04 | | | 0.08 | | |
| CD (G) at 5% | 0.08 | | | 0.17 | | |

Table 2: Estimates of stability parameters for 1000 seeds weight and yield in Indian mustard

Genotypes JD-6 and GM-2 showed average responsiveness for number of seeds per siliqua, while RH-0447 for 1000 seed weight. JD-6 was found to be suited for broad adaptation; Sej-2 under intensive practices; GM-2, NDRE-22, Uravshi and Local Yella for poor environmental conditions for the number of siliquae per plant. Genotype, GM-2 was the most adaptable with S²di value nearly approaching to zero (S²di = 0.033), bi near to unity and highest seed yield per plant (6.571g). Chauhan [7] had also reported stability of GM-2 under favourable environment. Apart from this, JD-6 can also be recommended for wide adaptation for seed yield per plant.

From the results presented above, it can be concluded that different genotypes reacted differently to varying seasons as indicated by the high significant G x E interaction hence, the supposition that environmental effects are important in understanding plant growth. It also emphasized about significant G x E effects and the necessity for multiple environments testing through time and space so as to characterise genotype difference and stabilities. Genotypes, GM-2, JD-6, NDRE-22 and Sej-2 having maximum stability could be commercially utilized and in future breeding programmes under Manipur valley conditions. In all, G x E interaction should not be ignored rather analysed using appropriate techniques in order to test new genotypes in the environment of intended use before release to farmers.

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