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Evaluation of yield and aphid resistance of Indian mustard (*Brassica juncea*) accessions under acidic soil of Meghalaya

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Indian mustard [*Brassica juncea* (L.) Czern and Coss] belonging to the family Brassicaceae is one of the 10 most economically important plant families (Rich 1991). *Brassica* is grown for vegetables, fodder, oil and condiments. Globally India ranks third in area and production of mustard (Kumawat *et al.* 2023). In India, they are grown under diverse agro-climatic conditions under irrigated or rainfed, timely or late sown, saline soils and mixed cropping. In Meghalaya, mustard production is 1.4 and 2.1 times below the national and global average. The soils of north-eastern hill regions (NEHR) are acidic, with Al^{3+} (Aluminium) toxicity and deficient in P (Phosphorous) and Zn^{2+} (Zinc). This gap in yield potential is mainly due to poor soil quality as well as severe aphid infestation. Since yield is the culmination of a series of attributing characters, the response to selection for yield is minimal. It is important to manipulate the yield attributes like the number of siliquaes, number of seeds/siliquae, test weight, plant height, maturity duration, oil quality, etc. The knowledge and understanding on the type and extent of genetic diversity as well as genetic gain of the attributes are important for further crop improvement. For an effective selection programme, it is essential to have knowledge of the level of genetic variability amount and associations between characters. India ranks second (15%) in the repository of *Brassica* germplasm in the world (Chand *et al.* 2021). These enormous materials form the hub for genetic variability, which is yet to be exploited. Aphid attack can cause yield loss from 20–90% (Rao *et al.* 2012). Aphids are sap-feeding insects and are a serious threat to mustard yield. *Lipaphis erysimi* is a 'specialist' aphid for mustard and the Green Peach Aphid (GPA) (*Myzus perisicae*) is the 'generalist' aphid that can feed over 50 families including mustard. Hence in the present study, 95 accessions of Indian mustard along with 4 widely adopted check varieties were tested for yield and its attributing characters under acidic soils (NEHR) of Meghalaya. Later, aphid proliferation was studied in selected high yielding genotypes to evaluate an elevated level of resistance to two aphids' species.

The present study was carried out during winter (*rabi)* season of 2021 at the Research Farm of College of Post Graduate Studies in Agricultural Sciences (Central Agricultural University, Imphal, Manipur), Umiam, Meghalaya. Indian mustard was collected from different parts of the country and ICAR-National Bureau of Plant Genetic Resources, New Delhi. A total of 95 genotypes were grown in augmented block design with four checks namely; Varuna, Kranti, Rohini, and NRCHB-101 replicated in the five blocks. Each genotype was grown with a spacing of 45 cm × 10 cm and 15 plants/genotype was maintained. Ten competitive plants/genotype were randomly selected for recording observations. Traits like germination and flowering were counted as days from sowing i.e. days to first germination (DT1G), days to 80% germination (DTEG), days to first flowering (DT1F), days to 50% flowering (DTFF), days to 80% bud formation (DTEBF) and days to maturity (DTM). Yield attributing traits were counted in numbers like number of primary branches/plant (NPB), number of secondary branches/plant (NSB), number of siliques/plant (NSQPP), and number of seeds/siliquae (NSPSQ). Traits like plant height (PH), stem diameter (SD), and siliquae length (SL) were measured in centimetres, and yield-related traits were weighed in grams, viz. seed yield/plant (SYPP), dry matter (DM), biological yield (BY), 1000-seed weight (TW) and a derived trait harvest index [HI = (SYPP/BY) × 100] was calculated. Based on principle component analysis (PCA), three high and three poor-yielding genotypes were selected and grown in smaller pots i.e. 1 plant/pot with 6 replications under controlled environment of 22°C, 70% RH, 14 h light and

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10 h dark. Ten mustard aphids and 15 green peach aphids were released in all the plants separately in each treatment and aphid proliferation was monitored at 24 h, 48 h and 72 h time points. The total aphid proliferation (TAP), measured in the absolute number including initial aphid release, real-time fold of aphid proliferation (RT-FAP), incremental aphid proliferation (IAP), and marginal aphid proliferation (MAP) at 24 h, 48 h, and 72 h were monitored. Every index is formulated below:

$$\text{i) RT-FAP}_{24\text{ h}} = \frac{\text{TAP at 24 h}}{\text{Tap at 0 h}}$$

$$\text{ii) RT-FAP}_{48\text{ h}} = \frac{\text{TAP at 48 h}}{\text{Tap at 24 h}}$$

$$\text{iii) RT-FAP}_{72\text{ h}} = \frac{\text{TAP at 72 h}}{\text{Tap at 48 h}}$$

iv) IAP 24 h = TAP at 24 h-TAP at 0 h

v) IAP 48 h = TAP at 48 h-TAP at 0 h

vi) IAP 72 h = TAP at 72 h-TAP at 0 h

vii) MAP 24 h = TAP at 24 h-TAP at 0 h

viii) MAP 48 h = TAP at 48 h-TAP at 24 h

ix) MAP 72 h = TAP at 72 h-TAP at 48 h

The soils of NE India are mostly acidic (Roy *et al.* 2022) along with this the occurrence of heavy rainfall, low light intensity, severe disease occurrence, and undulated topography make agriculture difficult in these areas. Limited works have been carried out on mustard crop improvement in NEHRs. The ANOVA obtained from augmented design analysis revealed that the treatments i.e. genotypes showed significant differences for 17 traits, except for DTEBF. A similar study by Singh *et al.* (2024a) also used the same design where they reported less variation for flowering and maturity days. The average days for first germination was 13.5 ± 0.8 days and 7 genotypes germinated in less than 4 days. Three genotypes PM-27, SEETA and NPJ-194 had 50% flowering in 53.6 ± 1.3days. The NSQPP and YPP were maximum in Vardhan which had 455.1 siliquae and 13.8 g/plant, respectively. NSPS was found the highest in CS-2009-332. Maximum SL was observed in CS2009-105 which was 9.6 ± 0.1 cm but was the late flowering and had DTEBF as 113.1 ± 0.5 days. RH119 was a poor yielding genotype with the lowest values of NPB, NSB, SD, DW, BY, and SYPP. Based on the adjusted means obtained from augmented design analysis, the maximum yield/plant was recorded in the genotypes, Vardan (13.8 g), followed by RH-0923 (13.33 g), RW-46-3 (12.35 g), RL-JEB-84 (11.78 g), KMR-53-3 (11.69 g) and DRMR-4001 (11.55 g). The highest GCV and PCV were seen in SYPP (73.67% and 86.89%), NSQPP (55.21% and 70.76), and BY (54.7 and 60.86%). Apart from these other traits like, DW, D1G, NSB, HI, DTEG, NPB, NSPS, TW and SD had high GCV and PCV. Similarly, high values of PCV and GCV was observed for NSQPP BY (Rout *et al.* 2019), SYPP (Lakra *et al.* 2020 and Hyder *et al.* 2021). The highest heritability was observed for DT1F (94%), followed by DTM (93%), whereas SYPP had a heritability of 72%. Genetic advance was found highest for NSQPP, followed by PH and BY. Genetic advance as percent mean (GAM) was found highest for DW followed by HI and BY. Kumar *et al.* (2021) also observed high heritability coupled high genetic gain for NPB. These findings revealed that these traits are governed by additive gene effects and selection for these traits would be rewarding in early generations. Correlation analysis revealed that SYPP was correlated with all the traits studied except for DW, it was highly correlated with NSQPP (0.89), NSPS (0.67) and NSB (0.673). Similar findings of positive correlation of SYPP with NSQPP and negative correlation with DTFF were obtained by Rout *et al.* (2019) and Patel *et al.* (2021). NSQPP had positive and highly significant correlation with PH, NPB, NSB, and NSPS (above 0.6). PCA for the 18 agro-morphological and yield-related traits gave a biplot in which the 63.9% of total variation was accounted by the first two principal components (Fig. 1). Generally, PCA was used in previous studies for grouping the genotypes based on set of correlated traits which can be used as a basis for selecting a genotype (Gosh *et al.* 2023, Singh *et al.* 2024a). SYPP, NSQPP, BY, DW, and NSB were the traits that contributed maximum towards the first principal component (PC1), whereas DTFF followed by DT1G was the most contributing trait for PC2. Vardan, RL-JEB-84, DRMR-4001, CS-2009-332, KMR-53-3, RH-781, RH-0923, PM24, JM-1, RW-46-3, RGN-73-JC and RMM-09-10 were the genotypes present at extreme of 1st quadrant in PCA individual's biplot (Fig. 1). These genotypes have higher yields coupled with higher values of other yield-contributing traits.

Aphids can proliferate in a very short time and can cause economic losses to many crops (Mondal 2020), in extreme cases they could cause yield loss of up to 90% (Rao *et al.* 2012). In the current study, mustard aphid (*Lipaphis erysimi* - LE) and green peach aphid (*Myzus persicae* -MP) were artificially inoculated in the seven selected genotypes, and their proliferation was studied individually**.** All the observations like TAP, derived RT-FAP, IAP, and MAP indices for aphids revealed significant differences for 11 traits out of 16 traits studied. Correlation analysis for the field traits and *in vitro* aphid count traits showed that all traits related to LE were positive and significantly associated with days to 80% bud formation (DTEBF). LE showed a negative non-significant correlation and MP showed a positive non-significant correlation with SYPP, respectively. Although we could not find any supporting reports, but the information could be used for indirect selection in field conditions. In the case of LEIAP (Fig. 2a) and LEMAP the genotypes RMM-09-10 and RL-JEB-84 showed no significant difference in aphid count between 24 h and 48 h hence they are more resistant over the other genotypes for LE. The genotypes CS-2009-332, RMM-09-10, PM24, RJ-JEB-84, and CS-2013-50 were considered as more resistant to MP over the other genotypes based on MP MAP (Fig.

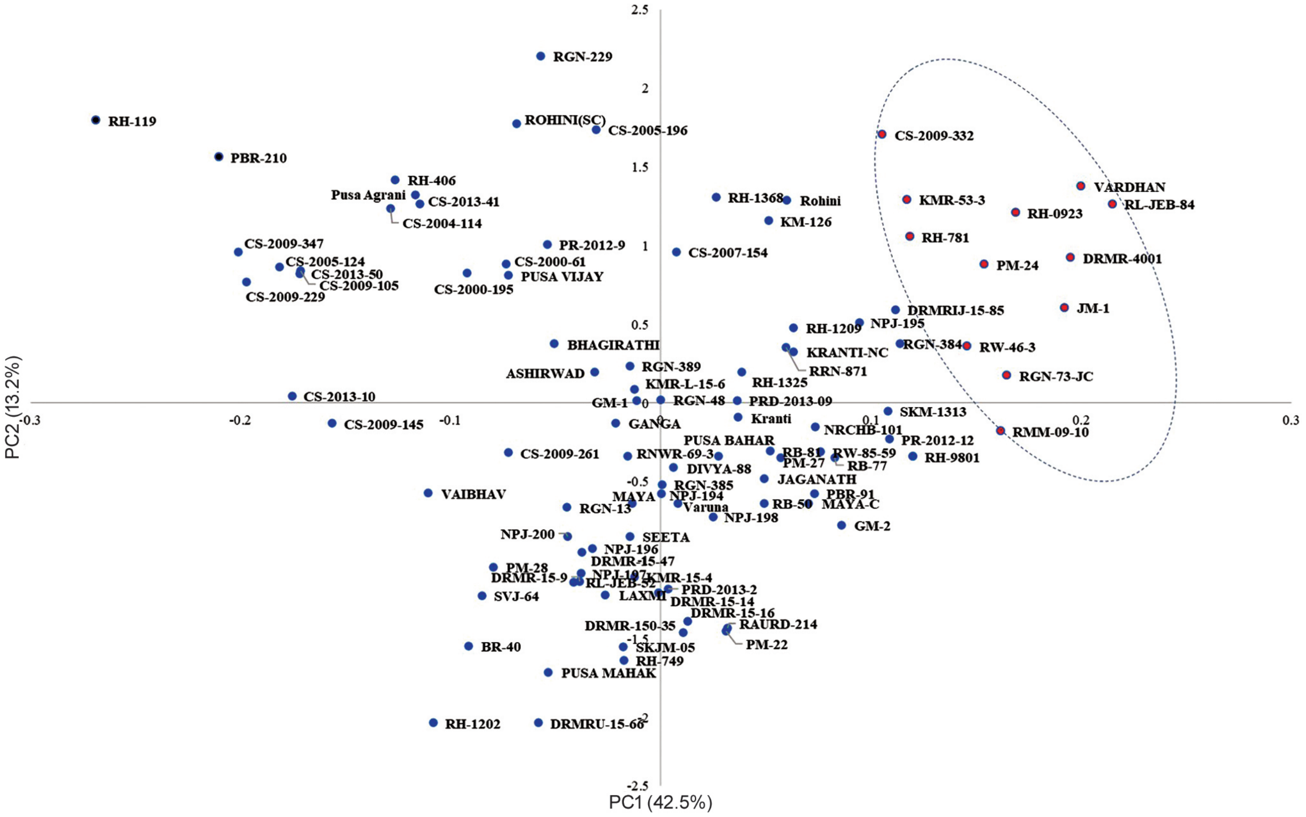

Fig. 1 Aphid proliferation index of *Lipaphis erysimi* (a) and *Myzus persicae* (a) of the selected seven accessions. Blue and orange bars represent the proliferation of aphids at 24 h, 48 h.

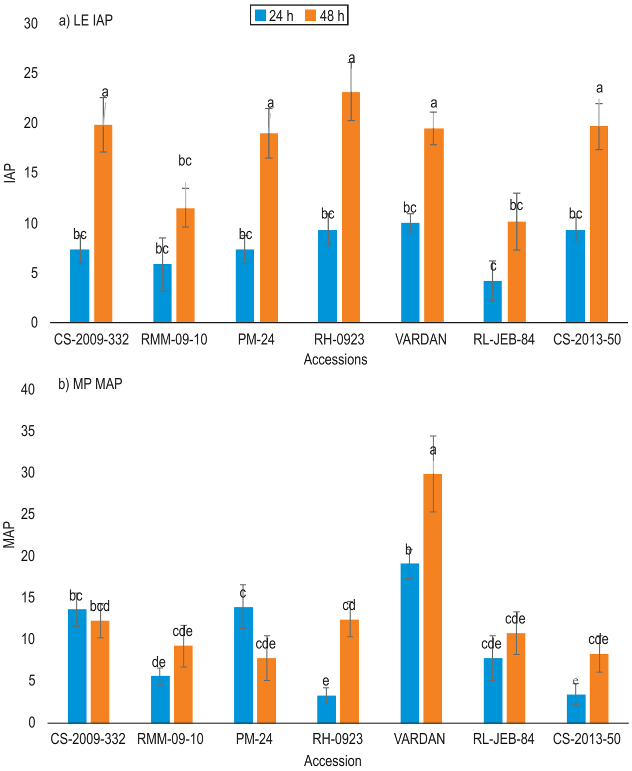

Fig. 2 Principle component analysis biplot of 99 genotypes used in the study.
Blue circle denoted cluster of superior genotypes.
IPA, Incremental aphid proliferation; MAP, Marginal aphid proliferation.

2b). The genotype CS-2013-510 was more resistant to MP but was poor yielding, whereas CS-2009-332, RMM-09-10 and PM24, RJ-JEB-84 were moderately resistant and were high yielding. In contrast to the previous reports that high yielding variety were tolerant to aphid infestation (Singh *et al.* 2024b). In our study, it was surprising that high-yielding genotypes like Vardhan, CS-2009-332, and RH-0923 were less resistant to aphids. Hence improving them by crossing with other identified high-yielding and more resistant genotypes will be rewarding.

SUMMARY

The present study was carried out during winter (*rabi)* season of 2021 at the Research Farm of College of Post Graduate Studies in Agricultural Sciences (Central Agricultural University, Imphal, Manipur), Umiam, Meghalaya to assess the yield and aphid resistance of Indian mustard accessions under acidic soil of Meghalaya. A total of 95 accessions were evaluated in the acidic soils of north-eastern hill regions (NEHR) of India with concomitant problems of low phosphorus availability and aluminum toxicity followed by a specialist and a generalist aphid resistance evaluation. The result evidenced that the number of siliques/plant (NSQPP), biological yield (BY), dry weight (DW), number of seeds/siliqua (NSPS), and number of secondary branches/plant (NSB) were found to be highly correlated with seed yield/plant (SYPP). Principal component analysis (PCA) gave a biplot with atleast two diverse groups. The extreme genotypes i.e. Vardan, RH-

0923, RL-JEB-84, and PM24 of the first quadrant in PCA had high yield and its attributing traits. Aphid resistance study using different indices in the selected genotypes evidenced an elevated resistance level. The genotypes RMM-09-10 and RL-JEB-84 could be considered as higher resistant against both two aphid spp., *Lipaphis erysimi* and *Myzus persicae*, a specialist and generalist aphid, respectively.

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