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Short communication

Screening quality protein maize germplasm for resistance to biotic stresses

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Abstract

The present investigation was carried out to screen 28 Quality Protein Maize (QPM) inbred lines along with two checks (Bajim Q-08-27 and Bajim Q-08-26) against turcicum leaf blight (TLB), maydis leaf blight (MLB), banded leaf and sheath blight (BLSB) and fall armyworm (FAW) under natural epiphytotic conditions at Palampur during *kharif* 2023. The resistant reaction was recorded in 12 lines for TLB and 18 lines for MLB while 22 lines for BLSB and 17 for fall armyworm exhibited moderate reaction. Multiple resistance was recorded in six inbreds *viz*., BJ QPM-13, BJ QPM-15, BJ QPM-19, DQL-1017-2, DQL-609-1-3 and DQL- 614-6 with resistance reaction to MLB and TLB along with moderate resistance to BLSB and FAW. These resistant lines can be used in QPM breeding program as resistance sources against TLB, MLB, BLSB and FAW after ascertaining resistance under in *vitro* and in *vivo* conditions over environments.

Keywords: Maize, Resistant inbreds, Biotic stresses, Blights, Fall armyworm

Maize (*Zea mays* L., 2n =20) is referred to as the golden crop due to its widespread use to mankind, livestock and industries. Along with wheat and rice, it provides around 30% of food calories to more than 4.5 billion people. Maize kernels are rich in carbohydrates (60-75%), crude protein (9-10%) and lipids (3-5%) making it a highly nutritious food source (Ranum *et al*. 2014). Maize is grown in India on about 10.04 million hectares predominantly as a rainfed crop with a production of 33.62 million tonnes and an average yield of 3.3 tonnes per hectare (Anonymous 2022). In India, it is utilised primarily as feed (63%) followed by food (23%), starch production (12%), seed and various other purposes (2%). The primary issue concerning human nutrition in developing countries is the low quality of cereal proteins. Therefore, development of nutritionally enhanced hybrids and varieties becomes crucial to address malnutrition and global food security.

Developed in the late 1960s, QPM provides 70% to 100% more lysine and tryptophan as compared to traditional and modern maize varieties. Despite its high yielding potential, a major constraint in the production of QPM remains its vulnerability to various pests and diseases. Approximately, 65 diseases of maize have been reported across various regions of India. Turcicum leaf blight (TLB)/Northern corn leaf blight (NCLB), Maydis leaf blight (MLB)/Southern corn leaf blight (SCLB) and Banded leaf and sheath blight (BLSB) remain the most prevalent across India. Approximately 13.2% of the total crop yield per year is lost due to attacks from various pathogens causing diseases. The warm and humid climate of the country is conducive to disease development. Over 40 insect species have been reported on maize in the field by Fenta and Dereje (2019). Among the pests, the invasive species of fall armyworm (FAW) Spodoptera frugiperda (J.E. Smith) has emerged as the primary insect pest causing significant yield losses from 10-30% (Urge *et al*. 2020).

TLB caused by fungus Exserohilum turcicum is favoured by moderate, wet and humid weather conditions (18-27°C). Long, narrow, greyish or tan lesions appear initially on leaves that align with the midrib. These lesions later expand into an oblong or characteristic “cigar” or spindle shape and may also

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develop on husks. The reduction of photosynthetic tissue causes yield losses from 25% to 90% of the total crop and a decline in silage quality. MLB caused by fungus *Bipolaris maydis* (Nisikado and Miyake) Shoemaker 1959 is prevalent in regions with warm temperatures (20-30°C) and high humidity (>80%) leading to yield losses of approximately 40% to 70% of total production (Haque *et al*. 2022). Small elliptical spots or lesions with dark brown margins and a straw to light brown center appear as symptoms which begin from the base of the plant till the flag leaf eventually progressing to complete foliage blight (Kumar *et al*. 2022). BLSB caused by the fungus *Rhizoctonia solani* also affects maize in hot and humid weather. This severe disease initially appears on the leaves and basal sheaths of maize as leaf sheath blight and later progresses to affect the ears as ear rot. Extensive gray, tan or brown snake-like, discolored patches interspersed with dark brown bands appear on the affected parts. The disease typically results in production losses of upto 60% in maize under natural conditions (Rai and Singh 2018). FAW is a polyphagous, lepidopteran pest which can be very destructive in warm and humid conditions (Sushmita *et al*. 2023). The capacity for rapid reproduction, migration and feeding on a diverse array of host plants collectively makes it challenging to control the pest (Fenta and Dereje 2019). The larvae cause damage by feeding on foliage resulting in characteristic holes. Severe damage by feeding causes "dead heart" giving the plant a torn or ragged appearance. Although diseases and pests can be managed with chemical treatments, these approaches are neither farmer-friendly nor environmentally sustainable besides has severe consequences on human health and therefore, genetic resistance is ideal and sustainable (Sharma *et al*. 2010 and 2025).

The genetic basis of resistance in maize to turcicum leaf blight (NCLB), maydis leaf blight (SCLB), banded leaf and sheath blight (BLSB), and fall armyworm has been extensively studied. For NCLB, qualitative resistance is conferred by genes like Ht1, Ht2 and Ht3, while quantitative resistance involves multiple QTLs, such as ZmWAK-RLK1 and ZmREM6.3. In case of SCLB, resistance includes both the recessive rhm-1 gene and QTLs like ZmCCoAOMT2. BLSB resistance has been linked to ZmFBL41, a gene regulating lignin biosynthesis, which restricts lesion expansion (Zhu *et al*. 2021). Several genetic loci have been associated with resistance to fall armyworm (FAW) in maize, with most resistance being polygenic and quantitative in nature. Key QTLs have been identified on chromosomes 1, 2, 4, 6, 7, 9 and 10, with consistent evidence highlighting major resistance regions on chromosome bins 4.06 and 9.03. However, reliance on a limited number of resistant sources, especially major R-genes, can lead to breakdown of resistance due to evolving pathogen or pest populations. For instance, the narrow use of T-cytoplasm led to the 1970 SCLB epidemic in the USA. Thus, diversifying resistant sources is crucial to avoid such vulnerabilities, enhance durability of resistance and ensure broad-spectrum and stable protection across diverse environments and evolving threats . Therefore, the present study was carried out to identify sources of disease and pest resistance, which is a crucial step for the advancement of the QPM breeding program.

The experimental material comprised 30 elite QPM lines including two checks *viz*., Bajim Q-08-27 and Bajim Q-08-26 which were evaluated against TLB, MLB, BLSB and fall armyworm under natural epiphytotic conditions in a randomized block design with three replications during *kharif*, 2023 at the Experimental Farm of the Department of Genetics and Plant Breeding, Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur (HP). Moderately resistant to resistant checks were used in the study for the three diseases assessed. Out of the 30 inbreds, 24 were procured from the Hill Agricultural Research and Extension Centre (HAREC), Bajaura, 4 were acquired from the Indian Institute of Maize Research (IIMR), Ludhiana and 2 were improved inbred lines developed by CSK HPKV, Palampur. The weekly average maximum and minimum temperatures ranged from 25.9°C to 28.5°C and 12.8°C to 19.8°C, respectively, while the relative humidity ranged from 64% to 92.05% during the crop period. The disease screening for TLB and MLB was done following a 0-9 scale given by Mitiku *et al*. (2014). The scale given by Muis and Quito (2006) was followed for recording disease reaction to BLSB. Disease rating for fall armyworm was done using the modified scale of Davis and Williams (1992). Disease and pest severity was assessed on five randomly selected plants per genotype within each replication. The scores thus obtained were averaged, and the mean score calculated across the three replications was used to classify genotypes as resistant or susceptible. To assess the relationship between disease and pest resistance, correlation analysis was performed using R software. The resistance scores for each genotype were analyzed to determine the strength and direction of the association between disease and pest resistance.

Under natural epiphytotic conditions, twelve genotypes exhibited resistance to TLB with infection rates below 30% (Table 1). Eighteen genotypes were found to be moderately resistant. Similar findings for TLB were also reported earlier by Sharma *et al*. (2021) and Sharma *et al*. (2022). None of the genotypes displayed moderate or high susceptibility to TLB suggesting that the genetic makeup of these lines may inherently possess traits that confer resilience against this disease. This uniform resistance across the tested genotypes warrants further investigation into the underlying genetic architecture, as it suggests the possibility of common resistance genes or regulatory pathways that might be efficiently targeted in breeding efforts.

For MLB, eighteen genotypes exhibited resistance with infection rates below 30% and twelve genotypes were found to be moderately resistant (Table 1). None of the genotypes displayed moderate or high susceptibility to MLB. These results highlight the genetic potential within these genotypes for use in breeding programs aimed at enhancing disease

Table 1: Disease reaction to turcicum leaf blight, maydis leaf blight and banded leaf and sheath blight under natural epiphytotic conditions

Degree of infection (%)	Rating scale	Reaction	Disease	No. of genotypes	Genotypes
<30%	$\leq$3.0	Resistant	TLB	12	Bajim Q-08-26, DQL-1017-2, DQL-614-6, DQL-609-1-3, BJ QPM-10 (HKI-193-1), BJ QPM-13, BJ QPM-15, BJ QPM-19, BJ QPM-14, BJ QPM-16, BJ QPM-18, BJ QPM-23
			MLB	18	Bajim Q-08-26, DQL-1017-2, DQL-609-1-3, BJ QPM-9 (HKI-163), BJ QPM-16, BJ QPM-6, DQL-774-171, Bajim Q-08-27, BJ QPM-19, BJ QPM-4, BJ QPM-12, BJ QPM-11, BJ QPM-2, BJ QPM-14, DQL-614-6, BJ QPM-24, BJ QPM-13, BJ QPM-15
30.1-50%	3.1-5.0	Moderately resistant	TLB	18	BJ QPM-22, BJ QPM-5, BJ QPM-6, Bajim Q-08-27, BJ QPM-11, BJ QPM-2, BJ QPM-4, BJ QPM-17, BJ QPM-24, BJ QPM-9 (HKI-163), BJ QPM-12, DQL-774-171, BJ QPM-1, BJ QPM-20, BJ QPM-21, BJ QPM-3, BJ QPM-7, BJ QPM-8
			MLB	12	BJ QPM-22, BJ QPM-20, BJ QPM-18, BJ QPM-17, BJ QPM-5, BJ QPM-3, BJ QPM-7, BJ QPM-10 (HKI-193-1), BJ QPM-1, BJ QPM-8, BJ QPM-23, BJ QPM-21
			BLSB	22	Bajim Q-08-26, BJ QPM-23, BJ QPM-12, BJ QPM-6, BJ QPM-19, BJ QPM-22, BJ QPM-18, DQL-1017-2, BJ QPM-13, BJ QPM-1, BJ QPM-3, BJ QPM-9 (HKI-163), Bajim Q-08-27, BJ QPM-4, BJ QPM-11, BJ QPM-15, BJ QPM-10 (HKI-193-1), BJ QPM-2, BJ QPM-24, BJ QPM-7, DQL-609-1-3, DQL-614-6
50.1-70%	5.1-7.0	Moderately susceptible	BLSB	7	BJ QPM-16, DQL-774-171, BJ QPM-17, BJ QPM-14, BJ QPM-20, BJ QPM-8, BJ QPM-21
>80%	>7.0-9.0	Susceptible	BLSB	1	BJ QPM-5

resistance in maize. The higher number of resistant genotypes for MLB compared to TLB suggest that resistance to MLB might be more prevalent in the test germplasm pool. This difference indicates different evolutionary pressures or selection histories in the development of these QPM lines. The absence of highly susceptible genotypes for either TLB or MLB reinforces the robustness of the genetic material against foliar blight pressures making them valuable candidates for developing durable, disease resistant maize varieties.

Twenty-two genotypes were found to be moderately resistant to BLSB with infection levels from 30% to 50%. Seven genotypes were moderately susceptible (Table 1). Only one genotype was categorized as susceptible to BLSB. The similar report have also been observed by Thakur *et al*. (2018) for BLSB.

Fall armyworm screening recorded none of the genotypes to be highly resistant or resistant to the pest. The results showed that seventeen genotypes exhibited moderate resistance to the pest with a rating of 3-5 (Table 2) which indicated that these genotypes possess useful traits for mitigating pest impact. Thirteen genotypes, however, fell into the susceptible category with a rating of 5-7 highlighting variability in pest resistance among the tested QPM inbreds indicating a need for targeted breeding strategies to reduce susceptibility further. These results align with previous studies of Sapkota *et al*. (2022) who have also reported variability in pest resistance levels in maize genotypes. None of the genotypes exhibited high susceptibility which suggests that genetic resistance to this pest may be relatively well represented within the population. Selecting genotypes that fall within the moderate resistance category would reduce pest induced yield losses and the need for chemical controls fostering more sustainable QPM production practices. Further investigation into the biochemical and morphological characteristics of such genotypes could reveal defensive mechanisms such as secondary metabolite production that contributes to reduced fall armyworm feeding and damage.

The correlation between disease and pest resistance scores was examined to understand any potential relationship between these two traits. The analysis revealed that at phenotypic level, TLB was found to be significantly positively correlated with BLSB (Fig. 1a). However, genotypic correlation coefficients showed a higher degree of association than their corresponding phenotypic correlation coefficients (Fig. 1b). This indicate that the traits under consideration had an inherent association and the environment had a smaller effect on these traits. TLB, MLB and BLSB exhibited significant and positive genotypic correlations among each other. However, all three diseases showed significant negative genotypic correlations with fall armyworm infestation. This negative association implies that genotypes more susceptible to fall armyworm tend to be less affected by these foliar blights and vice versa. This finding highlights a potential trade-off in resistance traits, suggesting that selecting for resistance to one factor may unintentionally influence susceptibility to the other. This should be considered when developing resistant genotypes for future breeding strategies and pest management practices.

The variation in resistance patterns across different biotic stresses observed in the study presents varied opportunities for breeding. Genotypes that

Table 2. Reaction to fall armyworm under natural epiphytotic conditions

S. No.	Modified Davis and Williams scale	Categorization	No. of genotypes	Genotypes
3	>3-5	Moderately resistant	17	BJ QPM-5, BJ QPM-6, BJ QPM-13, BJ QPM-14, BJ QPM-17, BJ QPM-19, BJ QPM-21, Bajim Q-08-27, BJ QPM-1, BJ QPM-2, BJ QPM-3, BJ QPM-11, BJ QPM-12, BJ QPM-15, DQL-609-1-3, DQL-614-6, DQL-1017-2
4	>5-7	Susceptible	13	BJ QPM-10 (HKI-193-1), BJ QPM-20, BJ QPM-22, BJ QPM-23, BJ QPM-24, BJ QPM-4, BJ QPM-7, BJ QPM-8, BJ QPM-9 (HKI-163), BJ QPM-16, DQL-774-171, Bajim Q-08-26, BJ QPM-18

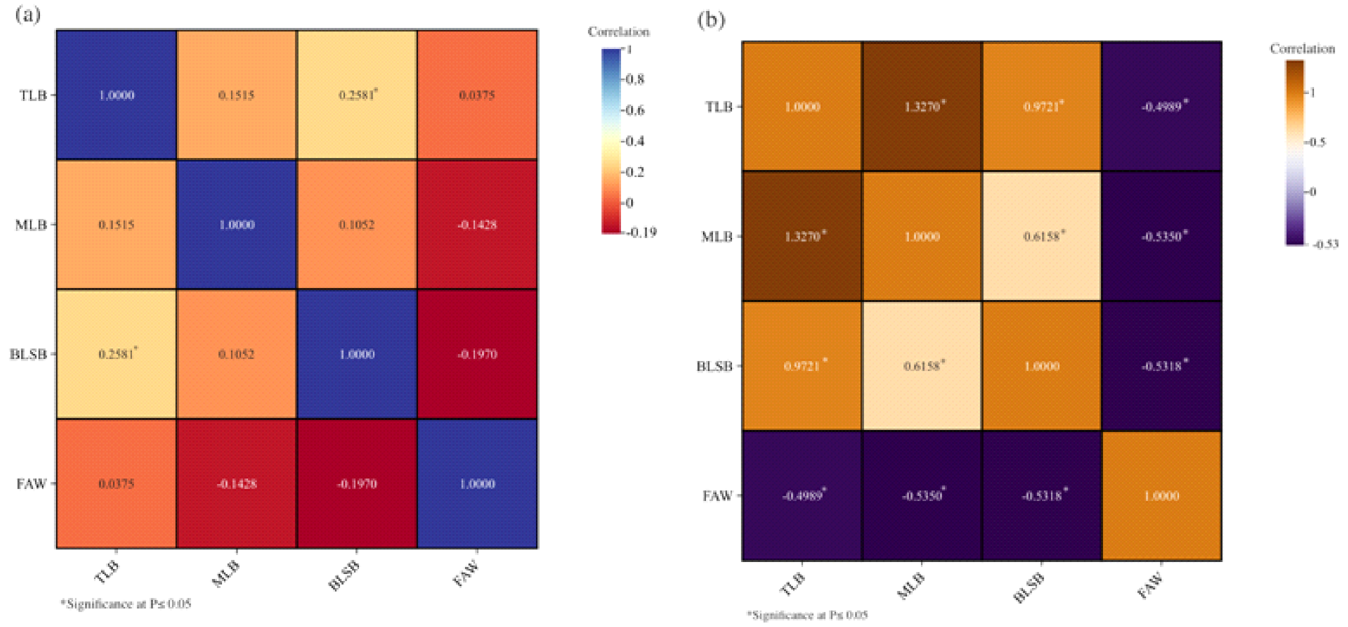

Fig. 1. Correlation between disease and pest scores at phenotypic (a) and genotypic (b) level

demonstrate resistance to multiple stresses could serve as valuable foundation material for developing resilient QPM varieties. Among all the genotypes studied, six genotypes *viz*., BJ QPM-13, BJ QPM-15, BJ QPM-19, DQL-1017-2, DQL-609-1-3 and DQL-614-6 exhibited resistance to TLB, MLB and moderate resistance to BLSB and fall armyworm. These genotypes are particularly noteworthy as they represent potential candidates for broad spectrum protection. They can be further utilized as sources of disease and insect pest resistance in QPM after screening under artificial epiphytotic conditions.

Conclusion

Across the pest and diseases evaluated, a total of six genotypes viz., BJ QPM-13, BJ QPM-15, BJ QPM-19, DQL-1017-2, DQL-609-1-3 and DQL- 614-6 exhibited moderate resistance to resistance against TLB, MLB, BLSB and FAW. These QPM inbreds can be further utilized as a source of resistance in the QPM breeding program.

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