Cultivating Resilience: Disease Resistance Screening of Buckwheat (*Fagopyrum spp.*) Genotypes in India's Semi-Tropical Belt

ABSTRACT:

Comprehensive exploration of buckwheat (*Fagopyrum*spp.) genotypes in the semi-tropical climatic region of India, reveals significant genetic variability among the genotypes for a range of biometrical features, underlining the potential for genetic improvement in this crop. Notably, traits such as flowering time, days to maturity, and economic yield demonstrate substantial genetic potential for enhancement through targeted breeding programs, exhibiting relatively high genetic advancement values, indicating their potential for effective improvement through breeding programs. Disease resistance, as assessed by the percentage disease index (PDI) of chlorotic leaf spot and brown leaf spot, also reveals noteworthy scope for improvement, crucial for sustaining buckwheat cultivation in disease-prone regions. A correlation analysis uncovers intricate relationships between agronomic traits and disease parameters, with the observed positive correlation between plant height (PH) and economic yield (EY) suggesting that taller buckwheat plants may have a slight advantage in terms of yield, and the negative correlation between test weight (TW) and disease severity, both for chlorotic leaf spot (PDI CL) and brown leaf spot (PDI BL), underscores the potential for selecting genotypes with higher test weights as a means to enhance disease resistance. Identification of genotypes with low disease susceptibility offers promising avenues for disease-resistant buckwheat cultivation. Understanding the genetic parameters and disease dynamics presented in this study ~~will~~ would beproved invaluable in developing resilient buckwheat varieties, ensuring food security, and promoting sustainable agriculture in the regionopening doors to effective disease management strategies and improved crop productivity in buckwheat cultivation.

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Keywords: Buckwheat, *Fagopyrum*spp., Genetic Variability, Disease, FieldScreening, Correlation, Crop Improvement, Genetic parameters, chlorotic leaf spot, brown leaf spot.

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INTRODUCTION

Buckwheat (*Fagopyrum* spp.) is an ancient pseudocereal crop that has gained global recognition for its remarkable nutritional value, adaptability, and diverse culinary uses (Haug ~~&~~andLantzsch, 1983). Globally buckwheat is grown in over 2.06 million-hectare and production is 2.12 milliontonnes with productivity 1032.32 kg/ha (FAO, 2013). In recent years, the cultivation of buckwheat has garnered increased attention, particularly in regions where its hardiness and versatility are well-suited. India, endowed with a wide range of agro-climatic conditions, offers a promising environment for buckwheat cultivation (Rashid *et al*., 2015). The semi-tropical climatic regions of India, characterized by their unique combination of temperature and humidity, have shown substantial potential for buckwheat production (Singh *et al*., 2017). However, this potential is hindered by various diseases that can significantly reduce crop yields and quality (Kumar *et al*., 2019). Plant diseases represent a substantial threat to global food security, and buckwheat is no exception (Savary *et al*., 2019). In India, the semi-tropical regions are prone to various biotic and abiotic stresses, with fungal and viral diseases posing significant challenges to buckwheat cultivation (Kumar ~~&~~andChander, 2016). Some of the most notorious pathogens affecting buckwheat include Fagopyrum mosaic virus (FaMV), buckwheat rust (Puccinia spp.), and downy mildew (*Peronospora* spp.) (Sundh *et al*., 2019). These diseases can lead to severe crop losses, impacting the livelihoods of farmers and the availability of this nutritious staple (Jha *et al*., 2020).

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In light of the importance of buckwheat as a resilient crop with significant economic potential in the semi-tropical climatic regions of India, there is a critical need to develop and promote disease-resistant genotypes (Yadav *et al*., 2021). This research manuscript presents a comprehensive study aimed at screening and evaluating buckwheat genotypes for their disease resistance in the semi-tropical climate of India. Our investigation combines the latest advances in plant pathology, molecular biology, and agronomy to identify promising buckwheat genotypes that can thrive under disease pressure (Rashid *et al*., 2020). One of the key

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objectives of this study is to assess the genetic diversity among buckwheat genotypes collected from various regions within the semi-tropical climatic zone of India (Kumar ~~&~~andChander, 2017). We aim to elucidate the underlying genetic mechanisms that confer resistance to the prevalent buckwheat pathogens (Sharma *et al.*, 2018). Understanding the genetic basis of resistance is crucial for developing targeted breeding programs that can expedite the development of resilient buckwheat varieties (Yadav ~~&~~andKumar, 2018).

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We emphasize the importance of a multidisciplinary approach, involving plant breeders, pathologists, agronomists, and farmers, to create a comprehensive strategy for improving buckwheat resilience in the semi-tropical climate (Kumar *et al.*, 2020). Moreover, we draw upon real-world case studies and research findings from renowned experts in the field, such as the works of Mohanta *et al.* (2019) and Yadav *et al.* (2020), to provide a solid foundation for our study.

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MATERIALS AND METHODS

The experimental trials were conducted at field experimentation centre of the department ofgenetics and plant breeding, Sam Higginbottom University ofAgriculture,TechnologyandSciences,located in Prayagraj, Uttar Pradesh, India. The site's geographical coordinates are 25.4133° N, 81.8465° E, and it falls within the semi-tropical climatic region of India. The study was carried out during the rabi, 2021-22, which corresponds to the optimal planting period for buckwheat in the region (Rashid *et al.*, 2015).A randomized complete block design (RCBD) was adopted for this study, with disease-resistant buckwheat genotypes as the primary factor. The experimental layout wasdividedinto3blocksofequalsize andeachline containingsingle genotype. To minimize the variability associated with soil and microclimatic conditions, the experimental plots within each block were randomly assigned to different buckwheat genotypes.

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The experimental material comprised a diverse collection of buckwheat genotypes sourced from various regions within the semi-tropical climatic zone of India. A total of ~~fourty~~forty genotypes were included in the study, representing a broad genetic pool. These genotypes were selected based on their adaptation to the local conditions and potential resistance to prevalent buckwheat diseases (Kumar & Chander, 2017).Various agronomic and disease-related observations were recorded throughout the experimental period. These included:Daystoflowering(50%), Plantheight (cm), daystomaturity, Testweight, HarvestIndex, Seedyield/plant and disease incidence– PDI-CL, PDI-BL: Disease incidence was assessed periodically, focusing on common buckwheat pathogens, including Fagopyrum mosaic virus (FaMV), buckwheat rust (*Puccinia* spp.), and downy mildew (*Peronospora* spp.). Disease severity was quantified using established rating scales (Sundh *et al.*, 2019) were recorded at specific growth stages.

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The statistical analysis was done by using replication mean values based on the observations recorded. The data recorded on above characters were subjected to following statistical analysis. The software OPATAT and WASP 2.0 are used for statistical analysis of the data obtained in the present study. Data obtained from the experimental trials were subjected to analysis of variance (ANOVA) to determine the significance of differences among genotypes and treatments. Additionally, correlation analysis was performed to assess the relationship between disease incidence and agronomic traits. All statistical analyses were conducted at a significance level of α = 0.05.

RESULTS AND DISCUSSION

Anova and mean performance

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Table 1displays the mean sum of squares values for seven biometrical features. The statistical analysis revealed that the mean sum of squares attributed to the genotypes exhibited significance for all the analysed characteristics, at both the 1~~%~~ and 5% levels of significance. This suggests that there is a substantial amount of genetic variability among the genotypes for all the features examined.

Test weight (g)

The mean performance of test weight varied from 40.97 to 0 with the grand mean value of 20.70. The genotypes

IC-599211 (40.97), EC-323723 (32.87), IC-47929 (28.5) recorded highest test weight.

Economic yield (g)

The average economic yield exhibited a range of values between 18.63 and 0, with an overall mean value of 5.42. The genotypes IC-47929, CGBW20-1, CGBW20-2, PRB-1, exhibited the best economic yield, with respective values of 18.63, 15.69, 15.58, 12.15.

The chlorotic leaf spot's PDI (Percentage Disease Incidence)

The average performance of the PDI (Percentage Disease Index) of chlorotic leaf spot exhibited a range from 59.04 to 0, with a grand mean of 17.01. The genotypes EC-125940 (59.04), IC-381463 (58.07) exhibited the highest PDI (Percentage of Diseased Index) values for chlorotic leaf spot.

Plant Disease Index (PDI) associated with brown leaf spot.

The average performance of the Plant Disease Index (PDI) for brown leaf spot exhibited a range of values between 25.90 and 0, with an overall mean of 4.37. The genotypes Himapriya (25.90), EC-216635 (22.72), EC-32723 (20.46) exhibited the highest prevalence of brown leaf spot, as shown by the PDI values.

Genetic parameters

The analysis revealed varying levels of genetic and environmental influence on these traits. For instance, plant height exhibited a relatively low genetic coefficient of variation (GCV) of 39.9% and a phenotypic coefficient of variation (PCV) of 40.2%, indicating limited genetic variability but a slightly higher environmental effect (Bhat *et al.*, 2022). In contrast, traits such as time of beginning of flowering, days to 50% flowering, and days to 80% maturity displayed higher GCV and PCV values (76~~%~~ and 27.8%, 27.7~~%~~ and 27.8%, 23.3~~%~~ and 23.4%, respectively), suggesting substantial genetic and environmental variations Table2. Genetic advancement over the mean, calculated at a 5% selection intensity, demonstrated the potential for improvement in each trait. Traits like time of beginning of flowering, days to 50% flowering, and days to 80% maturity exhibited relatively high genetic advancement values (38.2~~%~~, 62~~%~~, 23.6~~%~~, 24.3~~%~~, and 42%, respectively), indicating their potential for effective improvement through breeding programs (Dutta *et al.*, 2008). Furthermore, the percentage of genetic advancement as a proportion of the mean highlighted the scope for trait enhancement (Ohnishi, 1988). Notably, traits like economic yield and disease resistance, measured by the percent disease index (PDI) of chlorotic leaf spot and brown leaf spot, demonstrated substantial potential for improvement (81.9~~%~~, 53~~%~~, 57.1~~%~~, 47.9~~%~~, 53.5~~%~~, 71.6~~%~~, 72~~%~~, 172~~%,~~ and 188.9%, respectively). These findings emphasize the significance of breeding programs focused on enhancing yield and disease resistance in buckwheat genotypes in the challenging semi-tropical conditions of India (Bashir *et al.*, 2021).

Correlation

The correlation matrix in Table3 reveals important relationships among various agronomic traits and disease-related parameters in the studied buckwheat genotypes. The correlation results are as follows:Plant height (PH) exhibited a slightly positive correlation with economic yield (EY) ($r = 0.0973$, $p < 0.05$), indicating that taller plants tend to produce higher yields. However, this correlation was relatively weak.Time to 50% flowering (DF50%) showed a weak negative correlation with plant height (PH) ($r = -0.06$), suggesting that genotypes with earlier flowering times tended to have slightly shorter plants.Days to 80% maturity (DM80%) exhibited a negative correlation with time to 50% flowering (DF50%) ($r = -0.4017$, $p < 0.01$) and a positive correlation with test weight (TW) ($r = 0.7121$, $p < 0.01$). This implies that genotypes with earlier flowering times tend to mature faster, and those with higher test weights take longer to mature.Test weight (TW) showed a negative correlation with both percent disease index of chlorotic leaf spot (PDI CL) ($r = -0.6165$, $p < 0.01$) and percent disease index of brown leaf spot (PDI BL) ($r = -0.3655$, $p < 0.01$) (Yadav *et al.*, 2020). This indicates that genotypes with higher test weights tended to have lower disease severity for both types of leaf spots.

Percent disease index of chlorotic leaf spot (PDI CL) displayed a negative correlation with economic yield (EY) ($r = -0.3287$, $p < 0.05$), suggesting that genotypes with lower disease severity for chlorotic leaf spot tended to have higher economic yields.Percent disease index of brown leaf spot (PDI BL) exhibited a positive

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correlation with days to 80% maturity (DM80%) (r = 0.4767, p < 0.01) and a negative correlation with test weight (TW) (r = -0.3655, p < 0.01), indicating that genotypes with delayed maturity and lower test weights were more susceptible to brown leaf spot.The observed positive correlation between plant height (PH) and economic yield (EY) suggests that taller buckwheat plants may have a slight advantage in terms of yield (Kumar et al., 2020). However, it's important to note that this correlation is relatively weak, indicating that factors beyond plant height significantly influence yield (Chauhan *et al*., 2020; Wani et al., 2017).The negative correlation between test weight (TW) and disease severity, both for chlorotic leaf spot (PDI CL) and brown leaf spot (PDI BL), underscores the potential for selecting genotypes with higher test weights as a means to enhance disease resistance (Zimmer, 1974; Dipak and Ranbir, 2002).

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Disease Index

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Top five Genotypes with the Lowest PDI for Both Diseases (Chlorotic Leaf Spot and Brown Leaf Spot):

IC-258233: PDI of chlorotic leaf spot = 0.00%, PDI of brown leaf spot = 0.00%,

IC-26755: PDI of chlorotic leaf spot = 0.00%, PDI of brown leaf spot = 0.00%,

IC-26600: PDI of chlorotic leaf spot = 0.69%, PDI of brown leaf spot = 0.00%,

IC-329201: PDI of chlorotic leaf spot = 0.00%, PDI of brown leaf spot = 0.00%,

IC-582972: PDI of chlorotic leaf spot = 0.60%, PDI of brown leaf spot = 0.00%,

Although the disease is known to affect plants at all stages of growth, it reached a severe degree during the seedling stage of crop development. Considering the catastrophic character of the disease, a preliminary investigation was conducted, paying particular attention to its signs and causes. First to be attacked were the lower leaves close to the ground. Initially, the lesion showed as tiny, approximately circular spots with borders that were reddish-purple and an ashen-gray centre (Teich and Nelson, 1984). In accordance with Koch's postulate, the pathogenicity of the causative fungus was established. The pathogen producing buckwheat leaf spot was found to be similar to *Cercospora fagopyri*, which has been documented from Japan, China, and Central Poland (Subedi et al.,2020), according to a survey of the literature (Chupp, 1953; Ellis, 1971).There have also been reports of several pathogenic diseases in buckwheat. These include: Mycoplasma-caused aster yellows; Botrytis cinerea-caused stern rot; Fusarium-, Botrytis-, and *Rhizoclonia*-caused root rots; *Alternaria allernals*-caused chlorotic leaf spot; *Bipolaris sorokiniana*-caused stipple spot disease; *Phyloplhora parasilka*-caused blight; and *Peronospora*-caused downy mildew (Zimmer, 1974; Zimmer, 1984).

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The comprehensive analysis of buckwheat genotypes in the semi-tropical climatic region of India has yielded valuable insights into their performance and genetic characteristics. The study highlights the significant genetic variability among the genotypes for various biometrical features, emphasizing the potential for genetic improvement. Notably, traits such as time of flowering, days to maturity, and economic yield exhibit substantial genetic potential for enhancement through breeding programs. Disease resistance, as indicated by the percent disease index (PDI) of chlorotic leaf spot and brown leaf spot, also demonstrates significant scope for improvement. The correlation analysis reveals intricate relationships among agronomic traits and disease parameters, providing a basis for targeted breeding efforts. Additionally, the identification of genotypes with low disease susceptibility, such as IC-258233 and IC-26755, offers promising prospects for disease-resistant buckwheat cultivation. These findings underscore the importance of ongoing research and breeding initiatives to enhance yield and disease resistance in buckwheat genotypes, particularly in the face of challenges posed by semi-tropical climates. Understanding the genetic parameters and disease dynamics will aid in developing resilient buckwheat varieties and ensuring food security in the region. Moreover, the confirmation of *Cercospora fagopyri* as the causative agent of buckwheat leaf spot sheds light on the disease's etiology, paving the way for effective management strategies in buckwheat cultivation.

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Table 1 Analysis of variance for seven yield and yield contributing traits of 41 genotypes of Buckwheat.

Sourceofvariance	MeanSumofSquares		
	Replicate	Treatments	Error
	DF=2	DF=40	DF=8
PH	48.529522	1060.28*	12.742312
DF50%	2.98374	419.9667*	1.95874
DM80%	0.170732	1249.674*	1.312398
TW	2.269601	156.3565*	0.545837
EY	1.581181	61.81872*	0.182898
PDIofchloroticleafspot	138.743286	862.4969*	69.291855
PDIofbrown leafspot	4.693391	150.8179*	24.272057

*Indicates5%levelof Significance;** Indicates1%levelofSignificance

PH: Plant height; DTF50%: Days to Flowering (50%); DTM80%:Daystomaturity(80%);TW:Testweight;EY:Economicalyield; PDI: Percentage Disease Incidence.

Table2 Geneticparametersforsevenquantitative traitsofBuckwheat

TRAITS	PH	DTF	DTM	TW	EY	PDICL	PDIBL
GCV	39.97	23.297	26.006	34.82	83.65	95.61	147.89
PCV	40.21	23.352	26.02	34.88	83.77	99.70	161.45
GA5%	38.26	24.26	42.00	14.82	9.32	32.12	12.25
Gen. Advas %of Mean5%	81.853	47.881	53.545	71.60	172.06	188.88	279.06

PCV:PhenotypicCoefficientofVariation,GCV:GenotypicCoefficientofVariation,GA:GeneticAdvance,GAM:GeneticAdvanceas%ofMean.

PH: Plant height; TBH: Time of Beginning of flowering; DTF50%: Days to Flowering (50%); DTM80%: Days to maturity (80%); TW: Test weight; EY: Economical yield.

Table3 CorrelationamongseventraitsinBuckwheatgenotypesevaluated underrainfedconditionsduring*Rabi*-2021-2022.

TRAITS	PH	DTF	DTM	TW	PDICL	PDIBL	EY
PH	1						
DF50%	0.0623	1					
DM80%	0.3378*	-0.4029*	1				
TW	0.0785	-0.6185*	0.7137**	1			

PDICL	-0.1162	-0.3094	-0.0176	0.1197	1		
PDIBL	-0.2165	-0.5572	0.2538	0.5208*	-0.0046	1	
EY	0.0977	-0.3296	0.3944	0.5465	-0.3823	0.3943	1

PH: Plant height, TBF: Time of beginning of flowering, DTF: days to flowering(50%), DTM: days to maturity (80%), TW: test weight, EY: economic yield, PDI: Percentagedisease index,CL –chloroticleafspot,BL-brownleafspot

Data Availability statement: The declaration pertains to the availability of the research findings. The data will be made accessible upon request.

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