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SCREENING OF FINGER MILLET GENOTYPES FOR RESISTANCE TO MAGNAPORTHE GRISEA IN NORTHWESTERN ETHIOPIA

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ABSTRACT

Finger millet is one of the staple cereal crops cultivated in Ethiopia. However, its production is challenged by blast disease. This study aimed to screen finger millet genotypes for resistance to blast under natural epiphytotic conditions and to assess the yield potential of resistant genotypes during the 2022 and 2023 main cropping seasons. A total of 64 finger millet genotypes, including both standard and local checks, were evaluated using a square lattice design with two replications at the Adet and Finote Selam experimental sites. Disease severity was scored from the initial onset using a 0–9 rating scale for leaves and a 0–5 scale for necks and heads. At Adet in 2022, 13 genotypes (20.31%) were resistant, 4 (6.25%) moderately resistant, 17 (26.56%) moderately susceptible, and 30 (46.88%) susceptible. In 2023, 14 genotypes (21.88%) were resistant, 11 (17.19%) moderately resistant, 24 (37.50%) moderately susceptible, and 15 (23.44%) susceptible. At Finote Selam in 2022, 3 genotypes (4.69%) were moderately resistant, 7 (10.94%) moderately susceptible, 32 (50.00%) susceptible, and 22 (34.38%) highly susceptible. In 2023, 2 genotypes (3.13%) were moderately resistant, 6 (9.38%) moderately susceptible, 38 (59.38%) susceptible, and 18 (28.13%) highly susceptible. The variation in genotype responses across locations and years can be attributed to differing ecological factors. Notably, genotypes G7 and G20 demonstrated high yield potential but were susceptible to blast, whereas G13 and G61 showed low terminal disease severity but lower yields. Crossing high-yielding susceptible genotypes with resistant low-yielding ones may offer an effective breeding strategy. Incorporating resistant and moderately resistant genotypes into cultivation and breeding programs can improve production, mitigate blast impact, and reduce farmers' reliance on chemical fungicides, ultimately lowering production costs and minimizing environmental harm.

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INTRODUCTION

Finger millet (*Eleusine coracana* (L) Gaertn) is a staple food crop for millions of people living in the tropical, and subtropical regions of Asia, and Africa (Krishna *et al.*, 2020). Among the small millets, it is the most extensively cultivated, with the largest area under cultivation (Maharajan *et al.*, 2019). Finger millet is cultivated over 4.5 million hectares, about five million tons produced

worldwide, with over 25 countries in Africa, and Asia involved in its cultivation. The global millet production is estimated to be 27.8 million tons, experiencing a decline of 0.9% every year (FAO, 2022).

Finger millet is recognized as a vital plant genetic resource for agriculture, and food security, especially in areas with poor, and marginal soils (Gupta *et al.*, 2017). It has numerous agronomic benefits, including resistance to certain pests, and diseases, adaptability to various environmental conditions, good yield potential, a short growing season, less impute requirement, and tolerance to salinity, and waterlogging (Prasad *et al.*, 2020). Furthermore, finger millet outperforms staple cereals such as rice, and wheat in nutritional value, rich in dietary fiber, iron, zinc, calcium, phosphorus, potassium, vitamin B, and essential amino acids. This makes it advantageous for those suffering from diabetes, heart problems, and high blood pressure due to its health benefits (Teklu *et al.*, 2024; Srivastava and Sharma, 2014).

In Ethiopia, finger millet is an essential food crop, including in the Amhara region, where it is mainly cultivated under rain-fed conditions (Gebre *et al.*, 2018). In 2024, around 445,000 hectares of land were used for its cultivation, resulting in a production of 125,000 metric tons with an average yield of 2.47 metric tons per hectare. Yet, in the last five years, the yield has decreased by an average of 2% (CSA, 2024). The Amhara region accounts for half of Ethiopia's finger millet production (CSA, 2024). Despite its significance, the productivity lags compared to other cereals due to various biotic, abiotic, and socioeconomic factors (Gebreyohannes *et al.*, 2021). Key problems include blast disease, insect pests (Gashu *et al.*, 2024), drought, poor agronomic practices, and lodging (Admasu and Belete, 2020).

Among these constraints, blast disease caused by *Magnaporthe grisea*, is a significant biological threat to finger millet yield, utilization, and marketability, particularly in East Africa (Chung *et al.*, 2020). The disease can affect finger millet at any growth stage, leading to yield reductions of 20–50%, and in severe cases, total crop loss (Odeph *et al.*, 2020). In Ethiopia, it is a great constraint, with an incidence rate of 57.9%, and a severity of 23.7%, causing average yield losses of 41.4% (Gashaw *et al.*, 2014).

A variety of management strategies have been implemented to manage blast disease, such as cultural practices, fungicide applications, biocontrol agents, botanicals, and host plant resistance (Odeph *et al.*, 2021). Among these, host plant resistance is considered as the most sustainable and cost-effective method, especially for farmers with limited resources (Pathania *et al.*, 2021). Utilizing resistant varieties can reduce dependence on chemical inputs and support sustainable agricultural practices. However, research indicates that numerous farmers are not familiar with blast-resistant varieties, emphasizing the necessity for increased awareness, and application of blast-resistant varieties offer a practical solution(Mbinda and Masaki, 2021).

However, resistance is mainly controlled by major genes, which are susceptible to breakdown over time(Wang *et al.*, 2017). Therefore, identifying resistant genotypes specific to certain regions, and integrating them into local agricultural practices provides an effective, economical, and environmentally friendly approach to managing blast disease (Ranganatha *et al.*, 2022). This highlights the need for continuing efforts to develop high-yielder varieties with durable genetic resistance to blast. Although resistant varieties play a crucial role in sustainable agriculture, there is limited research on the resistance level of Ethiopian indigenous finger millet genotypes to blast disease. Assessing the resistance levels of these genotypes is vital not only for the development of improved varieties but also for ensuring food security in areas where blast disease significantly limits its production. Therefore, this study aims to evaluate the resistance levels of selected finger millet genotypes to blast disease, providing valuable insights for future breeding initiatives. The study also aimed to address research questions: what are the resistance levels of Ethiopian indigenous finger millet genotypes to blast disease, and how these results can support in improving finger millet production, and food security.

MATERIALS AND METHODS

Description of the Study Areas

The research was carried out in the experimental stations of Adet, and Finote Selam, which are located in the Yilmana Densa, and Jabitenan districts, respectively (Figure 1).

Adet is located at an elevation of 2,220 meters above sea level, found at 11°17'21.1"N latitude, and 37°28'45.2"E longitude. This area has a minimum temperature of 11.0°C, and a maximum temperature of 26.8°C, with an average annual rainfall of 1,372 mm. The main soil type found in Adet is Nitosols (Mihretie *et al.*, 2020).

Finote Selam is at an altitude of 1,947 meters, located at 10°41'43.6"N latitude, and 37°15'02.1"E longitude. The area receives an average annual rainfall of 1,250 mm, with temperatures ranging from a minimum of 14°C to a maximum of 32°C. The soil type in Finote Selam is also Nitosols, characterized by a pH of 5.3 (Mengesha *et al.*, 2020).

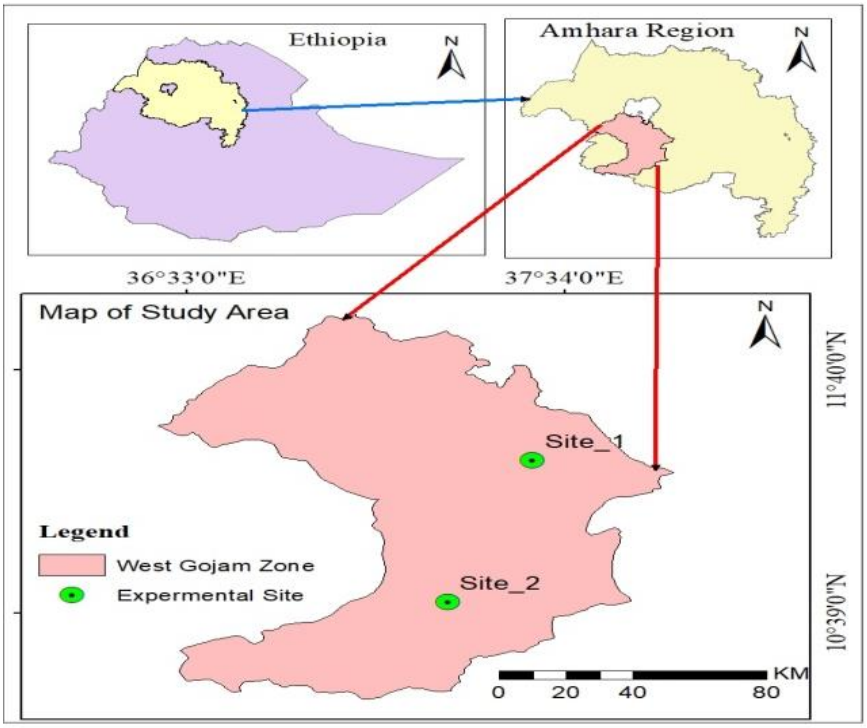


Figure 1. Map of the study area at Finote Selam (Site-1) and Adet (Site -2).

The daily weather data, which includes temperature, relative humidity, and precipitation, was collected for both experimental districts from the Western Amhara Meteorological Services Centre (WAMSC) located in Bahir Dar, Ethiopia. This information was analyzed to assess its relationship with disease severity (Wekesa *et al.*, 2019), and is illustrated in Figure 2.

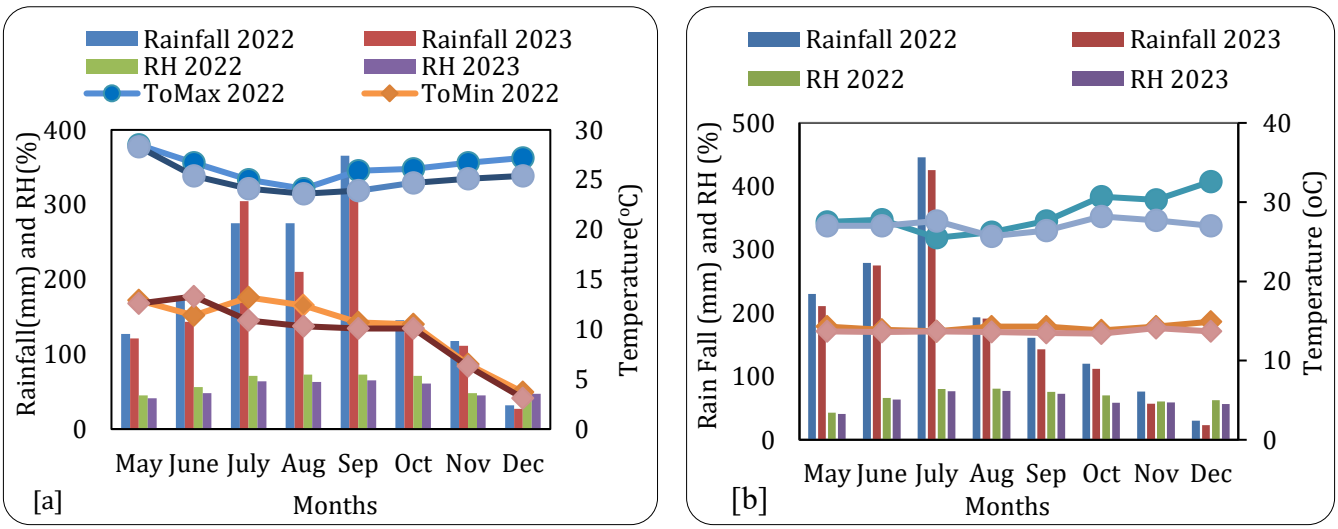


Figure 2. Mean monthly rainfall, relative humidity, and temperature of the study districts ([a] Adet, and [b] Fenotselam). (WAMSC, 2022 and 2023).

Understanding how environmental factors affect the spread of blast disease is essential for formulating disease management strategies fit to specific locations. These strategies could involve modifying planting dates or choosing appropriate genotypes that are well-adapted to specific agro-climatic environments (Asibi *et al.*, 2019).

Experimental Materials

The experiment included 62 germplasm genotypes (breeding lines) along with Jabi-blast resistance as a standard, and one local check. The genotypes were obtained from the Ethiopian Agricultural Research Institute (Adet Agricultural Research Centre) and listed below with their pedigrees (Table 1).

Table 1. Pedigrees of finger millet genotypes included in the study.

Genotype	Pedigree	Genotype	Pedigree	Genotype	Pedigree	Genotype	Pedigree
1	P*N-P#17	17	P*N-P#31	33	D*N-P#18	49	N*G-P#34
2	N*W-P#1	18	N*P-P#17	34	W*N-P#P1-1	50	N*B-P#5
3	W*N-P#5	19	N*G-P#30	35	N*T-P#17	51	W*N-P#8
4	W*N-P#3	20	N*T-P#19	36	N*D-P#1	52	W*N-P#6-2
5	N*G-P#18	21	N*G-P#35	37	N*T-P#16	53	N*G-P#22
6	N*P-P#8	22	N*T-P#4	38	N*T-P#21	54	N*G-P#26
7	N*B-P#19	23	N*P-P#10	39	N*G-P#33	55	N*G-P#20-2
8	W*N-P#1-2	24	N*T-P#20	40	B*N-P#25	56	N*G-P#11
9	N*T-P#7	25	P*N-P#5	41	P*N-P#35	57	N*G-P#10
10	D*N-P#7	26	N*P-P#24	42	W*N-P#11-1	58	N*G-P#8
11	N*T-P#25	27	N*B-P#6	43	N*T-P#28	59	N*G-P#30-1
12	N*T-P#2	28	N*G-P#1	44	B*N-P#1	60	N*W-P#4
13	N*T-P#12	29	P*N-P#32	45	N*P-P#9	61	W*N-P#6-3
14	P*N-P#13	30	N*G-P#20-1	46	N*G-P#32	62	B*N-P#10
15	N*T-P#22	31	N*G-P#31	47	P*N-P#30-2	63	St. check (Jabi)
16	N*B-P#7	32	N*P-P#4	48	P*N-P#27	64	Local check

Experimental Design and Procedure

A square lattice design (8 × 8) with two replications was used (Manyasa *et al.*, 2019). The plot sizes comprised four rows, each measuring 2 meters in length, and 1.2 meters in width, resulting in an overall plot area of 2 m × 1.2 m. The spacing between blocks, replications, plots, and rows was set at 1 m, 1.5 m, 0.5 m, and 0.3 m, respectively. A seed rate of 15 kg/ha was implemented, and hand-drilling was used for planting at intervals of 15 cm. Fertilizer application included 50 kg/ha of urea and 121 kg/ha of NPS. Urea was applied during the sowing and tillering stages, while NPS was applied at the time of planting. Other agricultural practices were conducted as recommended for the crop.

Data Collection

Disease assessment

Leaf blast disease was evaluated from seedling to booting stages by measuring the percentage of leaf area affected by blast lesions at 10-day intervals using 0–9 disease severity scale, following IRRI standards (IRRI, 2014).

For finger, and neck blast disease evaluations were performed at physiological maturity, and recorded using a modified scoring system (Bal *et al.*, 2020): 0 = No incidence, 1 = <5% infection, 2 = 5–10% infection, 3 = 11–25% infection, 4 = 26–50% infection, and 5 = >50% infection on neck, and finger areas. The categorization of genotypes for leaf blast resistance or susceptibility was determined by disease severity (%), dividing them into six classifications: Resistant (R): 0–5%, Moderately Resistant (MR): 6–25%, Moderately Susceptible (MS): 26–50%, Susceptible (S): 51–75%, and Highly Susceptible (HS) : >75% (Kumari *et al.*, 2022).

For neck, and finger blast, classification was determined as follows (Wekesa *et al.*, 2019): Highly Resistant (HR) : <10% infection, Resistant (R): 11–30% infected, Moderately Resistant (MR): 31–40% infected, Moderately Susceptible (MS): 41–50% infected, Susceptible (S): 51–70% infected, and Highly Susceptible (HS): 71–100% infection on neck, and finger parts.

Disease incidence was calculated by using the number of infected plants, and expressed as a percentage (DI%) of the

total number of plants assessed using the formula of Teng and James (2001). The percent disease intensity (PDI) was calculated by using the following formula as used by Patro *et al.* (2020), while The blast disease severity scores that were taken at different times were used to calculate the area under the disease progress curve (AUPDC) of each genotype using the formula used by Wekesa *et al.* (2019):

$$Disease\ incidence\ \% = \frac{Infected\ plants}{Total\ plants} \times 100$$

$$PDI\ for\ severity = \frac{sum\ of\ individual\ disease\ ratings}{No.of\ observations\ accessed\ \times Maximum\ disease\ rating} \times 100$$

$$\text{AUDPC} = \sum_{i=1}^{n-1} 0.5(\text{Xi} + \text{Xi} + 1)(ti + 1 - ti)$$

Where, "*x*i" is the cumulative disease severity expressed as a proportion at the ith observation; "ti" is the time (days after planting) at the ith observation and "n" is the total number of observations.

Yield and yield components

The following agronomic traits were assessed: Physiological Maturity (DM), Plant Height (PH), Number of Tillers per Plant (NTP), Number of Ears per Plant (NEP), and Grain Yield (GY) (kg/ha), among others.

Data Analysis

The collected data was statistically analyzed using SAS software (version 9.4) (SAS, 2009). Data was assessed for normal distribution, and homogeneity of error variance (F-test). Since the disease data did not meet the normality assumption, it was transformed using arcsine before analysis (Jalalifar *et al.*, 2023).

Data on DI%, PDI, AUDPC, grain yield, and yield components subjected to analysis of variance (ANOVA) to identify significant differences among treatment means, and error variances. Considering the variability in results across various locations, and years, separate analyses were performed for each.

To separate treatment means, Duncan's Multiple Range Test (DMRT) was used at a significance level of $p < 0.05$ (Gomez and Gomez, 1984). Furthermore, genotypes were clustered according to their AUDPC values using the unweighted pair group method with arithmetic mean (UPGMA) (Bhatta *et al.*, 2017).

RESULTS

Occurrence and Intensity of Blast disease in Various Finger Millet Genotypes

The statistical analysis revealed significant genotypic differences ($P<0.05$) in disease incidence (DI) and severity. Furthermore, the factors of location (Loc), year, treatment (TRT), and their interactions, particularly Loc × TRT and Loc × Year, significantly influenced the majority of disease, and agronomic parameters (Table 2). The average severity of leaf blast was greater in the 2022 cropping season (20.69%) in comparison to 2023 (14.73%) at Adet. Likewise, at Finote Selam, the mean leaf severity for the 2022 season (38.53%) exceeded that of 2023 (35.94%). In the 2022 assessment at Finote Selam, leaf incidence varied from 32.18% to 100%, with an average of 69.94%, while severity ranged from 16.02% to 55.41%. For the 2023 cropping season, blast incidence varied between 22.45% and 84.55%, yielding a mean of 58.38%, with severity ranged from 6.87% to 57.01% (Table 3).

Neck and Head Blast Incidence and Severity of Selected Finger Millet Genotypes

Analysis of variance revealed significant differences ($p < 0.05$) in neck blast incidence, and severity among the genotypes across both locations, and years, as illustrated in Table 4. In 2022, the incidence of neck blast at Adet varied from 0% to 77.54%, with an average of 51.52%, whereas at Finote Selam, it ranged from 40.87% to 100.00%, is an average of 78.28%. For 2023, the incidence at Adet ranged between 0% and 66.42%, with a mean of 47.16%, while at Finote Selam, it varied from 43.76% to 89.64%, is an average of 68.11%. In terms of severity, the range at Adet for 2022 was from 0% to 51.05%, and at Finote Selam, it was from 37.89% to 85.82%. During both growing seasons, the highest average neck blast severity scored at Finote Selam (56.09%) in comparison to Adet (38.83%) in 2022 and consistently higher at Finote Selam (62.51%) than at Adet (33.7%) in 2023. Some genotypes demonstrated greater resistance to neck blast compared to the standard check, Jabi (Table 4).

Table 2. The effect of locations, year, treatments, and their interactions on yield and yield components, and disease parameters.

Trait	Mean	SEM (±)	Mean square									
			Loc	Year	Year*Loc	TRT (df=63)	Year*TRT (df=63)	Loc*TRT (df=63)	Loc*Year* TRT (df=63)	Error (df=234)	CV (%)	R2 (%)
DM	147.41	3.12	285.01***	190.13**	1540.2***	58.87***	28.66*	33.75**	17.99^{ns}	19.52	3.16	0.73
PH	77.63	5.13	3533.3***	12053.2***	278.19*	528.15***	105.51^{ns}	45.77^{ns}	53.65^{ns}	52.62	9.83	0.85
NTP	3.77	0.52	33.21***	64.13***	13.52***	2.08***	0.77*	0.63^{ns}	0.52^{ns}	0.54	24.67	0.78
NEP	5.39	0.72	0.14^{ns}	0.01^{ns}	288.6***	3.84***	1.15ns	2.13***	1.11^{ns}	1.05	23.69	0.79
GY	3084	474	3700052**	106815857***	3121099.7**	2260674.2***	522327^{ns}	5483567^{ns}	158429.7^{ns}	448245	23.87	0.79
LBI	49.81	11.4	105276***	15607.4***	35.84ns	760.84***	219.1^{ns}	566.6***	160.54^{ns}	257.8	41.05	0.8
NBI	61.40	10.3	74528***	7265.02***	1292.45*	973.95***	140.5 ^{ns}	366.94**	159.4^{ns}	209.33	32.02	0.8
HBI	68.21	9.76	56988***	18239.9***	2885.86***	961.42***	123.12^{ns}	447.1***	98.6^{ns}	190.55	27.63	0.81
LBS	27.47	7.18	48756***	365.73^{ns}	2345.2***	271.44***	107.9^{ns}	209.5***	76.4^{ns}	103.1	36.39	0.81
NBS	47.79	9.02	67804***	55.62^{ns}	4230.3***	570.15***	202.3^{ns}	221.1^{ns}	302.9***	162.73	36.23	0.81
HBS	53.19	9.13	61139***	1343.2**	619.3^{ns}	927.99***	111.3^{ns}	357.4***	79.3^{ns}	166.64	31.29	0.81

Significance codes: '***' 0.001 '**' 0.01 '*' 0.05, Loc = location, df = Degree of freedom, TRT= treatment, SEM= standard error of the mean, DM= Days to physiological maturity, PH = Plant height (cm), NTP= number of tiller per plant, NEP = Number of ears per plant, GY = Grain yield (kg/ha), LBI= leaf blast incidence, NBI = neck blast incidence, HBI= head blast incidence, LBS= leaf blast severity, NBS = Neck blast severity, HBS = Head blast severity, LBAUDPC, NBAUDPC and HBAUDPC= leaf, neck and head area under disease progress curve respectively, and CV = Coefficient of variation.

Table 3. Percent Mean leaf incidence and severity in 2022 and 2023 cropping season.

	Adet				Finote Selam			
	2022		2023		2022		2023	
Genotypes	LBI	LBS	LBI	LBS	LBI	LBS	LBI	LBS
G5	52.16^{a-d}	25.09^{a-d}	47.33^{a}	21.3^{abc}	64.15^{c-j}	30.06^{f-p}	38.00^{h-l}	19.36^{mno}
G6	16.09^{b-e}	6.01^{bcd}	0.00^{bc}	0.00^{c}	77.52^{a-h}	43.19^{a-k}	42.22^{g-l}	25.05^{h-o}
G7	55.74^{a-d}	29.04^{a-d}	27.88^{abc}	13.60^{abc}	62.19^{c-j}	32.85^{d-p}	27.88^{abc}	13.60^{abc}
G10	25.60^{a-e}	14.15^{a-d}	0.00^{bc}	0.00^{c}	82.55^{a-e}	43.87^{a-i}	72.53^{a-e}	47.99^{a-h}
G13	26.76^{a-e}	15.43^{a-d}	35.56^{abc}	16.22^{abc}	43.32^{ijk}	18.92^{nop}	28.98^{kl}	20.62^{mno}
G14	0.00^{e}	0.00^{d}	0.00^{c}	0.00^{c}	58.44^{d-k}	31.10^{e-p}	53.51^{b-k}	31.46^{c-n}
G16	12.38^{cde}	3.03^{cd}	10.07^{abc}	3.03^{bc}	81.62^{a-f}	40.32^{a-m}	65.25^{a-h}	46.02^{a-j}
G19	26.76^{a-e}	15.97^{a-d}	10.07^{abc}	2.38^{bc}	76.54^{a-h}	40.24^{a-m}	45.93^{d-l}	28.33^{c-o}
G20	70.48^{a}	38.69^{a}	51.17^{a}	25.71^{ab}	94.97^{ab}	50.42^{a-d}	57.96^{a-k}	37.74^{a-n}
G21	45.09^{a-e}	19.39^{a-d}	38.26^{abc}	15.58^{abc}	50.01^{g-k}	25.48^{j-p}	33.25^{i-l}	17.98^{no}
G27	64.35^{ab}	38.22^{a}	46.32^{a}	24.64^{abc}	90.70^{abc}	51.05^{abc}	80.60^{ab}	55.38^{ab}
G30	51.17^{a-d}	27.77^{a-d}	10.07^{abc}	3.33^{bc}	65.32^{b-j}	36.62^{b-n}	43.32^{e-l}	24.54^{i-o}
G31	0.00^{e}	0.00^{d}	0.00^{c}	0.00^{c}	64.35^{c-j}	33.36^{c-p}	42.85^{f-l}	24.43^{i-o}

G32	16.09^{b-e}	5.41^{bcd}	0.00^{c}	0.00^{c}	60.13^{d-k}	29.29^{f-p}	72.45^{a-f}	49.10^{a-f}
G33	21.91^{a-e}	9.65^{a-d}	19.18^{abc}	8.66^{abc}	82.63^{a-e}	43.48^{a-j}	43.32^{e-l}	23.25^{j-o}
G35	12.38^{cde}	3.03^{cd}	10.07^{abc}	2.83^{bc}	75.54^{a-h}	36.56^{b-n}	69.15^{a-g}	47.37^{a-i}
G36	25.60^{a-e}	14.13^{a-d}	10.07^{abc}	2.38^{bc}	74.54^{a-h}	37.23^{b-m}	31.13^{jkl}	21.02^{l-o}
G39	26.76^{a-e}	15.01^{a-d}	14.34^{abc}	6.79^{abc}	80.59^{a-f}	41.23^{a-l}	75.54^{a-d}	51.28^{a-d}
G41	24.75^{a-e}	6.43^{bcd}	0.00^{bc}	0.00^{c}	70.50^{a-i}	35.69^{b-o}	46.16^{d-l}	27.91^{e-o}
G44	35.26^{a-e}	21.09^{a-d}	27.88^{abc}	14.89^{abc}	51.70^{f-k}	23.14^{l-p}	74.54^{a-d}	51.52^{abc}
G45	50.01^{a-e}	24.92^{a-d}	41.08^{abc}	18.83^{abc}	70.51^{a-i}	34.38^{b-o}	53.39^{b-k}	33.34^{b-n}
G49	36.79^{a-e}	15.54^{a-d}	19.18^{abc}	9.44^{abc}	90.75^{abc}	48.43^{a-e}	70.40^{a-g}	50.31^{a-e}
G50	49.79^{a-e}	26.44^{a-d}	32.95^{abc}	18.68^{abc}	56.39^{e-k}	16.02^{p}	67.34^{a-h}	41.11^{a-n}
G51	65.25^{ab}	35.57^{ab}	49.79^{a}	27.17^{ab}	100.00^{a}	55.41^{a}	80.54^{ab}	57.01^{a}
G52	48.64^{a-e}	22.45^{a-d}	39.05^{abc}	17.99^{abc}	48.78^{h-k}	22.83^{m-p}	56.73^{a-k}	38.08^{a-n}
G53	41.36^{a-e}	19.3^{a-d}	31.98^{abc}	12.57^{abc}	78.54^{a-h}	42.78^{a-k}	42.22^{g-l}	25.53^{g-o}
G57	27.76^{a-e}	9.94^{a-d}	0.00^{c}	0.00^{c}	71.51^{a-i}	37.11^{b-m}	53.79^{b-k}	37.05^{a-n}
G60	0.00^{e}	0.00^{d}	0.00^{c}	0.00^{c}	35.26^{jk}	18.47^{op}	63.28^{a-h}	44.47^{a-j}
G61	10.07^{de}	2.83^{cd}	34.48^{abc}	14.51^{abc}	51.97^{f-k}	25.18^{l-p}	70.50^{a-g}	48.81^{a-g}
G62	52.36^{a-d}	28.02^{a-d}	43.76^{abc}	21.38^{abc}	82.54^{a-e}	43.09^{a-k}	79.54^{abc}	54.91^{ab}
Std. check (Jabi)	25.6^{a-e}	13.18^{a-d}	19.18^{abc}	10.26^{abc}	61.19^{c-k}	28.38^{g-p}	22.45^{l}	6.87^{o}
Local check	53.48^{a-d}	31.61^{abc}	42.36^{abc}	26.23^{ab}	68.47^{b-i}	43.44^{a-j}	58.81^{a-j}	41.70^{a-m}
Mean	40.73	20.69	30.22	14.73	69.94	35.94	58.38	38.53
SEM(±)	3.20	2.46	2.44	2.17	2.47	1.91	2.44	2.17
CV (%)	41.05	42.02	38.13	39.57	19.89	24.76	32.23	36.96
Sig. (5%)	ns	ns	ns	ns	**	**	**	**

*Means with the same letter along the column are not significantly different

Table 4. Percent mean neck incidence and severity in western Amhara, Ethiopia.

	Adet				Finote Selam			
	2022		2023		2022		2023	
Genotypes	NBI	NBS	NBI	NBS	NBI	NBS	NBI	NBS
G5	38.27^{a-f}	44.36^{a-d}	61.19^{ab}	45.56^{a-d}	51.92^{uvw}	33.02^{uvw}	52.29^{r-w}	41.79^{tuv}
G6	24.41^{b-f}	52.65^{abc}	39.75^{a-h}	27.31^{a-i}	78.54^{d-s}	57.38^{g-q}	43.76^{w}	37.89^{v}
G7	61.16^{a-d}	25.01^{a-e}	54.64^{a-d}	38.95^{a-f}	89.06^{a-m}	59.26^{e-p}	79.54^{a-g}	73.02^{a-h}
G8	66.15^{abc}	58.71^{a}	57.95^{a-d}	43.23^{a-e}	91.93^{a-k}	73.73^{e-f}	82.55^{a-e}	79.15^{a-d}
G9	61.18^{a-d}	31.97^{a-e}	66.42^{a}	51.05^{a}	95.22^{a-g}	77.07^{a-e}	68.25^{e-q}	64.92^{d-o}
G11	68.47^{ab}	39.11^{a-d}	61.19^{ab}	47.89^{abc}	100.00^{abc}	78.68^{a-d}	70.50^{e-o}	65.22^{d-o}
G13	49.30^{a-e}	35.42^{a-e}	45.07^{a-f}	31.79^{a-g}	50.89^{vw}	32.42^{uvw}	55.67^{p-w}	50.92^{n-v}
G20	70.48^{ab}	47.12^{abc}	60.11^{ab}	44.66^{a-e}	90.83^{a-l}	68.76^{b-l}	71.52^{d-n}	66.63^{d-n}
G24	62.24^{abc}	54.81^{ab}	57.95^{a-d}	42.13^{a-e}	90.75^{a-l}	74.65^{a-h}	85.58^{a-d}	83.49^{abc}
G27	70.50^{ab}	46.40^{abc}	61.16^{ab}	45.73^{a-d}	95.38^{a}	86.65^{ab}	72.27^{d-n}	69.92^{b-k}

G35	12.38^{def}	56.38^{a}	10.07^{hi}	3.84^{hi}	65.87^{n-v}	39.63^{q-v}	64.15^{h-s}	59.51^{g-r}
G39	56.73^{a-e}	33.69^{a-e}	51.17^{a-f}	36.74^{a-f}	51.92^{uvw}	32.44^{uvw}	77.54^{a-i}	74.29^{a-g}
G46	68.47^{ab}	44.26^{a-d}	53.48^{a-e}	39.15^{a-f}	94.05^{ab}	80.36^{abc}	89.64^{a}	85.82^{a}
G49	42.22^{a-d}	53.94^{ab}	20.58^{f-i}	12.98^{f-i}	88.75^{a-m}	65.45^{c-n}	87.59^{ab}	85.35^{a}
G51	72.53^{ab}	50.80^{abc}	62.19^{ab}	47.26^{a-d}	96.19^{a}	89.75^{a}	86.64^{abc}	84.53^{ab}
G53	59.84^{a-d}	44.51^{a-d}	52.29^{a-e}	37.32^{a-f}	53.79^{t-w}	32.22^{uvw}	63.30^{i-t}	53.44^{l-u}
G55	64.30^{abc}	0.00^{e}	52.16^{a-e}	37.86^{a-f}	53.61^{t-w}	31.09^{vw}	47.59^{vw}	39.81^{uv}
G58	77.54^{a}	54.52^{ab}	64.34^{a}	49.45^{ab}	93.78^{a-i}	72.61^{a-j}	75.53^{a-k}	69.14^{c-l}
G60	10.07^{ef}	39.94^{a-d}	10.07^{hi}	3.22^{hi}	40.87^{w}	18.50^{w}	54.08^{q-w}	47.88^{p-v}
G61	12.38^{def}	54.50^{ab}	35.67^{a-h}	21.29^{c-i}	62.01^{q-v}	35.92^{s-w}	70.45^{e-o}	67.84^{d-m}
Std. check (Jabi)	28.98^{a-f}	43.42^{a-d}	23.18^{e-i}	17.53^{e-i}	67.88^{m-v}	39.65^{q-v}	79.54^{a-g}	51.49^{n-v}
Local check	57.78^{a-e}	47.08^{abc}	57.95^{a-d}	50.25^{ab}	96.23^{a-f}	75.91^{a-g}	75.54^{a-k}	69.67^{b-k}
Mean	51.52	38.83	47.16	33.74	78.28	56.09	68.11	62.51
SEM(±)	3.14	2.75	1.71	1.78	2.08	1.94	1.71	1.78
CV (%)	38.19	38.87	26.84	33.22	32.02	36.23	23.56	26.69
Sig. (5%)	ns	ns	***	***	***	***	***	***

*Means with the same letter along the column are not significantly different.

During the 2022 cropping season, at Adet the intensity of head blast varied between 0% and 65.85%. In contrast, the intensity in the 2023 ranged from 0% to 57.50%. At Finote Selam, the intensity in 2022 ranged from 36.23% to 99.03%, whereas in 2023, it ranged from 34.6% to 88.51%. When looking at the average mean intensity, Finote Selam reported a greater mean in 2022 (64.63%) than in 2023 (63.59%), while Adet had a mean of 44.97% in 2022, and 39.54% in 2023 (Table 5). Overall, Adet exhibited lower intensity than Finote Selam.

Table 5. Percent mean head incidence and severity in western Amhara, Ethiopia

	Adet				Finote Selam			
	2022		2023		2022		2023	
Genotypes	HBI	HBS	HBI	HBS	HBI	HBS	HBI	HBS
G3	77.54^{abc}	58.40^{a-d}	67.34^{a}	52.32^{a-d}	99.92^{a-g}	80.27^{b-i}	79.54^{a-f}	75.09^{a-h}
G5	68.44^{a-d}	54.31^{a-d}	67.45^{a}	50.43^{a-e}	55.83^{r}	38.83^{wxy}	57.42^{j-o}	50.43^{q-v}
G6	51.06^{a-h}	34.61^{a-i}	20.58^{fgh}	13.95^{g-j}	86.93^{e-o}	66.90^{f-q}	48.66^{no}	37.47^{vw}
G7	74.54^{a-d}	55.56^{a-d}	54.58^{a-f}	40.22^{a-h}	89.65^{b-m}	66.43^{f-q}	78.54^{a-f}	73.21^{a-j}
G8	74.48^{a-d}	58.53^{a-d}	66.41^{a}	51.10^{a-e}	91.06^{b-l}	71.74^{e-n}	82.56^{a-d}	79.75^{a-e}
G9	61.18^{a-f}	40.58^{a-h}	65.36^{ab}	50.08^{a-e}	100.00^{a-f}	81.82^{b-g}	72.45^{c-j}	65.31^{d-q}
G11	83.60^{a}	65.85^{a}	70.40^{a}	54.59^{ab}	100.00^{a-f}	80.82^{b-i}	73.53^{c-i}	69.89^{c-l}
G13	60.18^{a-g}	43.59^{a-g}	55.36^{a-f}	41.08^{a-h}	62.01^{qr}	36.23^{y}	60.86^{i-n}	55.29^{k-u}
G14	0.00^{i}	0.00^{i}	0.00^{h}	0.00^{j}	80.54^{g-q}	56.03^{n-v}	52.36^{mno}	45.13^{uvw}
G24	79.55^{ab}	62.32^{abc}	69.34^{a}	53.52^{ab}	97.03^{a-i}	81.26^{b-h}	82.58^{a-d}	81.19^{a-d}
G27	79.54^{ab}	64.12^{ab}	66.03^{ab}	50.96^{a-e}	100.00^{a-d}	91.88^{abc}	79.56^{a-f}	73.65^{a-i}

G31	17.69^{f-i}	7.26^{ghi}	27.76^{c-h}	11.37^{hij}	87.61^{e-n}	65.08^{g-q}	63.28^{g-n}	54.75^{l-u}
G32	21.91^{e-i}	11.35^{f-i}	0.00^{h}	0.00^{j}	76.46^{j-q}	48.14^{r-y}	66.41^{f-m}	57.49^{i-u}
G35	32.03^{d-i}	13.08^{e-i}	24.41^{e-h}	13.65^{g-j}	75.49^{j-q}	54.59^{o-w}	69.45^{c-k}	61.44^{f-t}
G36	56.84^{a-h}	39.19^{a-h}	46.67^{a-g}	31.15^{a-i}	93.87^{a-k}	76.23^{c-k}	74.51^{b-i}	68.57^{d-m}
G39	66.41^{a-e}	50.72^{a-d}	57.88^{a-e}	43.29^{a-g}	78.54^{i-q}	51.21^{q-y}	81.54^{a-e}	75.73^{a-g}
G46	66.03^{a-e}	48.58^{a-e}	67.25^{a}	48.97^{a-e}	98.15^{a-h}	82.64^{b-f}	91.72^{a}	88.51^{a}
G49	46.52^{a-h}	27.95^{b-i}	28.98^{b-h}	20.50^{e-j}	92.85^{a-k}	74.31^{e-l}	83.55^{abc}	81.47^{a-d}
G51	77.52^{abc}	59.70^{abc}	66.03^{ab}	51.29^{a-e}	100.00^{a}	99.03^{a}	88.69^{ab}	85.83^{abc}
G53	76.54^{a-d}	57.11^{a-d}	62.19^{a-d}	45.70^{a-f}	80.55^{g-q}	53.08^{p-x}	62.25^{h-n}	54.32^{l-u}
G55	71.48^{a-d}	56.04^{a-d}	64.35^{abc}	48.85^{a-e}	70.04^{n-r}	42.19^{v-y}	54.58^{k-o}	46.42^{s-w}
G57	59.84^{a-g}	42.19^{a-h}	51.17^{a-f}	35.97^{a-h}	79.58^{h-q}	62.87^{j-r}	72.53^{c-i}	64.60^{e-q}
G58	79.55^{ab}	61.16^{abc}	70.45^{a}	52.76^{abc}	98.08^{a-h}	74.45^{d-l}	73.48^{c-i}	68.15^{d-n}
G60	14.34^{hi}	5.80^{hi}	12.38^{gh}	4.12^{ij}	69.45^{n-r}	37.48^{xy}	54.31^{l-o}	45.66^{t-w}
G61	16.09^{ghi}	7.34^{ghi}	49.30^{a-f}	29.99^{a-j}	72.45^{l-r}	51.82^{q-y}	72.51^{c-i}	70.54^{b-l}
Std. check(Jabi)	34.24^{c-i}	22.45^{d-i}	25.60^{d-h}	17.13^{f-j}	74.48^{k-q}	41.28^{v-y}	78.54^{a-f}	51.11^{o-v}
Local check	74.54^{a-d}	62.12^{abc}	66.41^{a}	57.44^{a}	100.00^{a-e}	90.73^{a-d}	91.69^{a}	86.46^{ab}
Mean	61.26	44.97	54.07	39.54	87.1	64.63	70.42	63.59
SEM(±)	1.97	2.73	1.89	1.81	2.04	1.84	1.74	1.81
CV (%)	29.59	33.26	27.69	32.21	27.63	31.29	20.24	24.27
Sig. (5%)	**	**	***	***	***	***	***	***

*Means with the same letter along the column are not significantly different.

Finger Millet Genotype Category: Based on Response to Blast Disease Reaction

Genotypic diversity plays a crucial role in determining resistance or susceptibility to blast disease. This study classifies finger millet genotypes based on their responses to blast infection, providing valuable insights for breeding programs aimed at developing resistant cultivars.

At the Adet site in 2022, genotypes G14, G31, G60, G61, G35, G16, and G30 exhibited the lowest leaf blast incidence and severity scores. In 2023, genotypes G6, G10, G14, G31, G32, G41, G57, G60, G35, and G36 also showed reduced severity. All of these were classified as resistant ("R") in both cropping seasons.

Genotypes categorized as moderately susceptible ("MS") in 2022 included G7, G4, G26, G29, G12, G46, G31, G11, G51, G38, G27, and G20. In 2023, the genotypes grouped under the "MS" category were G59, G53, the local check, and G38.

At Finote Selam, moderately resistant ("MR") genotypes in 2022 included G50, G60, G13, G52, G44, G61, G21, and G32. In 2023, genotypes G63, G21, G5, G13, G36, G33, G31, G30, G6, and G53 showed "MR" responses. The most susceptible genotypes ("S") to leaf blast in 2022 were G49, G20, G27, G45, and G51, while in 2023, G39, G44, G62, G27, and G51 were the most affected (Table 3).

In terms of neck blast severity, the most resistant genotypes at Adet in 2022 were G55, G57, G3, and G36. In 2023, G14, G32, G60, G35, and G31 showed the highest resistance. At Finote Selam, genotypes categorized as "R" or "MR" in 2022 included G60, G55, G53, G13, G39, and G5. In 2023, G6 and G55 were identified as the most resistant.

Moderately susceptible and susceptible genotypes at Adet in 2022 included G61, G58, G24, G35, and G8, whereas in 2023, G51, G11, G58, G64, and G9 were the most susceptible. At Finote Selam, the genotypes most affected in 2022 were G46, G27, and G51, and in 2023, G24, G51, G49, and G46 showed the highest susceptibility (Table 4).

Based on head blast severity scores, genotype G14 was the most resistant at Adet across both years. The most susceptible genotypes in 2022 were G38,

G27, and G11, while in 2023, G45, G64, and G1 showed the highest susceptibility.

At Finote Selam, "MR" genotypes in 2022 included G13, G60, and G5, while in 2023, G4 and G6 were also classified as "MR." The most susceptible genotypes in 2022 were G27, G38, and G51, while in 2023, G51, G64, and G45 were the most affected (Table 5).

This study identified several genotypes—G14, G31, G60, G16, G35, and G32—that demonstrated consistent resistance to blast disease over two years (2022 and 2023) and across both testing sites (Adet and Finote Selam). Genotypes such as G33, the standard check (Jabi), G9, G8, G56, G39, G13, G49, G17, and G47 exhibited moderate resistance with lower disease severity compared to susceptible lines. In contrast, genotypes such as the local check, G1, G38, G20, and G51 remained consistently susceptible across seasons and locations.

Table 6. Reactions of 64 finger millet genotypes to blast diseases at Adet, and Finote Selam in 2022 and 2023 cropping seasons.

Location	Disease	2022						2023					
		HR	R	MR	MS	S	HS	HR	R	MR	MS	S	HS
Adet	LBS	0	7	33	24	0	0	0	13	46	5	0	0
	NBS	2	13	14	26	9	0	5	16	19	23	1	0
	FBS	4	9	4	17	30	0	3	11	11	24	15	0
Finote Selam	LBS	0	0	7	54	3	0	0	13	46	5	0	0
	NBS	0	1	14	9	26	14	0	0	2	7	44	11
	FBS	0	0	3	7	32	22	0	0	2	6	38	18

Note: LBS, = leaf blast severity, NBS= neck blast severity, HBS= head blast severity, HS= highly resistant, R= resistant, MR= moderately resistant, S= susceptible, HS= highly resistant

Cluster analysis

Cluster II consists of genotypes with final AUDPC more than 894.72, 1845.99, and 2081.41%–per day for leaf, neck, and head blast respectively, and showing high susceptibility. Cluster I consists of genotypes showing final AUDPC less than 747.87, 1509.28, and 1685.68 for leaf, neck, and head and thus "S" to blast. Cluster IV consists of genotypes having final AUDPC of 573.10, 1287.39, and 1530.24 for the above plant parts and showing "MS". Cluster III has a mean AUDPC of 479.62, 1192.14, and 1376.04 for leaf, neck, and head and shows "MR". Finally, cluster V consists of genotypes with final AUDPC of 327.07, 877.83, and 757.38 for leaf, neck, and head blast categorized as"R" (Table 7). No genotype was identified as immune to blast, as illustrated in Figure 3. From these findings, it can be concluded that accessions in Clusters III and IV may carry minor genes related to blast resistance, while those in the other clusters are likely lacking any resistance genes.

Table 7. Clustering of genotypes based on AUDPC rate per-day values

Group	LAUDPC	NAUDPC	HAUDPC	Disease reaction	No. of genotypes
1	747.87	1509.28	1685.68	S	20
2	894.72	1845.99	2081.41	HS	14
3	479.62	1192.14	1376.04	MR	17
4	573.10	1287.39	1530.24	MS	6
5	327.07	877.83	757.38	R	7

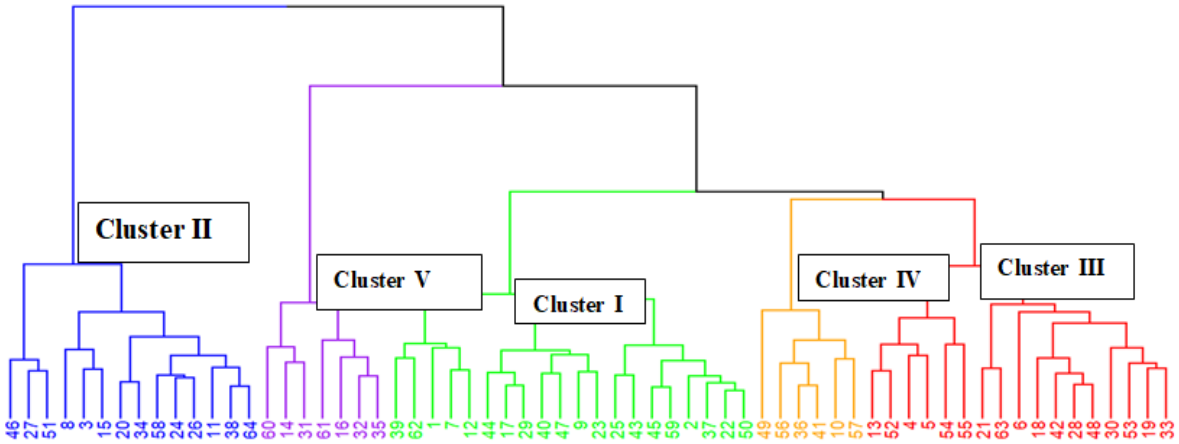


Figure 3. UPGMA dendogram based AUDPC of finger millet genotypes at Adet and Finote Selam in 2022 and 2023 cropping seasons.

Concerning yield, and its components, the genotypes categorized as "R" and "MR," including G56, G32, G57, G13, G49, G28, G62, G9, G48, G5, as well as the standard check (Jabi), are all classified as late-maturing. Similarly, the "R" and "MR" genotypes such as G30, G53, G25, G60, G35, G17, G54, G19, G40, G23, and G5 demonstrate significant plant growth. At Adet, genotypes G5, G48, G14, and G60, plus the standard check, also show high yields. In Finote Selam, the top yielders among the "R" and "MR" genotypes include G5, G21, G2, and G35, along with the standard check (Jabi). Furthermore, the genotypes G5, G60, G55, G53, G28, G48, G32, G37, G35, G4, G30, G52, and G42, including the standard check, are classified as late-maturing.

The scatter plot regression analysis revealed a negative correlation between blast severity, and grain yield. As the severity of the blast increases, the grain yield generally decreases. The fitted curve also shows that greater disease severity corresponds to reduced grain yield in the genotypes (Figure 3).

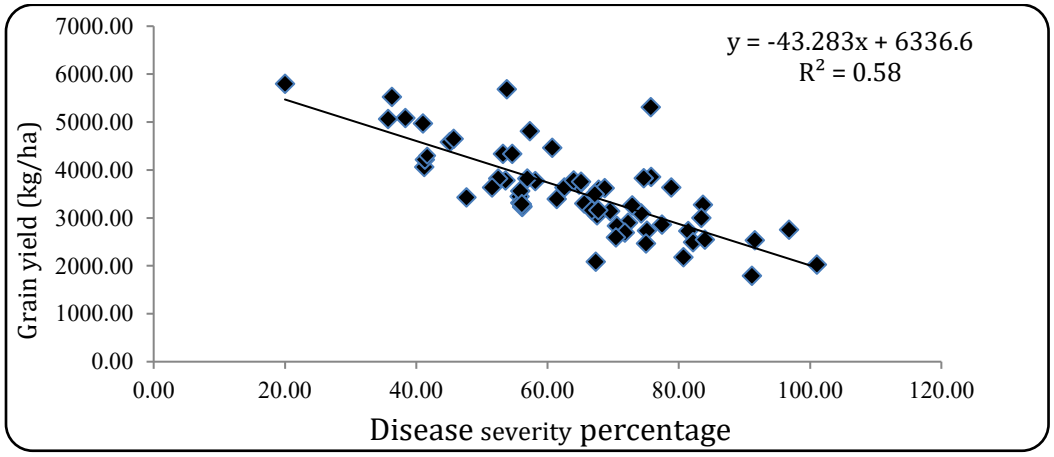


Figure **3**. Estimated linear regression between mean blast disease severity and grain yield.

DISCUSSION

The prevalence and severity of blast disease were greater in Finote Selam compared to Adet, with a more significant incidence noted in 2022 than in 2023. This trend is likely affected by environmental variables. The research highlights the notable effect of climatic conditions on blast disease severity in finger millet. In our research, we found that Finote Selam, with more favorable environmental factors like temperature, and humidity, showed higher levels of blast incidence, and severity in comparison to Adet. This explains how different environmental conditions can impact disease

prevalence, highlighting the necessity of considering local conditions when evaluating genotypes for resistance to blast disease.

It is documented that temperature, and relative humidity are vital factors in the sporulation, discharge, and germination of blast conidia (Wekesa *et al.*, 2019). Elevated temperatures along with high humidity provide optimal conditions for leaf blast disease development. On the other hand, neck, and panicle blast are more sever in cooler temperatures with moderate to high humidity. Moreover, persistent humidity following rainfall significantly progresses disease spread by supporting spore dispersal. To reduce the threat of blast disease, controlling humidity within the crop canopy, implementing crop rotation, and adopting early planting can effectively lower infection rates and improve disease management (Ojha *et al.*, 2024).

The differences in blast severity observed among the genotypes imply that the pathogen may exhibit host specificity, given the genetic diversity existing in the genotypes. The difference in resistant genotypes between locations may come from variations in pathogen populations, environmental conditions, or a combination of these factors. Similar inconsistencies in disease severity among genotypes, influenced by environmental conditions, have been reported by Kumari *et al.* (2022) and Manyasi *et al.* (2022).

Additionally, genotypes containing dark-colored seeds, and compact heads were found to exhibit greater resistance than those with white seeds, and open heads. The high levels of phenolic compounds and tannins found in dark seeds provide antifungal activities, while the compact head formation decreases humidity and restricts physical entry of spore and conidia of the pathogen, thus lowering rates of infection (Shivhare *et al.*, 2022). This might be also attributed to the increased susceptibility of open-headed genotypes to airborne pathogen inoculum readily entered open-headed genotypes compared to their compact-headed ones (Wekesa *et al.*, 2019).

The findings of this research indicated considerable differences in blast resistance among various finger millet genotypes. The categorization of genotypes as either resistant or susceptible to blast is probably attributed to genetic variations among them. A crucial element influencing the difference resistance of plant genotypes to particular diseases might be the existence of specific resistance (R) genes within their genetic structure. These R genes produce proteins that recognize pathogen-associated molecular patterns (PAMPs) or distinct pathogen effectors, which initiate defense responses such as the hypersensitive reaction (HR) and systemic acquired resistance (SAR). The variability of these R genes among different plant genotypes is essential in determining a plant's resistance or susceptibility to diseases (Sett *et al.*, 2022).

Conversely, the fungal pathogen may overcome the host plant defense by developing resistance structures like haustoria. Moreover, reduced enzyme activity, along with the pathogen's long-term evolution, including mutations within its tissues, can result in intensified susceptibility of the genotypes (Pawlowski and Hartman, 2016).

In related research, Thakur *et al.* (2025) evaluated the resistance of 26 finger millet genotypes under field conditions during the 2021 growing season. Their results demonstrated notable differences in disease resistance and yield loss among the genotypes. Karishma *et al.* (2022) investigated 85 finger millet genotypes for their resistance to leaf, neck, and finger blast in natural field environments, noting that only one genotype, IC0477045, was resistant to leaf blast. The other genotypes showed a range of responses: 30 were moderately resistant, 32 moderately susceptible, 15 susceptible, and seven highly susceptible. Ojha *et al.* (2024) assessed 200 finger millet accessions in natural conditions for their resistance to leaf, neck, and finger blast diseases. Their findings revealed that nine accessions displayed strong resistance to all forms of blast.

Classifying finger millet genotypes according to their resistance to blast disease has important values for yield performance. Genotypes that are resistant are expected to produce higher yields than those that are susceptible, particularly in environments with high disease pressure. This is due to the fact that resistant genotypes can lessen the yield losses by the disease, while susceptible ones may experience reduced grain development, lodging, and overall plant vigor, ultimately resulting in reduced productivity (Ojha *et al.*, 2024). Research findings indicate that breeding for disease resistance in key crops can improve yields, and lessen the reliance on chemical treatments, providing economic advantages for smallholder farmers. Kumari *et al.* (2022) emphasizes that using blast-resistant finger millet varieties can improve sustainability and yield in its cultivation.

Pearson correlation coefficients revealed notable

associations between different agronomic and disease parameters. Specifically, there is a weak positive correlation (r = 0.3*) between grain yield (GY) and the number of ears per plant (NEP), indicating that plants with a greater number of NEP are likely to have higher yields. The negative correlations between neck, and head blast severity with agronomic traits such as NEP, and days to maturity (DM) imply that late-maturing genotypes, like G60 and G13, may avoid blast infections due to less favorable microclimatic conditions. This observation is consistent with studies by Gani and Tunwari (2023), and Kumari *et al.* (2022) which indicate that late-maturing genotypes generally show less disease severity. This may be due to the susceptible stage of the crop (panicle emergence) may not coincide with favorable weather conditions and virulent pathogens. Genotypes that mature later attain these stages when temperatures and humidity are decreased, which in turn mitigates the severity and dissemination of the blast fungus (Thakur *et al.*, 2024).

Additionally, there exists a strong negative correlation (r = –0.03*) between grain yield, and blast severity, supporting findings from Das *et al.* (2021). Ojha *et al.* (2024) revealed that all forms of blast showed a negative correlation with various studied agronomic traits. Moderate (r = 0.57**) and strong (r = 0.70**) significant correlations between leaf, neck, and head blasts suggest that a high level of leaf blast severity may result in increased neck or finger blast infections in the later growth stages. Other studies indicate a weak to moderate correlation between leaf blast, and neck or finger blast, implying that early leaf blast inoculation may not lead to severe neck or finger blast later on. This could be due to differential gene expression for resistance against leaf, neck, or finger blast infections (Thakur *et al.*, 2024).

The average Area under the Disease Progress Curve (AUDPC) value exhibits a gradual increase during the growing season. The strong negative correlation between mean AUDPC, and grain yield (r = –0.05*) may be due to the damage and death of leaf cells, and tissues caused by blast lesions. This indicates that the pathogen is infecting most aboveground plant parts, with neck and finger blast being the most detrimental stages of the disease. The growth rate of the crop, and leaf area development sharply decline during the onset of the disease, and persist until maturity, leading to a substantial decrease in total dry matter and grain yield (Bhatta *et al.*, 2017). Manyasi *et al.* (2022) also observed that the mean AUDPC value increases throughout the growing season, with the disease spreading more quickly in "S" genotypes, at a slower rate in "MR" genotypes, and at a reduced rate in "R" genotypes.

CONCLUSION

This research highlighted several finger millet genotypes with significant yield potential, and improved resistance to blast disease, presenting valuable resources for improving production in major finger millet growing areas of Ethiopia. The substantial genetic diversity found among these genotypes offers important opportunities for genetic improvement, especially through breeding programs aimed at creating high-yield, and disease-resistant varieties.

Genotypes: G6, G4, G60, G35, G31, G61, G32, G5, G30, G42, G48, G16, G28, and G18-exhibited strong resistance to blast disease, and should be prioritized for future breeding initiatives. Incorporating these genotypes into on-going genetic improvement programs can promote long-term yield stability while decreasing dependence on chemical control methods, thus reducing production expenses for farmers with limited resources.

A focused breeding strategy should aim to cross high yielding but susceptible genotypes such as G7 (5208.3 kg/ha) and G20 (4208.3 kg/ha) with resistant genotypes like G4, G14, and G60, which show low terminal severity. The subsequent steps involve controlled hybridization, field trials, and the selection of promising progeny that merges high yield with blast resistance. National and regional breeding initiatives, especially those led by the Adet Agricultural Research Centre, and similar institutions, should take the lead in these efforts to guarantee genetic improvement, and widespread adoption of improved varieties.

In the short term, farmers in the studied areas, and similar agro-ecological regions can gain advantages by cultivating resistant and high-yielding genotypes, thus minimizing yield losses attributed to blast disease. Additionally, genotypes that have shown susceptibility to blast-such as G62, G49, G41, G23, G56, G7, G24, G36, and G41 in Finote Selam, and G58, G9, G52, G12, G8, G1, and G21 in Adet-should be utilized with caution, while significantly susceptible genotypes like G27, G51, and G11 can serve as useful checks in future studies.

Despite the expected advantages, enacting these

breeding suggestions may encounter obstacles such as environmental variability impacting disease occurrence, financial constraint, lack of commitment to implementing the study findings, and the need for farmers to adopt newly developed varieties. To overcome these challenges, a collaborative approach involving researchers, extension services, and policymakers is crucial. Furthermore, understanding environmental factors influencing the spread of blast disease will aid in refining management techniques, including optimizing planting dates, and selecting appropriate landraces for various agro-climatic contexts. By emphasizing the improving and distribution of blast-resistant finger millet varieties, breeding initiatives can aid in adopting sustainable food security and economic resilience for smallholder farmers. These results offer essential guidance for shaping future breeding, and disease management strategies in Ethiopia, and similar agro-ecological environments.

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CONFLICT OF INTEREST

The authors declare that there are no conflicts of interest.

AUTHORS' CONTRIBUTION

Melkamu Andargie was responsible for performing the experiment, collecting, and organizing the data, and drafting the original manuscript. Merkuz Abera, Tesfaye Alemu, and Berhanu Bekele contributed to the formatting, editing, and revisions of the manuscript before submission.

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