Genetic Screening for Blast Resistance in Finger Millet (*Eleusine coracana*)

Abstract

Finger millet (*Eleusine coracana*), a vital staple crop, faces significant yield losses globally due to blast disease caused by *Pyricularia oryzae*. Deployment of resistant cultivars remains the most sustainable and cost-effective approach for disease management. Therefore, the identification of reliable resistance sources is critical for breeding programs aimed at developing durable blast-resistant varieties. In the present study, fifty-two diverse finger millet genotypes, including a known resistant check (Indaf-7) and a susceptible check (Uduru), were evaluated for leaf blast resistance during the Rabi season of 2022–2023 at the PG Research Farm, Centurion University of Technology and Management, Paralakhemundi, Odisha. Screening was conducted under both natural field conditions and controlled greenhouse environments supplemented with artificial pathogen inoculation. Disease severity was assessed using a standardized 0–9 disease rating scale, and quantitative measurements included calculation of the Area Under Disease Progress Curve (AUDPC). Additionally, the Area Under the Chlorophyll Decline Curve (AUCDC) was estimated using SPAD meter readings to quantify chlorophyll depletion associated with disease progression. Four genotypes—Bada Mandia, Lalsuru Mandia, VR 1233, and VR 1220—demonstrated robust resistance to blast infection. Meanwhile, a group of thirteen genotypes, including Telugu Mandia, Badtara, Dangardi, Chilli, Chaitanya, PR 202, VR 1220 FM, DPLM 3FM, VR 1214FM, CFMV1, VL 400FM, and FIN 6164, exhibited moderate resistance. Conversely, genotypes such as TNEC 1335FM, FIN 5167, Arjun, VR 1176, VR 1221, VR 1217, KMR 711, and FIN 5169 were identified as highly susceptible. The findings of this investigation offer a valuable genetic resource for finger millet breeding programs, laying a strong foundation for the development of ~~improved~~ cultivars with ~~enhanced~~ blast resistance and contributing to the sustainable production of this nutritionally important crop.

Keywords: Area Under Disease Progress Curve, Area Under Chlorophyll Decline Curve, Blast disease, disease resistance, Finger millet, and Genotypic screening,

INTRODUCTION

Finger millet (*Eleusine coracana* L.), commonly known as ragi, is a nutritionally rich and highly adaptable crop predominantly cultivated across the semi-arid regions of Eastern and Southern Africa and South Asia (Ascari et al., 2024). Globally, finger millet accounts for approximately 10% of the total millet cultivation area, which spans about 34.18 million hectares (Dubey et al., 2021). India alone contributes nearly 32% of the global acreage, covering approximately 1.09 million hectares, with major production hubs in Karnataka, Uttarakhand, Maharashtra, Tamil Nadu, Odisha, Andhra Pradesh, and Gujarat (Chapman et al., 1997). Notably, Karnataka leads national production, accounting for about 60% of India's finger millet area.

The grain is highly valued for its superior nutritional profile, offering a rich source of easily digestible proteins, minerals, and fibers. It is versatile in consumption, either raw, boiled, or processed into porridge and cakes (De Wet, 2006). Among all small millets, finger millet is particularly distinguished by its high calcium content (300–350 mg/100 g) (Sandeep et al., 2019). Its role in combating malnutrition is increasingly recognized, fueling the development and popularization of value-added finger millet-based products to meet evolving consumer demands (Amadou et al., 2011).

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However, the productivity of finger millet is critically constrained by blast disease, caused by the fungal pathogen *Pyricularia oryzae* (Cooke) Sacc. (teleomorph: *Magnaporthe grisea* (Hebert) Barr). This disease, particularly prevalent during the rainy season, manifests in three major forms: leaf blast (LB), neck blast (NB), and finger blast (FB), affecting plants at all developmental stages. Leaf symptoms initially appear as oval or diamond-shaped lesions with chlorotic halos and water-soaked centers, which may coalesce to form extensive necrotic areas. In advanced stages, infection extends to the peduncle and panicle, leading to neck and finger blast, respectively, resulting in shriveled or chaffy grains and significant yield losses (Bhardwaj et al., 2007).

The disease thrives under conducive environmental conditions—temperatures ranging from 25°C to 30°C, high relative humidity (>90%), and frequent overcast days accompanied by intermittent rainfall. The yield loss due to blast is substantial, with average reductions reported between 28% and 36%. Specifically, leaf blast can cause up to 40% loss, neck blast 20%–40%, and finger blast as high as 60% (ICAR-Indian Institute of Millets Research, 1958). Please include the reference

Quantitative disease assessment is crucial for understanding and managing blast epidemics. Disease severity is defined as the proportion of the plant surface area

affected, expressed as a percentage (Nutter Jr et al., 1991), a measure widely applied in various crops, including soybean rust (Godoy et al., 2006), pecan scab (Yadav et al., 2013), and rice brown spot (Schwank and Del Ponte, 2014). The Area Under Disease Progress Curve (AUDPC), calculated using the trapezoidal integration method, offers a robust measure of cumulative disease intensity over time, enabling comparisons across different genotypes, environments, and management practices (Madden et al., 2007).

Furthermore, the assessment of physiological damage, particularly chlorophyll loss, is increasingly being integrated into disease screening protocols. Chlorophyll concentration, commonly measured using SPAD meters, provides a non-destructive and rapid proxy for assessing plant health. However, SPAD readings are sensitive to the sampling position along the leaf blade, with significant variability observed from the leaf base to the apex (Debaeke et al., 2006; Víg et al., 2012). The thin leaf sections near the base, often with a prominent midrib, can introduce measurement inconsistencies due to incomplete coverage of the SPAD meter's optical window, leading to increased standard deviation in readings (Lin et al., 2010). These limitations highlight the need for refined calibration protocols and standardized sampling strategies to ensure the accuracy and reliability of SPAD-based chlorophyll estimations (Chapman and Barreto, 1997).

Thus, integrating traditional disease scoring with quantitative tools like AUDPC and chlorophyll analysis via SPAD provides a comprehensive framework for the accurate evaluation of blast resistance, facilitating the development of resilient finger millet cultivars. is the aim of the present study.

2. Materials and Methodology

2.1. Experimental Site & Design

The field experiment was conducted during November to March (2022–2023) at the Postgraduate Research Farm, Centurion University of Technology and Management, Paralakhemundi, Odisha. The experimental site is characterized by a tropical monsoon climate with moderate winter temperatures and occasional humidity fluctuations. Prior to sowing, the field was prepared by crosswise ploughing using a tractor-drawn harrow, followed by manual removal of weeds to ensure a clean seedbed. A Randomized Complete Block Design (RCBD) was employed, comprising 52 treatments with three replications. Seedlings were initially raised in a nursery bed and transplanted to the main field after 30 days. The main field layout covered an area of 25 × 14 m², bordered by 0.5 m wide irrigation

channels. Each replication was maintained at a plot size of 4 m in width, with a 0.5 m separation provided for irrigation. Seedlings were transplanted at a spacing of 22.5 cm (row-to-row) × 10 cm (plant-to-plant), maintaining uniform density across the field. The randomization of treatments within each block was performed meticulously to minimize positional effects and ensure experimental validity.

2.2. Experimental Materials

The experimental materials consisted of fifty two diverse genotypes of finger millet (*Eleusine coracana* L.), sourced from various germplasm collections: Fifteen landraces from M.S. Swaminathan Research Foundation (MSSRF), Jeypore, Odisha, fifteen improved varieties from the All India Coordinated Research Project (AICRP) on Small Millets, Mandya, Karnataka, four elite lines from the Indian Institute of Millets Research (IIMR), Hyderabad, and eighteen genotypes from the Agricultural Research Station, Vizianagaram, Andhra Pradesh. Details of the genotype accessions, their origins, and pedigree information are presented in Table 1

2.3. Assessment of Pathological Traits

2.3.1. Disease severity [%]:

Blast disease severity was assessed based on the percentage of the plant surface area exhibiting visible disease symptoms, following the definition proposed by Bock et al. (2022). Disease assessments commenced with the initial appearance of symptoms and were recorded at 10-day intervals, culminating in 10 observations per treatment across the growing season. Disease scoring utilized a standardized 0–9 scale based on lesion characteristics and the proportion of affected leaf area like: 0: No visible lesions, 1–3: Minor lesions covering up to 25% of leaf area, 4–6: Moderate lesions covering 26–50% of leaf area and 7–9: Severe lesions affecting more than 75% of leaf area (Supplementary Figure 1 for a visual guide to the disease rating scale.). Disease severity (%) for each plot was calculated using the formula proposed by Shrestha and Mishra (1994): Ref. missing, please include

$$Disease\ Severity\ (\%) = \frac{\Sigma(Class\ frequency\ \times Score\ of\ rating\ class)}{(Total\ number\ of\ plants\ observed\ \times Maximal\ disease\ index)} \times 100$$

$$\%\ \text{Disease incidence} = \frac{No.of\ infected\ plants}{Total\ no.of\ plants} \times 100$$

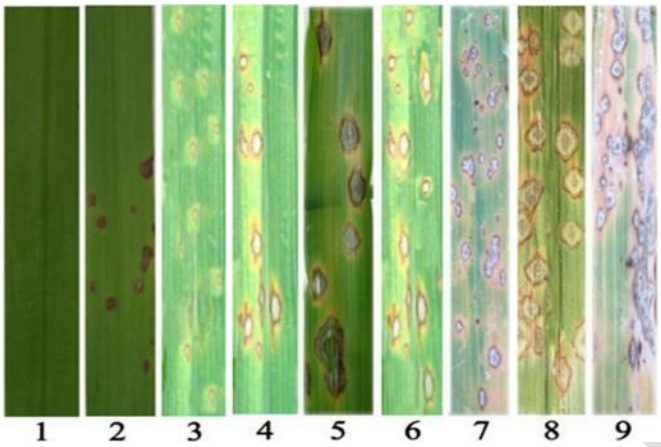

Fig-1: (1-9) Disease Scale of Finger Millet

The accessions were divided into four groups depending on disease severity: 0-15% resistant (R), 15.01-20.10% moderately resistant (MR), 21-30% moderately susceptible (MS), and more than 30% highly susceptible (S).

2.3.2. Area under disease progress curve (AUDPC)

The area under the disease progress curve (AUDPC) is a common method for combining several observations of disease progression into a single number. Our research reveals that this method significantly underestimates the impact of the first and final observations (Madden *et al*.,2007). Ref. missing, please include

$$\text{AUDPC} = \sum_{i=1}^{n} [(+ xi + 1)/2] * t$$

The AUDPC was estimated using the method provided by Das *et al*.,(1992). The Area under disease Progress Curve (AUDPC) is a quantitative indicator of disease intensity across time. It is used in plant pathology to identify and compare disease resistance levels among crop cultivars.

$$\text{AUDPC}=\sum_{i=1}^{n-1} \left(\frac{y_i+y_{i+1}}{2}\right) (t_{i+1} - t_i)$$

Where,

y_i= Disease Severity % on the i^{th} scoring

t_i = Number of days from sowing to i^{th}scoring

n = Total numbers of scoring

Among all the fifty-two genotypes of finger millet that includes two check varieties Indaf-7 (resistant) and Uduru (susceptible), were screened under field epiphytotic

condition for occurrence of disease reaction to leaf blast according to method standardized at ICRISAT, as well as in greenhouse condition in replication of three for each genotype.

2.3.3. Area under chlorophyll declined curve (AUCDC)

The Area Under Chlorophyll decline curve were calculated by using the SPAD meter. The SPAD values were also taken for both healthy and disease infected leaves to know the effect of disease on the chlorophyll content.

2.4.1. Isolation, characterization, and preservation of the pathogen

To isolate the pathogen, symptomatic leaves showing blast disease were collected and cut into small pieces measuring 5 x 5 mm on Potato Carrot Agar (PCA) media, composed of 120 gm potato, 200 gm carrot, 20 gm sugar, and 10 gm agar. The infected areas underwent surface sterilization using a 1% NaOCl solution for one minute. Prior to the experiment, all equipment intended for use was sterilized in an autoclave, followed by treatment in a hot air oven. Individual fungal colonies emerged during the 7-10 days following inoculation (Supplementary Fig. 2). The plates containing the isolates were kept at 28 ± 2 ºC in a BOD incubator. Cultures were maintained through periodic sub-culturing every 10-15 days on the same media plant.

2.4.2. Inoculation method using pot culture in a controlled environment

A pot culture experiment was conducted under controlled greenhouse conditions to assess the pathogenicity of the isolated fungus on the 52 finger millet genotypes. The genotypes were transplanted into individual plastic pots, ensuring that they were arranged in a randomized layout to reduce positional bias. The greenhouse environment was carefully regulated to maintain optimal conditions for pathogen growth, with temperature, humidity, and light cycles controlled to simulate natural conditions conducive to disease development. After 10 days post-transplantation, the fungal culture was scraped from the PCA plates, filtered through sterile gauze, and suspended in distilled water to create a spore suspension. The spore concentration was adjusted to 1 × 10^6 spores/mL using a haemocytometer for precise spore counting. The spore suspension was then applied to the finger millet plants using a hand-held sprayer, ensuring even coverage of the plant surfaces. Inoculation was performed in the evening to avoid the effects of heat stress on the plant and fungal spores. Following inoculation, the plants were transferred to a polyhouse, where they were enclosed in polypropylene bags (36 × 48 inches) to maintain high humidity levels (70–90%) necessary for fungal spore germination and disease progression. This environment facilitated optimal

disease development, as described by Murphy et al. (2008) (Supplementary Fig 3).

3. Results and Discussion

3.1. Disease Severity (%)

Field screening of fifty-two genotypes against leaf blast disease showed a wide range of resistance responses. Four genotypes namely, Bada Mandia, Lalsuru Mandia, VR1220FM and VR1233 were found to be highly resistance while eleven genotypes namely, Telugu Mandia, Badtara, Chilli, Dangardi, Chaitanya, PR202FM, DPLM3, VR1214FM, CFMV1, VL400FM, FIN6164 were moderately resistant to leaf blast disease. A total of twenty-two genotypes, including Bhairabi, Taya, Bada Kumnda, Madi Muskuri, VL Mandua352, VL352, FMCFMV2, VR1185FM, KOPN1056, PR1639, KMR656, FMDPLM2, FeZN15, VR1218FM, VR1225FM, VR1228FM, FeZn84, FIN5146, PR1506, GPV67, WN572, and BR9FM, exhibited varying degrees of susceptibility to the disease. The remaining genotypes were found to be highly susceptible to leaf blast. The disease severity across all fifty-two genotypes ranged from 3.11% to 39.56%, with no genotypes demonstrating an immune response to leaf blast disease. These findings indicate that while resistance is observed in certain genotypes, there is no complete immunity to the disease in the studied material (Supplementary Table 3, Supplementary Fig 4).

3.2. Area under disease progress curve (AUDPC)

The Area Under Disease Progress Curve (AUDPC) was computed from the disease severity data, representing the extent of disease-induced damage to the plant tissues over time. The severity of the disease in the genotypes was measured at regular intervals, and the corresponding AUDPC values are depicted in Supplementary Figure 5. The genotypes exhibited varied levels of resistance to leaf blast disease. The genotypes Bada Mandia, Lalsuru Mandia, VR 1233, and VR 1220 were categorized as highly resistant. On the other hand, Telugu Mandia, Badtara, Dangardi, Chilli, Chaitanya, PR202, VR1220 FM, DPLM 3FM, VR 1214FM, CFMV1, VL 400FM, and FIN 6164 were classified as moderately resistant. Several other genotypes, including Bhairabi, Taya, Bada Kumnda, Madi Muskuri, Muskuri, VL Mandua352, VL 352, FM CFMVZ, VR 1185FM, KOPN 1056, KMR 656, FM DPLM2, FeZN 15, VR 1218FM, VR1225, VR1228 FM, PR 1639, VR 1226, VR 1222, FeZN 84, BR 9FM, WN 572, GPV 67, and PR1506, exhibited moderate susceptibility. Finally, genotypes such as TNEC 1335FM, FIN 5167, Arjun, VR 1176, VR 1221, VR 1217, KMR 711, and FIN 5169 were categorized as highly susceptible to the leaf blast disease.

3.3. Area under chlorophyll decline curve (AUCDC)

Chlorophyll content was measured in each genotype using a SPAD meter over a six-day period to monitor the progressive decline in chlorophyll levels associated with disease development. The AUCDC values for all 52 genotypes are summarized in Supplementary Table 4. Initially, prior to disease infestation, chlorophyll content ranged from 6.00 to 9.92. However, as the disease progressed, a significant decrease in chlorophyll content was observed across all genotypes. The genotypes Bada Mandia and Lalsuru Mandia exhibited the highest resistance, with chlorophyll values of 9.92, indicating minimal decline. In contrast, genotypes like VR1217 and FIN5169 recorded the lowest chlorophyll values (6.00), with OEB610 showing a chlorophyll content of 7.00, reflecting higher susceptibility to the disease (Supplementary Figure 6).

3.4. Mahalanobis D^2 Analysis

Suryanarayana et.al., (2014) stated that the clustering pattern showed that genotypes from various geographic regions formed own distinct clusters, demonstrating that geographic diversity is not the primary determinant of genetic variation. According to the aforementioned findings, in order to choose genotypes with different genetic backgrounds, the material should be examined for important characteristics such as grain yield per plot, flag leaf area, days to maturity, plant height, harvest index, and days to 50% flowering. The production of the finger millet crop is facilitated by these qualities. Accordingly, there is no correlation between geographic variety and genetic diversity, and selecting these traits increases the production of finger millet. These findings matched those of earlier research by Haradari et al. (2010), Mittal et al. (2010), Pandora et al. (2013), Kumar et al. (2016), and Suryanarayana et al. (2014).

Mean intra and inter cluster distance

The intra-cluster and inter-cluster distances, as shown in Supplementary Table 5, provide insights into the genetic relationships among the genotypes within and between clusters. The intra-cluster D^2 values ranged from 0.00 to 148.90, with Cluster III exhibiting the maximum D^2 value (148.90), followed by Cluster II (113.78) and Cluster I (95.83). The highest inter-cluster distance was observed between Cluster I and Cluster V (229288.68), indicating the greatest genetic divergence, while the smallest inter-cluster distance was found between Cluster II and Cluster IV (32515.21). These findings suggest significant genetic variability between the clusters (Supplementary Fig 7).

Grouping of fifty-two finger millet genotypes based on D^2 analysis

The estimated values of D^2 between genotypes were utilized to cluster the genotypes as the sum of squares of the differences between the mean values of all the examined features i.e., yield and its attributing characters with the pathological traits (Supplementary Table no.6). All the fifty-two genotypes were divided into five primary clusters, with cluster I having the maximum number of the genotypes (22 genotypes) comprises KMR656, FIN5164, FeZn84, DPLM2, VR 1225, PR-1639, TAYA, KOPN1056, Bhairabhi, PR202, VL 352, PR1506, BR9, VR1185, VR1222, FMCFMVZ, VR1218, VR1228, Muskuri, FeZn15, VR1226, and Indaf-7. Cluster III (17 genotypes), includes Chilli, DPLM3, FM1, FIN6164, Dangardi, Badtara, CFMV1, Telugu Mandia, VR1214, Lalsuru Mandia, Bada Mandia, VR1220, VR1233, GPV67, Bada Kumunda, and VL400. The cluster II had 6 genotypes comprises TNEC1335, VR1217, VR1221, OEB610, KMR711, and FIN5169 while, cluster IV also contain 6 genotype like, WN572, Uduru, PR1630, FIN5167, FM4, DPLM3. Cluster V had a single genotype, VR1176. This clustering is based on the torcher's approach, Sandeep et al. (2021), provided a comprehensive understanding of the genetic diversity among the genotypes, which is crucial for the identification of superior genotypes for breeding and disease management strategies.

4. Discussion

Identification of Resistant Genotypes and Disease Severity Assessment in Finger Millet

Identifying genotypes that are resistant to blast is essential, as there are currently no well-established and proven resistant variants of finger millet. The severity of blast infestations further emphasizes this need. Disease Severity and Area Under Disease Progress Curve (AUDPC), also known as Area Under Disease Progress Curve of Cumulative Disease and Area Under Chlorophyll Decline Curve (AUCDC) are two crucial indicators utilized in the screening process for blast resistance. The evaluation of disease infestation through both quantitative and qualitative approaches is known as disease severity. The symptoms of finger millet blast are manifested through leaf lesions and lesions on the stems, and panicle blast may be visually seen to determine the severity of the illness. Severity is frequently graded using a quantitative scale (% of afflicted plant tissue) or a qualitative scale (e.g., 0-9). Genotypes that exhibit lower severity of disease are thought to be more tolerant or resistant to blast during screening. Quantitative metrics like AUCDC and AUDPC are used to evaluate how a disease is developing over time. Rather than at discrete intervals, they offer a thorough assessment of disease progression over the course of the growing season. Mapping disease severity against a timeline clarifies the disease progression curve.

Genotypes exhibiting lower AUCDC or AUDPC scores demonstrate slower disease development and are considered to have greater resistance to pathogens. Several finger millet genotypes are screened and their response to blast infection is assessed in a controlled environment. This entails introducing the pathogen into plants by inoculation and monitoring disease signs over time. At several intervals, information on the severity of the disease is gathered, and AUDPC or AUCDC values are computed using this information. Based on illness severity, AUDPC, and AUCDC, statistical analysis is then used to compare genotypes and determine which have the highest levels of resistance. It is significant to highlight that a variety of variables, including as genetic background, climatic circumstances, and the availability of particular resistance genes, might impact resistance to blast in finger millet. Therefore, in order to achieve an accurate and trustworthy assessment of genotype performance, screening efforts should take these parameters into account. Furthermore, a more thorough evaluation of blast resistance in finger millet genotypes may be obtained by integrating several disease resistance indices, such as disease severity, AUDPC, and AUCDC. This can assist breeders in choosing the best candidates for advancement and use in agriculture.

Genotypic Classification and Clustering

Using Torcher's method, fifty-two genotypes were grouped into five clusters Among the five clusters, the cluster I was the largest comprising of (22 genotypes) followed by cluster III (17 genotypes), cluster II (6 genotypes), cluster IV (6 genotype) and cluster V (one genotype). Additionally, depending on the intra and inter cluster distances, genotypes within a cluster show a limited range of genetic variation whereas those between the clusters show a greater range of variability. Such clusters may emerge as a result of extreme isolation, which prevents gene flow founder effect or genetic drift or through intense natural or human selection for a variety of adaptive complexes. It is desirable to select genotypes from the clusters having high inter cluster distance to get select the diversified parents for future crossing programme.

Genotype Resistance to Leaf Blast

Genotypes Bada Mandia followed by Lalsuru Mandia, VR 1233, VR1220 are the four genotypes that were resistant to leaf blast infection while, Telugu Mandia, Badtara, Dangardi, Chilli, Chaitanya, PR202, VR1220, DPLM 3, VR 1214, CFMV1, VL 400, FIN 6164 genotypes were moderately resistant to leaf blast disease. The genotypes namely, Bhairabi, Taya, Bada Kumnda, Madi Muskuri, Muskuri, VL Mandua-352, VL 352, CFMVZ,

VR 1185, KOPN 1056, KMR 656, DPLM2, FeZN 15, VR 1218, VR1225, VR1228, PR 1639, VR 1226, VR 1222, FeZN 84, BR 9, WN 572, GPV 67, PR1506, were found to be moderately susceptible, while TNEC 1335FM, FIN 5167 , Arjun , VR 1176, VR 1221, VR 1217, KMR 711, and FIN 5169 genotypes were susceptible to leaf blast disease.

The genotype VR1176 (AUDPC = 636.53) exhibited the highest AUDPC value, indicating high susceptibility, while Lalsuru Mandia (AUDPC = 33.22), followed by Bada Mandia (AUDPC = 43.89), VR1220 (AUDPC = 57.4), and VR1233 (AUDPC = 58.36), demonstrated the lowest AUDPC values, signifying strong resistance to leaf blast. Breeding these resistant genotypes with high-yielding varieties can potentially produce superior progeny that combine both high yield and disease resistance. Reference?

Chlorophyll Decline and Disease Progression

The chlorophyll content in the leaf tissues of the genotypes was measured using a SPAD meter, with data collected over a six-day interval from the onset of disease symptoms. A gradual decline in chlorophyll content was observed as disease severity increased. Maximum chlorophyll levels (9.83 mm/g) were recorded in resistant genotypes, while the minimum chlorophyll content (6.00 mm/g) was observed in susceptible varieties. The decline in chlorophyll content directly correlated with the progression of the disease, further highlighting the impact of blast on plant health. Reference?

5. Conclusion

The analysis of variance revealed significant differences among genotypes for disease resistance traits, including AUDPC, AUCDC, and disease severity, as well as agronomic traits such as yield and its components. These findings suggest that there is substantial genetic variation within the genotypes studied, making it possible to select the most resistant varieties for breeding programs aimed at improving finger millet resistance to leaf blast. The results emphasize the importance of using comprehensive resistance indices (disease severity, AUDPC, and AUCDC) for selecting the best candidates for crop improvement programs. Moreover, integrating these findings with marker-assisted selection can accelerate the development of high-yielding, blast-resistant finger millet varieties. The landraces Bada Mandia and Lalsuru Mandia can serve as valuable donor parents for blast resistance in future breeding programs. Further research should expand beyond leaf blast to include neck blast and finger blast resistance, ultimately broadening the scope of disease resistance in finger millet. Combining resistant, yet low-yielding genotypes, such as Bada Mandia and Lalsuru Mandia, with susceptible, high-yielding genotypes, such as FIN5169, KMR711, and KMR656, will likely result in the development of high-yielding, blast-resistant

lines. ✓

COMPETING INTERESTS DISCLAIMER:

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper. ✓

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Only high lighted references are in the text.

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SUPPLIMENTARY

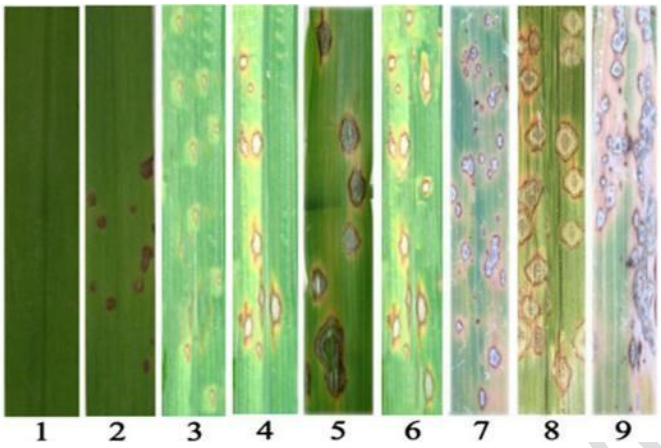
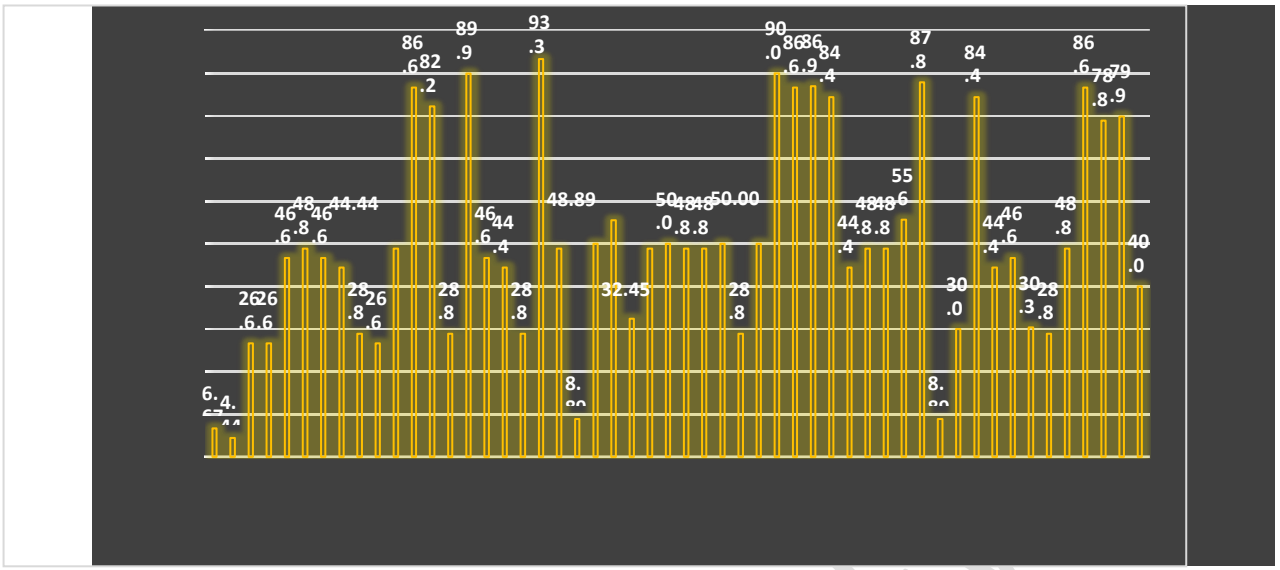


Fig1: (1-9) Disease Scale of Finger Millet

Fig.2. Spores of *Pyricularia oryzae*

Fig.3. **Spraying of inoculum in green house**

Should be in TNR



What are on the X and Y axes?

Fig. 4: Disease severity for fifty-two genotypes of finger millet

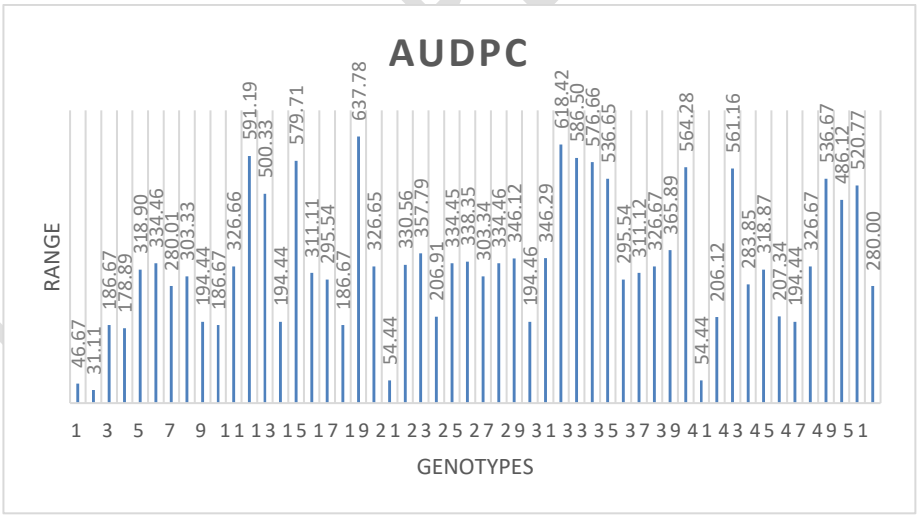


Fig 5: AUDPC for fifty-two genotypes of finger millet

Table 1: List of finger millet Genotypes along with respective collectedinstitutions.

Sl. No	Variety	Collected from
1	Bada Mandia	M.S. Swaminathan Research Foundation, Jeypore, Odisha
2	Lalsuru mandia	M.S. Swaminathan Research Foundation, Jeypore, Odisha
3	Telugu Mandia	M.S. Swaminathan Research Foundation, Jeypore, Odisha
4	Badtara	M.S. Swaminathan Research Foundation, Jeypore, Odisha
5	Bhairabi	M.S. Swaminathan Research Foundation, Jeypore, Odisha
6	Taya	M.S. Swaminathan Research Foundation, Jeypore, Odisha
7	Bada kumunda	M.S. Swaminathan Research Foundation, Jeypore, Odisha
8	Madi Muskuri	M.S. Swaminathan Research Foundation, Jeypore, Odisha
9	Chilli	M.S. Swaminathan Research Foundation, Jeypore, Odisha
10	Dangardi	M.S. Swaminathan Research Foundation, Jeypore, Odisha
11	Muskuri	M.S. Swaminathan Research Foundation, Jeypore, Odisha
12	Arjun	M.S. Swaminathan Research Foundation, Jeypore, Odisha
13	VL mandua- 352	M.S. Swaminathan Research Foundation, Jeypore, Odisha
14	Chaitanya	M.S. Swaminathan Research Foundation, Jeypore, Odisha
15	OEB610	M.S. Swaminathan Research Foundation, Jeypore, Odisha
16	VL352	All India Coordinate Research Project (AICRP) Mandya, Karnataka
17	FMCFMVZ	All India Coordinate Research Project (AICRP) Mandya, Karnataka
18	PR202	Agricultural Research Station, Vizianagaram
19	VR1176	Agricultural Research Station, Vizianagaram
20	VR1185	Agricultural Research Station, Vizianagaram
21	VR 1220	Agricultural Research Station, Vizianagaram
22	KOPN1056	Agricultural Research Station, Vizianagaram
23	PR-1639	Agricultural Research Station, Vizianagaram
24	DPLM 3	Agricultural Research Station, Vizianagaram
25	KMR656	All India Coordinate Research Project (AICRP) Mandya, Karnataka

26	DPLM2	All India Coordinate Research Project (AICRP) Mandya, Karnataka
27	FeZN15	All India Coordinate Research Project (AICRP) Mandya, Karnataka
28	VR1218	Agricultural Research Station, Vizianagaram
29	VR1225	Agricultural Research Station, Vizianagaram
30	VR1214	Agricultural Research Station, Vizianagaram
31	VR1228	Agricultural Research Station, Vizianagaram
32	TNEC1335	All India Coordinate Research Project (AICRP) Mandya, Karnataka
33	VR1221	Agricultural Research Station, Vizianagaram
34	PR1639	Agricultural Research Station, Vizianagaram
35	VR1217	Agricultural Research Station, Vizianagaram
36	VR1226	Agricultural Research Station, Vizianagaram
37	VR1222	Agricultural Research Station, Vizianagaram
38	FeZN84	All India Coordinate Research Project (AICRP) Mandya, Karnataka
39	BR9	All India Coordinate Research Project (AICRP) Mandya, Karnataka
40	KMR711	All India Coordinate Research Project (AICRP) Mandya, Karnataka
41	VR1233	Agricultural Research Station, Vizianagaram
42	CFMV1	All India Coordinate Research Project (AICRP) Mandya, Karnataka
43	WN572	All India Coordinate Research Project (AICRP) Mandya, Karnataka
44	GPV67	All India Coordinate Research Project (AICRP) Mandya, Karnataka
45	PR1506	Agricultural Research Station, Vizianagaram
46	VL400	All India Coordinate Research Project (AICRP) Mandya, Karnataka
47	FIN6164	Indian Institute of Millets Research, Hyderabad

48	FIN5146	Indian Institute of Millets Research, Hyderabad
49	FIN5169	Indian Institute of Millets Research, Hyderabad
50	FIN5167	Indian Institute of Millets Research, Hyderabad
51	Uduru(Susceptible)	All India Coordinate Research Project (AICRP) Mandya, Karnataka
52	Indaf 7(Resistant)	All India Coordinate Research Project (AICRP) Mandya, Karnataka

Table 2: Mean performance of AUDPC and AUCDC fifty-two genotypes in finger millet

Cite this in the text

S.N.	Genotype	AUDPC		AUCDC		GY	
		M	SD	M	SD	M	SD
1	Bada Mandia	43.89	2.83	9.92	0.74	21.99	2.80
2	Lalsuru Mandia	33.22	1.96	9.92	0.77	17.67	2.73
3	Telugu Mandia	180.56	5.85	9.49	0.38	19.94	2.62
4	Badtara	187.7	6.72	9.46	0.36	19.42	1.31
5	Bhairabi	311.7	3.04	9.41	0.38	18.50	2.71
6	Taya	315.85	3.51	9.41	0.39	19.03	0.79
7	Bada Kumunda	255.6	4.17	9.41	0.37	14.47	1.14
8	Madi Muskuri	303.99	4.36	9.11	0.87	17.56	1.80
9	Chilli	194.73	2.45	9.71	0.15	17.51	2.69
10	Dangardi	189.61	2.79	9.71	0.16	18.76	0.62
11	Muskuri	280.38	4.43	9.35	1.28	19.30	0.93
12	Arjun	479.84	1.76	8.00	1.28	18.66	1.97
13	VL Mandua-352	381.82	4.07	8.00	0.28	18.14	1.18
14	Chaitanya	193.76	2.94	9.44	1.07	19.19	1.02
15	OEB610	593.63	2.68	8.34	0.52	19.33	0.51

16	VL352	311.25	3.68	9.42	0.44	19.44	2.35
17	CFMVZ	284.75	4.63	9.39	0.28	20.72	1.60
18	PR202	174.51	4.44	9.57	1.12	21.24	1.54
19	VR1176	636.53	3.48	8.32	0.44	18.64	3.08
20	VR1185	342.58	3.46	9.39	0.02	19.31	0.50
21	VR 1220	57.4	2.79	9.96	0.44	20.58	1.33
22	KOPN1056	314.68	3.24	9.39	0.37	19.91	3.77
23	PR-1639	334.3	3.77	9.43	0.28	24.53	2.39
24	DPLM 3	194.4	4.12	9.57	0.36	21.34	0.46
25	KMR656	352.62	4.53	9.43	0.44	23.03	2.06
26	FMDPLM2	322.45	3.80	9.39	0.43	20.05	0.75
27	FeZN15	281.31	4.85	9.30	0.51	23.40	2.81
28	VR1218	345.11	3.49	9.22	0.41	21.58	0.75
29	VR1225	334.23	3.13	9.38	0.25	18.75	3.95
30	VR1214	177.82	2.87	9.54	0.40	17.70	1.30
31	VR1228	347.47	4.92	9.34	1.02	17.49	1.22
32	TNEC1335	592.25	7.25	8.50	1.25	18.56	1.36
33	VR1221	556.41	3.77	8.14	1.19	20.28	0.63
34	PR1635	457.87	2.93	8.17	1.25	19.23	0.80
35	VR1217	592.3	5.54	8.14	0.40	18.07	0.79
36	VR1226	283.45	3.29	9.34	0.40	19.44	1.53
37	VR1222	298.7	2.27	9.34	0.40	18.55	1.12
38	FeZN84	326.78	4.38	9.34	0.49	18.06	1.80
39	BR9FM	344.4	5.36	9.34	1.25	19.98	0.98
40	KMR711	553.29	4.91	8.14	0.07	25.16	3.54
41	VR1233	58.36	3.87	9.81	0.42	21.08	2.53
42	CFMV1	183.7	2.67	9.33	1.11	22.23	1.23
43	WN572	385.34	4.19	8.66	0.40	23.53	0.28
44	GPV67	257.56	4.95	9.33	0.40	20.29	0.75
45	PR1506	311.42	3.88	9.34	0.25	25.63	1.36
46	VL400	206.87	4.59	9.58	0.24	21.30	1.02

47	FIN6164	196.31	1.87	9.62	0.40	20.83	2.38
48	FIN5146	325.72	4.81	9.34	1.19	22.90	3.22
49	FIN5169	539.02	2.9	8.14	1.03	19.46	3.08
50	FIN5167	404.23	3.47	8.47	1.28	22.38	1.67
51	Uduru(Susceptible)	460.47	1.87	7.90	0.20	19.94	1.98
52	Indaf (Resistant)	284.41	3.94	9.66	0.45	20.44	1.36
	Mean	314		9.71		24.88	
	SE(m)	20		0.32		3.02	
	CV%	46		24.0		92	
	CD%	19.51		8.2		1.4	
	SD	67.7		2.3		22.8	
	σ^2G	199.2		68.43		10.46	
	σ^2P	206.4		68.74		17.33	
	GCV	15.05		16.31		4.16	
	PCV	15.28		16.35		5.36	
	h^2	96.98		99.55		60.39	
	GA	286.76		17.00		8.10	
	GA as % ofmean	30.53		0.66		0.13	

Note: AUCDC: Chlorophyll content, AUDPC: Area under disease progress curve, GY: Grain Yield/plant. SE: Standard Error, CV %: Coefficient of Variation, CD%: Critical difference, SD: Standard Deviation, M: Mean, σ^2G: Genotypic Variance, σ^2P: Phenotypic Variance, GCV : Genotypic co-efficient of variation, PCV: Phenotypic co-efficient of variation, GA: Genetic advance, h^2 :heritability

Table 3: Disease severity (%) for fifty-two finger millet genotypes under natural field condition. ✓

S.N.	Genotype	Obs.1	Obs.2	Obs.3	Obs.4	Obs.5	Obs.6	Obs.7	Obs.8	Obs.9	Obs.10	Avg.
1	Bada Mandia	0.00	0.00	2.22	2.22	4.44	4.44	6.67	6.67	6.67	6.67	4.00
2	Lalsuru Mandia	0.00	0.00	2.22	2.22	4.44	4.44	4.44	4.44	4.44	4.44	3.11
3	Telugu Mandia	0.00	4.44	6.67	13.33	15.56	20.00	24.44	24.44	26.67	26.67	16.22
4	Badtara	0.00	6.67	8.89	11.11	17.78	20.00	22.22	24.44	24.44	26.67	16.22
5	Bhairabi	0.00	4.44	8.89	11.11	17.78	20.00	22.22	35.56	44.44	46.67	21.11
6	Taya	4.44	4.44	11.11	15.56	17.78	24.44	26.67	42.22	46.67	48.89	24.22
7	Bada Kumunda	2.22	4.44	11.11	13.33	17.78	20.00	24.44	28.89	33.33	46.67	20.00
8	Madi Muskuri	2.22	6.67	13.33	11.11	20.00	22.22	26.67	31.11	42.22	44.44	22.00
9	Chilli	0.00	4.44	13.33	17.78	17.78	20.00	22.22	22.22	26.67	26.67	17.33
10	Dangardi	0.00	6.67	11.11	13.33	17.78	20.00	22.22	24.44	26.67	26.67	16.89
11	Muskuri	0.00	4.44	11.11	17.78	13.33	20.00	24.44	40.00	44.44	48.89	22.44
12	Arjun	4.44	6.67	15.56	20.00	22.22	24.44	40.69	75.66	82.22	86.69	37.89
13	VL Mandua-352	0.00	4.44	11.11	13.33	17.78	26.67	33.33	51.11	60.69	82.26	30.07
14	Chaitanya	0.00	4.44	13.33	17.78	20.00	20.00	22.22	24.44	26.67	28.89	17.78
15	OEB610	2.22	6.67	15.56	17.78	24.44	26.67	31.11	64.44	75.66	89.97	35.45
16	VL352	2.22	4.44	6.67	13.33	17.78	22.22	24.44	35.65	42.22	46.67	21.57
17	CFMVZ	2.22	4.44	11.11	15.56	22.22	22.22	28.89	37.78	40.00	44.44	22.89
18	PR202	0.00	2.22	8.89	11.11	15.56	17.78	20.00	22.22	24.44	28.89	15.11
19	VR1176	2.22	6.67	15.56	17.78	26.67	28.89	44.44	68.89	88.89	93.33	39.33
20	VR1185	0.00	6.67	8.89	15.56	22.22	22.22	24.44	42.22	44.44	48.89	23.56
21	VR 1220	0.00	2.22	2.22	4.44	4.44	4.44	6.67	6.67	6.67	8.89	4.67
22	KOPN1056	0.00	4.44	11.11	15.56	17.78	20.00	26.67	42.22	44.44	50.00	23.22
23	PR-1639	2.22	4.44	11.11	11.11	17.78	24.44	26.67	44.44	46.67	55.56	24.44
24	DPLM 3	0.00	6.67	11.11	15.56	15.56	17.78	20.00	24.44	26.67	32.45	17.02
25	KMR656	0.00	6.67	8.89	15.56	24.44	20.00	28.89	33.33	46.67	48.89	23.33
26	FMDPLM2	2.22	4.44	11.11	17.78	17.78	22.22	28.89	40.00	46.67	50.00	24.11
27	FeZN15	0.00	8.89	15.56	17.78	22.22	22.22	26.67	33.37	37.78	48.89	23.34
28	VR1218	2.22	6.67	8.89	13.33	20.00	20.00	28.89	44.44	46.67	48.89	24.00

29	VR1225	0.00	6.67	11.11	15.56	20.00	20.00	26.67	46.67	48.89	50.00	24.56
30	VR1214	2.22	6.67	11.11	15.56	17.78	20.00	20.00	24.44	26.67	28.89	17.33
31	VR1228	2.22	6.67	13.33	13.33	20.00	24.44	37.78	40.00	48.89	50.05	25.67
32	TNEC1335	4.44	8.89	13.33	20.00	22.22	31.11	40.00	82.22	86.69	90.00	39.89
33	VR1221	2.22	6.67	13.33	22.22	31.11	42.22	51.11	68.89	80.88	86.69	40.53
34	PR1635	0.00	4.44	11.11	13.33	17.78	20.00	40.49	51.11	77.79	86.97	32.30
35	VR1217	4.44	6.67	11.11	20.00	26.67	33.33	42.22	60.00	68.89	84.44	35.78
36	VR1226	0.00	6.67	8.89	8.89	20.00	24.44	26.67	37.78	40.00	44.44	21.78
37	VR1222	0.00	4.44	13.33	17.78	22.22	26.67	26.67	37.78	40.00	48.89	23.78
38	FeZN84	2.22	4.44	13.33	15.56	15.56	20.00	37.78	40.00	44.44	48.89	24.27
39	BR9	2.22	6.67	15.56	26.67	28.89	33.33	40.00	44.44	48.89	55.65	30.23
40	KMR711	4.44	6.67	15.56	20.00	22.22	26.67	44.44	68.89	73.33	87.89	37.01
41	VR1233	0.00	2.22	2.22	4.44	4..44	4.44	6.67	6.67	6.67	8.89	4.67
42	CFMV1	0.00	2.22	17.78	15.56	17.78	20.00	24.44	24.44	28.89	30.00	18.11
43	WN572	2.22	6.67	11.11	15.56	20.00	24.44	33.33	53.33	75.89	84.44	32.70
44	GPV67	0.00	6.67	13.33	17.78	20.00	22.22	28.89	31.11	36.64	44.46	22.11
45	PR1506	0.00	6.67	13.33	13.33	20.00	22.22	24.44	40.00	44.44	46.67	23.11
46	VL400	0.00	6.67	11.11	13.33	20.00	22.22	26.67	28.89	28.89	30.35	18.81
47	FIN6164	2.22	4.44	8.89	15.56	17.78	20.00	22.22	26.67	26.67	28.89	17.33
48	FIN5146	0.00	6.67	11.11	15.56	20.00	22.22	24.44	42.22	44.44	48.89	23.56
49	FIN5169	2.22	11.11	15.56	24.44	31.11	42.22	55.55	60.00	66.67	86.67	39.56
50	FIN5167	0.00	4.44	13.33	13.33	17.78	20.00	26.67	48.89	60.00	78.89	28.33
51	Uduru(Susceptible)	0.00	6.67	13.33	15.56	22.22	26.67	28.89	53.33	68.89	79.90	31.55
52	MR1(Resistant)	0.00	4.44	8.89	13.33	22.22	24.44	24.44	33.33	40.00	40.00	21.11

Table 4: Area Under Chlorophyll Decline Curve for fifty-two finger millet genotypes

TNR

S.N.	Genotype	Obs.1	Obs.2	Obs.3	Obs.4	Obs.5	Obs.6	Obs.7	Obs.8	Obs.9	Obs.10	Avg.
1	Bada Mandia	10.00	10.00	10.00	9.97	9.97	9.95	9.84	9.84	9.84	9.83	9.92
2	Lalsuru Mandia	10.00	10.00	10.00	9.97	9.97	9.96	9.84	9.84	9.83	9.82	9.92
3	Telugu Mandia	10.00	10.00	9.80	9.61	9.58	9.50	9.34	9.11	9.00	8.97	9.49
4	Badtara	10.00	10.00	9.60	9.58	9.58	9.50	9.34	9.11	9.00	8.97	9.46
5	Bhairabi	10.00	10.00	9.53	9.48	9.47	9.37	9.30	9.22	8.98	8.84	9.41
6	Taya	10.00	10.00	9.53	9.48	9.47	9.37	9.30	9.22	8.98	8.84	9.41
7	Bada Kumunda	10.00	10.00	9.53	9.48	9.47	9.37	9.30	9.22	8.98	8.84	9.41
8	Madi Muskuri	10.00	10.00	9.53	9.48	9.47	9.37	9.30	8.89	7.60	7.54	9.11
9	Chilli	10.00	10.00	9.67	9.65	9.67	9.64	9.64	9.63	9.63	9.62	9.71
10	Dangardi	10.00	10.00	9.69	9.68	9.66	9.64	9.63	9.61	9.60	9.59	9.71
11	Muskuri	10.00	10.00	9.53	9.50	9.50	9.50	9.42	9.39	9.36	9.20	9.54
12	Arjun	10.00	10.00	8.87	7.68	8.34	7.62	7.50	6.87	6.75	6.40	8.00
13	VL Mandua-352	10.00	10.00	9.53	9.53	9.52	9.49	9.38	9.36	8.98	8.64	9.44
14	Chaitanya	10.00	10.00	9.68	9.68	9.66	9.50	9.42	9.39	9.36	9.09	9.44
15	OEB610	10.00	10.00	8.97	8.57	8.36	8.11	7.84	7.34	7.21	7.00	8.34
16	VL352	10.00	10.00	9.54	9.54	9.50	9.50	9.42	9.39	9.36	9.20	9.54
17	FMCFMVZ	10.00	10.00	9.54	9.54	9.53	9.47	9.31	9.10	8.78	8.69	9.39
18	PR202	10.00	10.00	9.60	9.68	9.66	9.50	9.42	9.39	9.36	9.09	9.57
19	VR1176	10.00	10.00	9.10	8.57	8.36	8.11	7.84	7.34	7.00	6.89	8.32
20	VR1185	10.00	10.00	9.53	9.53	9.53	9.47	9.31	9.10	8.78	8.69	9.39
21	VR 1220	10.00	10.00	9.98	9.98	9.98	9.96	9.94	9.93	9.93	9.93	9.96
22	KOPN1056	10.00	10.00	9.53	9.53	9.53	9.47	9.31	9.10	8.78	8.69	9.39
23	PR-1639	10.00	10.00	9.53	9.53	9.40	9.36	9.34	9.34	9.00	8.88	9.43
24	DPLM 3	10.00	10.00	9.68	9.68	9.66	9.50	9.42	9.39	9.36	9.09	9.57
25	KMR656	10.00	10.00	9.53	9.53	9.40	9.36	9.34	9.34	9.00	8.88	9.43
26	DPLM2	10.00	10.00	9.53	9.53	9.53	9.47	9.31	9.11	8.78	8.69	9.39
27	FeZN15	10.00	10.00	9.50	9.43	9.31	9.11	9.06	8.98	8.86	8.79	9.30
28	VR1218	10.00	10.00	9.51	9.36	9.25	9.08	8.99	8.85	8.86	8.79	9.22

29	VR1225	10.00	10.00	9.50	9.40	9.40	9.34	9.32	9.24	8.98	8.64	9.38
30	VR1214	10.00	10.00	9.62	9.50	9.48	9.43	9.43	9.41	9.39	9.21	9.54
31	VR1228	10.00	10.00	9.49	9.34	9.31	9.26	9.21	9.14	9.01	8.70	9.34
32	TNEC1335	10.00	10.00	9.00	8.79	8.66	8.21	8.04	7.64	7.49	7.19	8.50
33	VR1221	10.00	10.00	8.84	8.31	8.16	8.05	7.68	7.49	6.89	6.00	8.14
34	PR1635	10.00	10.00	9.49	9.34	9.31	9.26	9.21	9.14	9.01	8.70	9.34
35	VR1217	10.00	10.00	8.84	8.31	8.16	8.05	7.68	7.49	6.89	6.00	8.14
36	VR1226	10.00	10.00	9.49	9.34	9.31	9.26	9.21	9.14	9.01	8.70	9.34
37	VR1222	10.00	10.00	9.49	9.34	9.31	9.26	9.21	9.14	9.01	8.70	9.34
38	FeZN84	10.00	10.00	9.49	9.34	9.31	9.26	9.21	9.14	9.01	8.70	9.34
39	BR9	10.00	10.00	9.49	9.34	9.31	9.26	9.21	9.14	9.01	8.70	9.34
40	KMR711	10.00	10.00	8.84	8.31	8.16	8.05	7.68	7.49	6.89	6.00	8.14
41	VR1233	10.00	10.00	9.87	9.86	9.86	9.86	9.85	9.64	9.64	9.54	9.81
42	CFMV1	10.00	10.00	9.64	9.64	9.59	9.51	9.60	9.54	9.46	9.24	9.62
43	WN572	10.00	10.00	9.43	9.34	9.31	9.26	9.21	9.14	9.01	8.70	9.34
44	GPV67	10.00	10.00	9.42	9.34	9.31	9.26	9.21	9.14	9.01	8.70	9.33
45	PR1506	10.00	10.00	9.44	9.34	9.31	9.26	9.21	9.14	9.01	8.70	9.34
46	VL400	10.00	10.00	9.64	9.64	9.59	9.51	9.60	9.54	9.46	9.24	9.62
47	FIN6164	10.00	10.00	9.70	9.64	9.59	9.51	9.60	9.54	9.46	9.24	9.62
48	FIN5146	10.00	10.00	9.48	9.34	9.31	9.26	9.21	9.14	9.01	8.70	9.34
49	FIN5169	10.00	10.00	8.84	8.31	8.16	8.05	7.68	7.49	6.89	6.00	8.14
50	FIN5167	10.00	10.00	9.12	8.79	8.66	8.21	8.04	7.64	7.49	7.19	8.51
51	Uduru(Susceptible)	10.00	10.00	9.73	9.68	9.66	9.62	9.59	9.50	9.46	9.34	9.65
52	MR1(Resistant)	10.00	10.00	8.87	7.68	8.34	7.62	7.50	6.87	6.75	6.40	8.00

Table 5: Mean intra and inter cluster distance in finger millet

Cluster	I	II	III	IV	V
I	**9183.57** (95.83)	130051.12 **(360.62)**	74855.96 **(273.59)**	59904.32 **(244.75)**	229288.68 **(478.84)**
II		**12947.61** (113.78)	118925.65 **(344.85)**	32515.21 **(180.31)**	65545.81 **(256.01)**
III			**22172.45** (148.90)	122965.99 **(350.66)**	95475.27 **(308.99)**
IV				**0.00**	150456.87 **(387.88)**
V					**0.00**

***The values in brackets core D values**

Table 6: Grouping of fifty-two finger millet genotypes based on D^2 analysis

Cluster	Number of genotypes	Genotypes
I	22	KMR656, FIN5146, FeZn84, DPLM2, VR 1225,PR-1639, Taya, KOPN1056, Bhairabhi, PR202, VL352, PR1506, BR9, VR1185, VR1222, CFMVZ, VR1218, VR1228, Muskuri, FeZn15, VR1226, INDAF,
II	6	TNEC1335, VR1217, VR1221, OEB610, KMR711, FIN5169
III	17	Chilli, DPLM3, FM1, FIN6164, Dangardi, Badtara, CFMV1, Telugu mandia, VR1214, Lalsuru mandia, Bada mandia, VR1220, VR1233, GPV67, Bada kumunda, VL400
IV	6	WN572, UDURU, PR1630, DPLM3 FIN5167, FM4
V	1	VR1176

Table 7: Based on the disease severity the finger millet genotypes were classified under 4classes TNR

Rating scale	Symptoms and lesions	Disease reaction	Name of Genotypes	Numbers of genotypes
1	No lesion to small brown specks of pinhead size.	Highly resistant	Bada mandia, Lalsuru mandia, VR 1220, VR 1233,	4
2-3	Large brown specks. Small, roundish to slightly elongated, necrotic gray resistant. Spots, about 1-2 mm in diameter with a brown margin	Moderately resistant	Telugu mandia, Badtara, Chilli, Dangardi, FM1, PR202, DPLM3, VR1214, CFMV1, VL400, FIN6164	11
4-5	Typical blast lesions, elliptical, 1-2 cm long, usually confined to the area between main veins, covering	susceptible	Bhairabi, Taya, Bada kumunda, Madi muskuri, FM4, VL352, FMCFMV2, VR1185, KOPN1056, PR-1639, KMR656, DPLM2, FeZN15, VR1218, VR1225, VR1228, FeZn84, FIN5146,PR1506, GPV67,WN572, BR9	22
6-9	Typical blast lesions covering 10-25% of the leaf area. Typical blast lesions covering 26-50% of the leaf area.	Highly Susceptible	FIN5169, KMR711, VR1217, VR1221, VR1176, OEB610, FM2	7

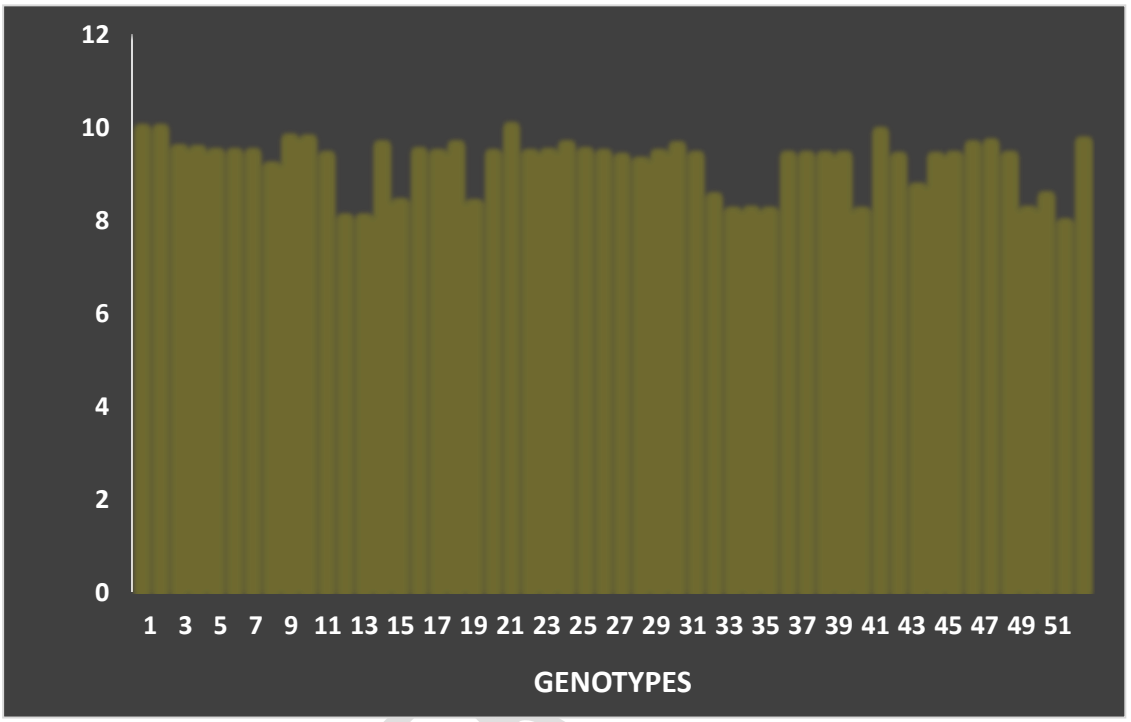


Fig 6: AUCDC for fifty-two genotypes of finger millet

Label Y axes

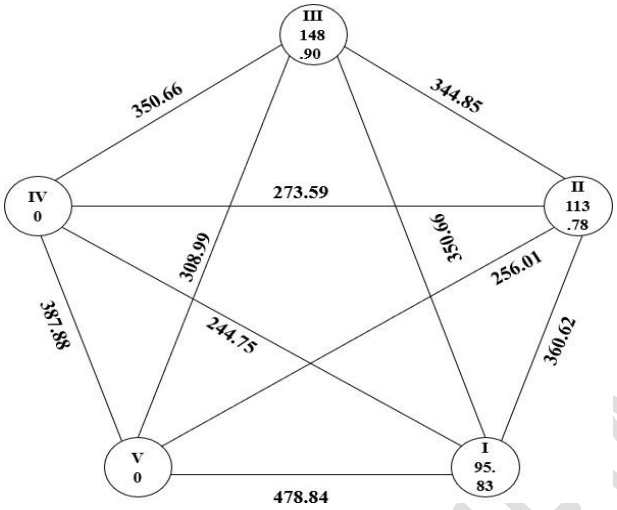


Fig 7: Mahalanobis Euclidean distance using Torcher's method

TNR