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# Multifaceted characterisation of *Bipolaris maydis* isolates causing maydis leaf blight of maize in India

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## Abstract

Maydis leaf blight (MLB), caused by *Bipolaris maydis*, is a major foliar disease of maize in India, causing yield losses ranging from 20 % to 85 %. Its prevalence has increased with rising temperature regimes. The present study characterised the cultural, morphological, pathogenic and molecular variability among 22 isolates of *B. maydis* collected from five agro-climatic zones across India. Radial growth on potato dextrose agar (PDA) ranged from 49.00 to 90.00 mm and the growth rate from 4.9–9.0 mm day$^{-1}$. Colony colour varied from creamy white to black and texture from smooth to rough. Conidial length and width ranged between 36.62–72.12 µm and 9.45–14.45 µm, respectively, with the number of septa varying from 5 to 9. Significant positive correlations were observed among conidial length, width and septation ($r > 0.80$, $p < 0.01$). All isolates were pathogenic, showing considerable variation in virulence. The incubation period varied from 39.6 to 57.6 hr and the latent period from 67.2 to 91.2 hr across genotypes. Mean lesion length ranged from 14.34 to 19.35 mm and lesion breadth from 2.45 to 2.90 mm. Disease severity ranged from 5.3 to 7.5 on a 1–9 scale. Isolate Bm-7 (Pantnagar-2) was the most virulent, with the highest disease score (7.5), shortest incubation (39.6 hr) and latent (67.2 hr) periods and longest lesion length (19.35 mm). It formed a distinct cluster in pathogenic grouping and was the most divergent in internal transcribed spacer (ITS)-based phylogeny. Sequencing of the ITS (≈ 589 bp) region grouped all isolates into a single major clade, indicating limited molecular differentiation. Dendrograms derived from morphological and pathogenic data were congruent, whereas no association was found between molecular grouping and geographic origin. The virulent Bm-7 isolate can serve as a reference for host–pathogen interaction and screening studies in maize breeding programs.

**Keywords:** *Bipolaris maydis*; maydis leaf blight; maize, phylogenetic tree; sequencing; variability

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## Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops globally, valued for its diverse industrial, nutritional and feed applications. In India, maize occupies a significant share of the kharif and rabi cropping systems across varied agro-climatic regions. In India, maize is cultivated on 10.7 million hectares, with a total production and average productivity of 38 million tons and 3.5 tonnes/ha, respectively (1). However, its productivity is severely constrained by several foliar diseases, among which maydis leaf blight (MLB), caused by *Bipolaris maydis* (Y. Nisik. & C. Miyake). Shoemaker, is of major economic importance. Among the biotic stresses, MLB is a severe fungal leaf disease affecting maize and other crops, such as sorghum and teosinte, globally. Severe attacks of MLB can reduce crop yields by up to 40 % (2–4). In India, MLB has emerged as one of the most widespread and severe diseases, particularly affecting regions such as Jammu and Kashmir, Himachal Pradesh, Sikkim, Meghalaya, Punjab, Haryana, Rajasthan, Delhi, Uttar Pradesh, Bihar, Madhya Pradesh, Gujrat, Maharashtra, Andhra Pradesh, Karnataka and Tamil Nadu. Under projected climate warming, the pathogen's prevalence and aggressiveness are expected to intensify, posing a significant challenge to sustainable maize production.

The pathogen *B. maydis* exhibits considerable variation in its cultural, morphological and pathogenic traits, which often complicates the breeding of durable resistance in maize (5, 6). Differences in colony characteristics, sporulation and conidial morphology have been widely

documented in *Bipolaris* spp., reflecting the influence of genetic diversity and ecological adaptation. Likewise, pathogenic variability among isolates from distinct geographical regions can lead to differential host responses, necessitating region-specific screening and management strategies. Comprehensive characterisation of *B. maydis* populations is therefore critical for understanding pathogen evolution, host–pathogen interactions and for identifying virulent isolates useful in resistance breeding (3, 4). Molecular markers such as the internal transcribed spacer (ITS) gene regions have proven effective for delineating intraspecific variability and phylogenetic relatedness among fungal populations. Combining phenotypic and genotypic assessments provides deeper insights into the population structure, epidemiological potential and evolutionary dynamics of fungal pathogens (7, 8). In this context, the present investigation was undertaken to decipher (i) variability in phenotypic and pathogenic traits under standardised laboratory and greenhouse conditions, (ii) examine interrelationships among morphological and pathogenic parameters and (iii) evaluate molecular diversity based on ITS gene sequencing. The findings provide a comprehensive understanding of the diversity and virulence patterns in *B. maydis* populations, which can aid in developing regionally adapted and durable disease management strategies for maize improvement programs.

## Materials and Methods

### Sampling and fungal strain isolation

Roving surveys were conducted during the kharif 2020 season in major maize-growing districts of Haryana, namely Ambala, Jind, Kaithal, Kurukshetra, Panchkula, Panipat, Sonipat and Yamunanagar to collect samples infected with MLB. Additional infected leaf samples were procured from Bihar, Delhi, Jammu and Kashmir, Punjab, Uttarakhand and Uttar Pradesh, representing five distinct agro-climatic zones of India. In total, 22 isolates of *B. maydis* were obtained and designated as Bm-1 to Bm-22 (Table 1). Isolation of the pathogen was carried out following a previously described method (9). Diseased leaf segments (2–3 mm) were washed under running tap water, surface-sterilised with 2.5 % sodium hypochlorite for 15–30 sec and rinsed thrice with sterile distilled water. The sterilised bits were placed aseptically on potato dextrose agar (PDA) medium (10) amended with streptomycin (100 mg $L^{-1}$) to suppress bacterial contamination. Plates were incubated at 28 ± 1 °C in a biochemical oxygen demand (BOD) incubator and examined after 24 hr for fungal growth. Emerging colonies were sub-cultured on fresh PDA to obtain pure cultures. Single-hyphal tip cultures were prepared by spreading a loopful of mycelial suspension on 2% water agar. Under an inverted microscope, a single germinated hyphal tip was identified and aseptically transferred to PDA slants. These were incubated at 28 ± 1 °C for seven days and pure cultures were maintained at 4 °C on PDA slants for further studies.

**Table 1.** Details of *Bipolaris maydis* isolates used in the study

| Sl. No. | Isolate Designation | Location | State | Latitude and longitude | Agro climatic zones | NCBI Accession No. Based on ITS |
|---|---|---|---|---|---|---|
| 1. | Bm-1 | Motipur | Bihar | 26.2525° N, 85.1609° E | Middle Gangetic Plains | PP712917 |
| 2. | Bm-2 | Delhi | Delhi | 28.7041° N, 77.1025° E | Trans-Gangetic Plains | PP712918 |
| 3. | Bm-3 | Srinagar | Jammu and Kashmir | 34.0837° N, 74.7973° E | Western Himalayan region | PP712919 |
| 4. | Bm-4 | Palampur | Himachal Pradesh | 32.1109° N, 76.5363° E | Western Himalayan region | PP712920 |
| 5. | Bm-5 | Hyderabad | Telangana | 17.3850° N, 78.4867° E | Southern Plateau and Hills | PP712921 |
| 6. | Bm-6 | Pantnagar-1 | Uttarakhand | 29.0222° N, 79.4908° E | Western Himalayan region | PP712922 |
| 7. | Bm-7 | Pantnagar-2 | Uttarakhand | 29.0222° N, 79.4908° E | Western Himalayan region | PP712923 |
| 8. | Bm-8 | Almora | Uttarakhand | 29.5892° N, 79.6467° E | Western Himalayan region | PP712924 |
| 9. | Bm-9 | Kasganj | Uttar Pradesh | 27.8085° N, 78.6461° E | Middle- Gangetic Plains | PP712925 |
| 10. | Bm-10 | Rusulpur Kalan (Karnal-1) | Haryana | 29.6686° N, 77.0651° E | Trans-Gangetic Plains | PP712926 |
| 11. | Bm-11 | Uchani (Karnal-2) | Haryana | 29.7322° N, 76.9823° E | Trans-Gangetic Plains | PP712927 |
| 12. | Bm-12 | Kunwar Kheri Kurukshetra | Haryana | 29.8945° N, 76.8116° E | Trans-Gangetic Plains | PP712928 |
| 13. | Bm-13 | Yamunanagar | Haryana | 30.1290° N, 77.2674° E | Trans-Gangetic Plains | …… |
| 14. | Bm-14 | Nirzan (Jind-1) | Haryana | 29.3156° N, 76.3898° E | Trans-Gangetic Plains | …… |
| 15. | Bm-15 | Sunderpur(Jind-2) | Haryana | 29.5621° N, 76.0892° E | Trans-Gangetic Plains | PP712929 |
| 16. | Bm-16 | Bhotwala(Jind-3) | Haryana | 29.3573° N, 76.3941° E | Trans-Gangetic Plains | PP712930 |
| 17. | Bm-17 | Aterna(Sonipat-1) | Haryana | 28.9031° N, 77.1550° E | Trans-Gangetic Plains | …… |

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| | | | | | | |
|---|---|---|---|---|---|---|
| 18. | Bm-18 | Manouli(Sonepat-2) | Haryana | 28.9083° N, 77.1794° E | Trans-Gangetic Plains | PP712931 |
| 19. | Bm-19 | Smalkha (Panipat) | Haryana | 29.2405° N, 77.0118° E | Trans-Gangetic Plains | PP712932 |
| 20. | Bm-20 | Ambala | Haryana | 30.3752° N, 76.7821° E | Trans-Gangetic Plains | PP712933 |
| 21. | Bm-21 | Derabassi | Punjab | 30.5887° N, 76.8471° E | Trans-Gangetic Plains | …… |
| 22. | Bm-22 | Morni (Panchkula) | Haryana | 30.6942° N, 76.8606° E | Trans-Gangetic Plains | …… |

NCBI: National Center for Biotechnology Information; ITS: internal transcribed spacer.

## Morpho-cultural characterisation of isolates

**To investigate the morphological and cultural characteristics of various isolates of *Bipolaris maydis,* isolates were individually cultured**

A 5 mm mycelial disc from an actively growing culture of each isolate was transferred to 90 mm PDA plates with three replications each and plates were incubated at 28 ± 1 °C. Cultural variability was assessed following the methods of (9). After 10 days, observations of cultural phenotypes were recorded including colony colour, texture, margin and zonation. Colony diameter was measured on the 3$^{rd}$, 5$^{th}$, 7$^{th}$ and 10$^{th}$ days after inoculation and growth rate (mm day$^{-1}$) was calculated based on the increase in colony diameter over time. After this, morphological characterisation was done using slides prepared from seven-day-old cultures mounted in lactophenol cotton blue. Observations were made at 20×, 40× and 100× magnifications using a phase-contrast microscope (Carl Zeiss Imager.M2, Germany) equipped with an Axiocam 503 mono camera. Measurements of conidial length, width, septation number, conidiophore structure and mycelial diameter were taken from 30 conidia per isolate, using a 10 µm ocular scale calibrated with a stage micrometer. Representative photomicrographs were captured to document morphological variation. A dendrogram was generated to cluster isolates based on their cultural and morphological characteristics using Euclidean squared distance and Ward's minimum variance method (11–13).

## Pathogenic variability

Pathogenic variability among *B. maydis* isolates was evaluated under controlled polyhouse conditions at CCS HAU, Regional Research Station, Karnal. Ten maize genotypes exhibiting differential reactions to MLB, HQPM-1, HQPM-4 (R), HM-10, HKI 1105 × HKI 488 (MR), Punjab Sweet Corn Composite, Vivek (MS), HM-8, HM-9, HKI-327 T and HKI 536 CBT (S)-were used to quantify isolate virulence. Seeds were sown in sterilised soil– farmyard manure (FYM) (2 : 1) mixture in 12-inch earthen pots, with 3 plants per pot and 4 replications per genotype. Each isolate was mass-multiplied on sorghum grains and a small pinch of ground inoculum was placed in the leaf whorl of 20–25-day-old plants. Humidity was maintained (> 90 %) by covering plants with plastic sheets for 48 hr post-inoculation (14). Data were recorded for incubation period (IP), latent period (LP), lesion shape, size and colour and disease severity (DS, %) at 20 days after inoculation. Lesion dimensions were measured with a digital vernier caliper. Disease severity was scored using the 1–9 scale of All India Coordinated Research Project (AICRP) on maize and isolates were grouped based on their virulence (15). Pathogenic clustering was performed by constructing a dendrogram using Euclidean squared distance and Ward's minimum variance method (13).

## Isolation of genomic DNA

Genetic variability among the *B. maydis* isolates was analysed through ITS-rDNA gene sequencing. For DNA extraction, isolates were grown in potato dextrose broth (PDB) prepared by pouring 100 mL into 250 mL conical flasks, sterilised at 121 °C and 15 psi for 15 min. A 5 mm mycelial disc from a seven-day-old culture was inoculated into each flask and incubated for 15 days at 28 ± 1 °C in a BOD shaker incubator. The resulting mycelial mats were harvested aseptically under laminar airflow, filtered through Whatman No. 1 paper, air-dried and stored at -20 °C for subsequent molecular analysis. Genomic DNA was extracted using the Wizard® Genomic DNA Purification Kit (Catalogue No. A1120; Promega Corporation, USA) following the manufacturer's protocol with minor modifications. Approximately 40 mg of mycelium was ground to a fine powder in liquid nitrogen using a pre-chilled mortar and pestle. The powdered tissue was transferred to 1.5 mL microcentrifuge tubes containing 600 µL nuclei lysis solution and incubated at 65 °C for 15 min in a water bath. In the last step, the pellet was washed with 600 µL of 70 % ethanol and centrifuged at 13000–16000 × g. DNA concentration and purity were determined using a Nanodrop spectrophotometer (Thermo Scientific) by loading 1 µL of each sample. Readings were expressed as ng µL$^{-1}$ concentration and $A_{260}/A_{280}$ ratio used to evaluate purity.

## Polymerase chain reaction amplification

A set of species specific ITS gene primer was used for amplification which includes ITS-1 f (5'-TCCGTAGGTGAACCTGCGG-3'), ITS-4 r (5'-TCCTCCGCTTATTGATATGC-3'). The primer was synthesised by Spectrum technologies, New Delhi. A 20 µL polymerase chain reaction (PCR) reaction was undertaken with 10 µL master-mix, 1 µL of forward and reverse primers each, 2 µL DNA and 6 µL of water. The amplification reactions were performed on 96 gradient thermo cycler (Thermo scientific) with aninitial pre-denaturation at 95 ºC for 5 min followed by 30 cycles each at denaturation at 95 ºC for 30 sec, annealing at 55.5 ºC for 30 sec, extension at 72 ºC for 45 sec followed by final extension at 72 ºC for 7 sec. All isolates were amplified by using these primer pairs and amplified products were electrophoresed in 1.5 % agarose gel (Agarose – LE, MB grade, Affymetrix) for 2 hr and analysed for banding pattern in gel documentation (gel-doc) system (Thermo scientific, Fusion Solo S). Amplified

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PCR products were purified using the Wizard® SV Gel and PCR Clean-Up System (Promega Corporation, USA) to remove unincorporated primers, nucleotides and other reaction components prior to sequencing. Then, the purified DNA was stored at –20 °C for further sequencing.

### Sequencing, alignment and construction of phylogenetic tree

The PCR purified product obtained after PCR clean-up system from different *B. maydis* isolates were selected for ITS region and β-tubulin gene sequencing by using Big Dye® Terminator v 3.1 Cycle Sequencing Kit (ABI, USA) in an automated DNA sequencer (Applied Biosystem 3130XL Genetic Analyzer) available in the Department of Animal Biotechnology, College of Veterinary Science, LUVAS, Hisar. The sequencing PCR reaction mixture (10 µL) includes nuclease free water (1.9 µL), dilution buffer 5x (2 µL), Big dye terminator master mix (0.5 µL), DMSO (0.6 µL), forward and reverse sequencing primer (2 µL), template (3 µL). The reactions for sequencing PCR were carried out in verity thermo cycler (ABI, USA) using the optimum conditions required for sequencing with an initial pre- denaturation at 96 ºC for 1 min followed by 25 cycles each of having denaturation at 96 ºC for 10 sec, annealing at 50 ºC for 5 sec, primer extension at 60 ºC for 5 min followed by final extension at 72 ºC for 10 min. After the final extension step, PCR products were purified through Big Dye® Terminator v 3.1 clean up method (Tube method). In this, PCR reaction product was transferred to 1.5 mL micro-centrifuge tube and 12 µL of master mix 1 (10 µL Milli-Q water and 2 µL f 25 mM EDTA) was added to tube containing 10 µL of reaction product. The contents were mixed properly and 52 µL of master mix II (2 µL of 3M sodium acetate of pH 4.6 and 50 µL of ethanol) was added to each tube. Contents were mixed well and incubated at room temperature for 15 min. Samples were centrifuged at 12000 rpm for 20 min at room temperature. Supernatant was decanted and pellet obtained was washed with 250 µL of 70 % ethanol followed by the air-drying process. The pellet was re-suspended in 13 µL of Hi-Di formamide by slight vortexing and short centrifugation and then samples were loaded in 96 well sequencing plate. A 96 well sequencing plate was loaded in automated DNA sequencer (Applied Biosystem 3130 XL Genetic Analyzer). Sequencer used the Foundation Data Collection Software v 3.0 and Sequence Analysis software v 5.2.

The raw sequences obtained after sequencing were searched against the NCBI database using BLAST (https://blast.ncbi.nlm.nih.gov) to confirm their identity with the organism under study. After blast analysis of raw sequences contig's were generated by using CAP-3 software. Contig's after blast were aligned by using Clustal-W, phylogenetic tree was constructed by using Neighbor-joining method at 1000 bootstrap value by using Tamura-Nei model in MEGA-X software.

### Statistical analysis

The data for various factors was statistically analysed by the methods of analysis of variance (ANOVA). Critical differences (CD) were determined as described by previous researchers (16). Data analysis was done by using OP stat and SPSS software. For molecular data analysis NCBI, CAP3 and MEGA-X were used. Completely randomised design (CRD) used in lab conditions.

## Results

### Cultural variability

Variability in colony characters like radial growth, growth rate per day, colony colour, texture were studied on PDA media. Significant variability was observed among different isolates as shown in Table 2. Fig. 1. Mycelial radial growth of all isolates under study ranged from 49.00 to 90.00 mm and growth rate varied from 4.9 mm/day to 9.0 mm/day. Among the 22 *B. maydis* isolates maximum radial growth 90.00 mm was shown by Bm-19 isolate from Smalkha (Panipat) followed by Bm-8 (77.50 mm), Bm-5 (77.00 mm) and Bm-2 (76.50 mm), whereas minimum radial growth was observed in Bm-7 (49.00 mm). Maximum growth rate was seen in Bm-19 (9.0 mm/day) followed by Bm-8 (77.50 mm/day) and least growth rate observed in Bm-7 (4.9 mm/day). The colour of isolates varied from creamy white to black. Other colony characters like texture, margins, zonation and type of colony for all *B. maydis* isolates also varied and isolates were classified into two textural classes smooth and rough. Smooth textural class shown by Bm-2, Bm-3, Bm-6, Bm-7, Bm-9, Bm-15, Bm-16, Bm-17, Bm-19 and Bm-22 isolates whereas Bm-1, Bm-4, Bm-5, Bm-8, Bm-10, Bm-11, Bm-12, Bm-13, Bm-14, Bm-18, Bm-20, Bm-21 showed rough texture. The colony pattern of majority of isolates was raised type except 9 isolates Bm-2, Bm-4, Bm-6, Bm-9, Bm-15, Bm-16, Bm-17, Bm-19 and Bm-22 which showed appressed pattern. Majority of isolates showed irregular margins whereas Bm-2, Bm-5, Bm-8, Bm-10, Bm-11, Bm-14, Bm-21, Bm-22 isolates showed regular margin. Zonation was not shown by any isolate.

### Morphological variability

The conidial length and breadth of different isolates varied between 36.62–72.12 µm and 9.45–14.45 µm respectively. Maximum mean conidia length was shown by Bm-12 (Kurukshetra) isolate whereas minimum mean length observed in Bm-8 (Almora) isolate. The largest size of conidia was recorded by Bm-12 (72.12 × 12.79 µm) from Kurukshetra and minimum size reported in case of Bm-8 (36.62 × 9.45 µm). Average number of septa varied from 5.2 to 8.6 and number from 3 to 11. Maximum number of septa observed in Bm-5 (8.6) whereas minimum was observed in Bm-8 (5.2). Mycelia width of different *B. maydis* isolates ranged from 3.58 µm to 7.51 µm, maximum mycelia width was observed in Bm-16 (7.51 µm) whereas minimum in Bm-8 (3.58 µm). Conidia shape of maximum isolates was curved, while in some both curved and straight shapes observed. Colour of conidia was observed to be brown to dark brown in maximum isolates, whereas in Bm-2 isolate yellowish brown colour observed as shown in Fig. 2 and Table 3.

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**Table 2.** Radial growth, growth rate (per day) and colony characters of different isolates of *Bipolaris maydis*

| Sl. No. | Isolates | Radial growth (mm) | | | | Growth rate | Colony colour | Colony texture | Zonation | Margins |
|---|---|---|---|---|---|---|---|---|---|---|
| | | 3rd day | 5th day | 7th day | 10th day | | | | | |
| 1 | Bm-1 | 25.50 | 38.25 | 43.50 | 65.25 | 6.53 | Dark grey | Rough raised | No | Irregular |
| 2 | Bm-2 | 41.50 | 44.00 | 56.75 | 76.75 | 7.68 | Dark grey | Smooth appressed | No | Regular |
| 3 | Bm-3 | 24.50 | 31.75 | 34.40 | 54.50 | 5.45 | Grey | Smooth raised | No | Irregular |
| 4 | Bm-4 | 17.30 | 26.70 | 32.50 | 59.50 | 5.95 | Grey | Rough appressed | No | Irregular |
| 5 | Bm-5 | 34.25 | 40.00 | 48.75 | 77.00 | 7.70 | Greyish white | Raised in center, smooth in periphery | No | Regular |
| 6 | Bm-6 | 24.75 | 31.50 | 39.50 | 53.50 | 5.35 | Black | Smooth appressed | No | Irregular |
| 7 | Bm-7 | 18.50 | 27.50 | 33.50 | 49.00 | 4.90 | Greyish-brown | Smooth raised | No | Irregular |
| 8 | Bm-8 | 36.20 | 44.50 | 52.65 | 77.50 | 7.75 | Light grey | Rough raised | No | Regular |
| 9 | Bm-9 | 34.60 | 44.50 | 47.60 | 55.50 | 5.55 | Black | Smooth appressed | No | Irregular |
| 10 | Bm-10 | 14.00 | 20.50 | 39.00 | 60.30 | 6.03 | Greyish white | Rough raised | No | Regular |
| 11 | Bm-11 | 20.00 | 33.86 | 38.90 | 58.50 | 5.85 | Grey | Central raised, ridged, appressed | No | Regular |
| 12 | Bm-12 | 14.00 | 41.00 | 46.00 | 60.30 | 6.03 | Light grey | Rough raised | No | Irregular |
| 13 | Bm-13 | 18.50 | 29.50 | 38.60 | 71.00 | 7.08 | Whitish-Dark grey | Rough raised | No | Irregular |
| 14 | Bm-14 | 22.50 | 31.50 | 39.50 | 73.00 | 7.30 | Light grey | Rough raised | No | Regular |
| 15 | Bm-15 | 19.75 | 28.00 | 37.00 | 54.60 | 5.46 | Dark grey | Smooth appressed | No | Irregular |
| 16 | Bm-16 | 14.00 | 22.00 | 28.50 | 65.50 | 6.55 | Dark grey | Smooth appressed | No | Irregular |
| 17 | Bm-17 | 17.00 | 26.00 | 33.00 | 60.00 | 6.00 | Light Grey | Smooth appressed | No | Irregular |
| 18 | Bm-18 | 19.75 | 22.60 | 29.50 | 53.50 | 5.35 | Grey | Rough raised | No | Irregular |
| 19 | Bm-19 | 32.50 | 48.00 | 67.50 | 90.00 | 9.00 | Creamy white | Smooth appressed | No | Irregular |
| 20 | Bm-20 | 23.90 | 36.75 | 44.60 | 71.25 | 7.13 | Dark grey | Rough raised | No | Irregular |
| 21 | Bm-21 | 22.20 | 38.25 | 32.50 | 52.00 | 5.20 | Dark grey | Rough raised | No | Regular |
| 22 | Bm-22 | 26.30 | 44.00 | 53.00 | 72.60 | 7.26 | Greyish brown | Smooth appressed | No | Regular |
| CD at 5 % | | 4.953 | 3.880 | 4.210 | 4.788 | | | | | |

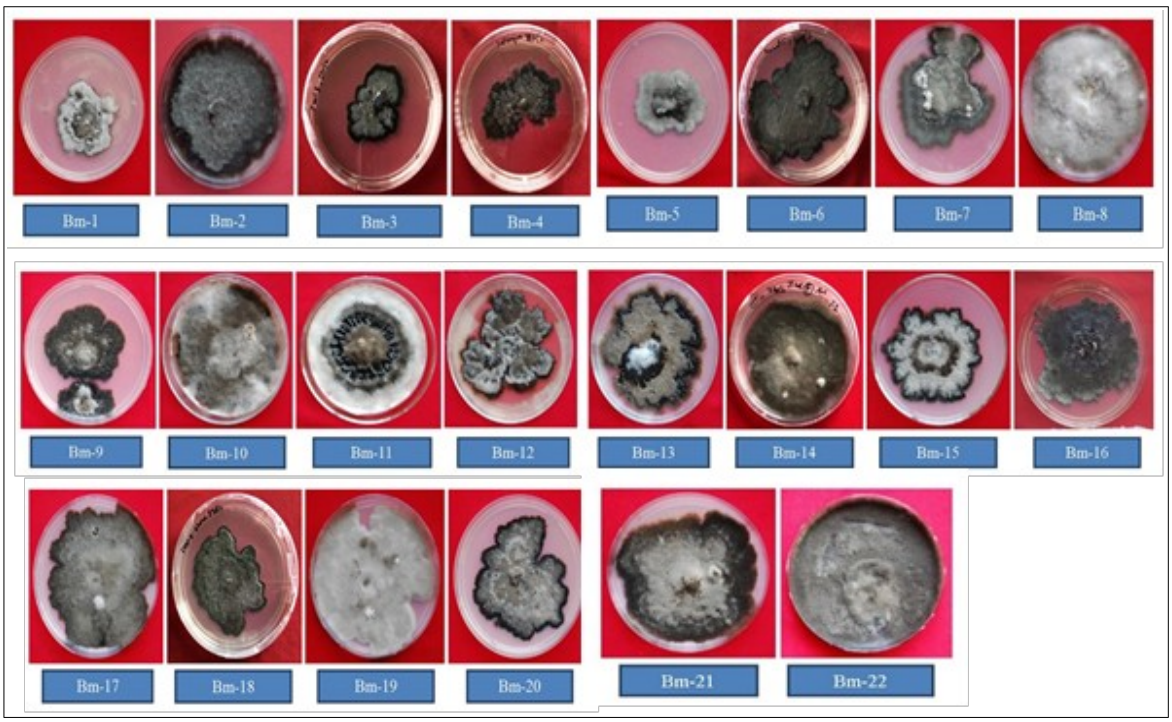



**Fig. 1.** Radial growth and colony characteristics of *Bipolaris maydis* isolates under study.

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**Table 3.** Morphological characters of *Bipolaris maydis* isolates under study

| Sl. No. | Isolates | Conidia length (µm) | Breadth (µm) | No. of septa | Mycelia width (µm) | Conidia shape | Conidia colour |
|---|---|---|---|---|---|---|---|
| 1. | Bm-1 | 58.14 (35.27–89.38) | 12.52 (7.58–15.03) | 7.5 (4–10) | 4.29 | Curved | Brown |
| 2. | Bm-2 | 52.77 (36.06–78.07) | 12.86 (10.44–32.06) | 6.2 (3–10) | 4.66 | Curved | Yellowish Brown |
| 3. | Bm-3 | 42.55 (23.34–60.29) | 10.94 (7.40–12.78) | 5.9 (3–9) | 5.10 | Curved and Straight | Brown |
| 4. | Bm-4 | 49.74 (26.38–69.85) | 13.25 (8.81–14.93) | 5.9 (3–9) | 5.20 | Curved and Straight | Dark brown |
| 5. | Bm-5 | 66.85 (20.64–98.29) | 14.79 (11.02–17.04) | 8.6 (3–12) | 5.06 | Curved and Straight | Brown |
| 6. | Bm-6 | 44.87 (24.40–69.40) | 12.01 (10.15–18.05) | 6.7 (3–9) | 5.49 | Curved | Brown |
| 7. | Bm-7 | 61.47 (37.76–82.69) | 13.81 (10.22–16.39) | 7.4 (4–10) | 6.39 | Curved | Brown |
| 8. | Bm-8 | 36.62 (12.03–53.84) | 9.45 (6.33–21.74) | 5.2 (4–9) | 3.58 | Curved and Straight | Brown |
| 9. | Bm-9 | 37.54 (10.13–61.75) | 10.55 (6.97–13.12) | 5.3 (3–9) | 4.59 | Curved and Straight | Brown |
| 10. | Bm-10 | 43.58 (23.45–68.04) | 12.78 (9.50–17.93) | 5.8 (3–8) | 5.11 | Curved and Straight | Brown |
| 11. | Bm-11 | 53.87 (18.26–80.93) | 11.63 (6.67–14.08) | 6.0 (3–9) | 5.73 | Curved and Straight | Brown |
| 12. | Bm-12 | 72.12 (50.43–89.30) | 12.79 (11.09–13.35) | 7.1 (3–9) | 4.35 | Curved | Brown |
| 13. | Bm-13 | 39.87 (20.70–62.46) | 11.45 (7.96–13.95) | 5.4 (3–9) | 5.69 | Curved | Dark brown |
| 14. | Bm-14 | 43.14 (14.55–73.20) | 11.73 (6.53–15.02) | 6.1 (3–9) | 6.05 | Curved | Brown |
| 15. | Bm-15 | 58.84 (91.49–91.53) | 12.35 (6.65–15.28) | 6.6 (3–9) | 4.65 | Curved | Brown |
| 16. | Bm-16 | 50.30 (22.16–75.44) | 12.13 (7.58–16.06) | 7.0 (3–10) | 7.51 | Curved | Brown |
| 17. | Bm-17 | 51.26 (28.15–75.44) | 12.99 (8.94–14.87) | 6.8 (3–9) | 5.55 | Curved and Straight | Brown |
| 18. | Bm-18 | 49.96 (19.87–74.91) | 11.51 (8.07–14.12) | 7.1 (3–10) | 6.32 | Curved and Straight | Dark Brown |
| 19. | Bm-19 | 52.37 (15.49–83.32) | 14.45 (11.82–16.97) | 6.7 (3–11) | 5.49 | Curved and Straight | Brown |
| 20. | Bm-20 | 64.19 (32.14–96.99) | 14.94 (11.58–17.03) | 7.4 (3–10) | 5.77 | Curved | Brown |
| 21. | Bm-21 | 62.73 (28.67–96.82) | 13.45 (10.00–16.06) | 6.8 (3–9) | 6.10 | Curved and Straight | Brown |
| 22. | Bm-22 | 57.77 (18.38–81.45) | 12.81 (8.41–15.62) | 6 (3–10) | 5.36 | Curved and Straight | Brown |
| CD at 5 % | | 3.365 | 0.802 | 0.781 | 0.313 | | |

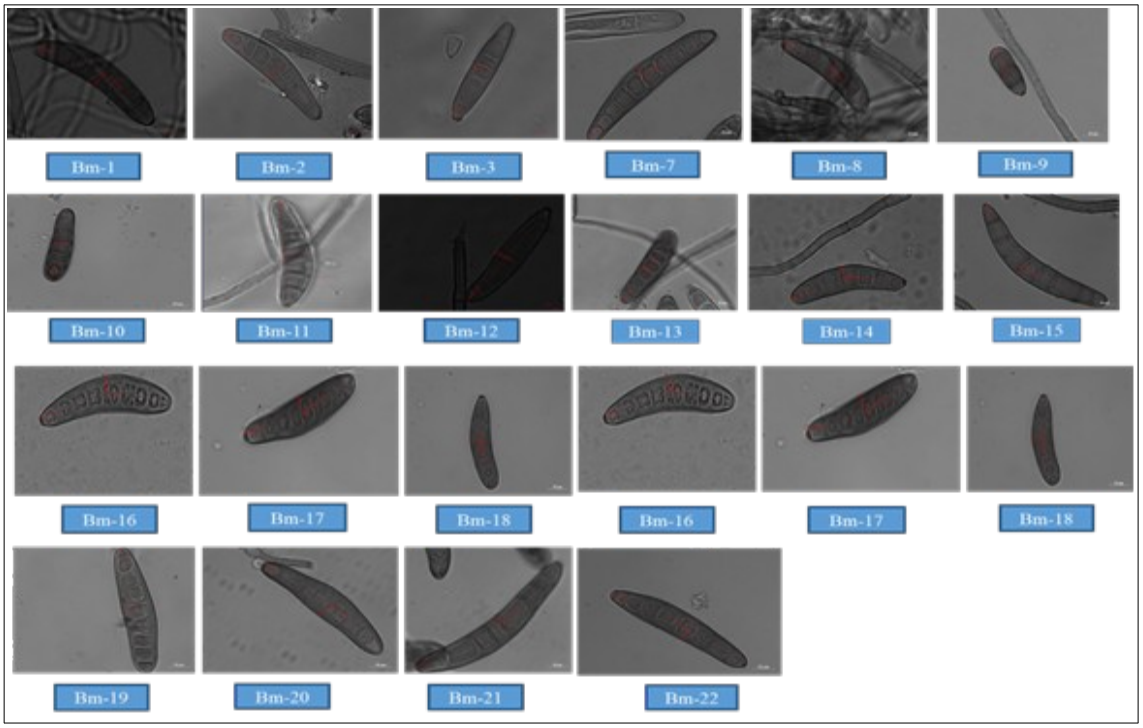



**Fig. 2.** Conidial morphology of 22 different isolates of *Bipolaris maydis*.

The correlation between various cultural and morphological traits was determined as shown in Fig. 3a. A highly significant positive Karl Pearson's Co-relation coefficient was observed between length, breadth and number of septa. In between length and breadth positive and significant co-relation coefficient of 0.738 was observed, whereas in between length and number of septa co-relation coefficient was 0.747 and in breadth

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and number of septa a signficant positive co-relation coefficient of 0.610 was observed. These co-relation coefficients clearly indicate that the isolate have greater conidia length have greater breadth, greater the length and breadth more the number of septa observed. However, no significant co-relation was found between other cultural and morphological characters. The clustering of different isolates on basis of cultural and morphological quantitative characters was performed by using Ward's method based on squared Euclidean distance and five clusters were formed at 2.5 squared Euclidian distance (Fig. 3b). All clusters showed significant difference in all characters (Supplementary Table 1). On mean basis, Cluster 1 isolates were found to have maximum conidia length, breadth, number of septa and mycelia width, whereas minimum in case of cluster 5 isolates. Growth rate was found to be maximum in case of cluster 5 isolates and minimum in cluster 4 isolates.

### Pathogenic variability

A comprehensive assessment of 22 *B. maydis* isolates revealed substantial pathogenic diversity, indicating the presence of multiple virulence phenotypes within the pathogen population. Significant variation was observed across all evaluated pathogenic traits, including IP, LP, lesion dimensions, lesion colour and DS.

### Incubation period as an indicator of aggressiveness

Marked variation in IP was detected among isolates. The most aggressive isolate, Bm-7 (Pantnagar-2), exhibited the shortest IP (39.6 hr), followed by Bm-4 and Bm-8 (45.6 hr). Conversely, isolates Bm-5 and Bm-11 required the longest IP (57.6 hr). Shorter IPs are widely associated with faster fungal colonisation and earlier host penetration, which generally correspond to increased aggressiveness. The current findings corroborate this relationship, as isolates with shorter IPs also exhibited higher disease scores. Genotypic differences were equally prominent. HQPM-4 and HQPM-1 showed prolonged IPs (62.7 and 62.2 hr, respectively), suggesting a slower pathogen establishment, whereas HKI-327T supported the most rapid infection (44.2 hr). These results highlight substantial host-based modulation of pathogen development as shown in Supplementary Table 2.

### Latent period

Latent period also varied significantly, ranging from 67.2 to 91.2 hr. Isolate Bm-7 again demonstrated the shortest LP (67.2 hr), whereas Bm-11 exhibited the longest (91.2 hr). The strong negative correlation ($r$ = -0.651***) between LP and disease score clearly demonstrates that isolates producing symptoms earlier tend to be more virulent. This aligns with established epidemiological theory, where shorter LPs accelerate secondary infection cycles, enhancing epidemic development. HQPM-1 and HQPM-4, with longer LPs (97.1 and 94.9 hr), appear to possess partial resistance or delayed tissue colonisation, while HM-8 showed the earliest symptom expression (68.7 hr), making it more susceptible (Supplementary Table 3).

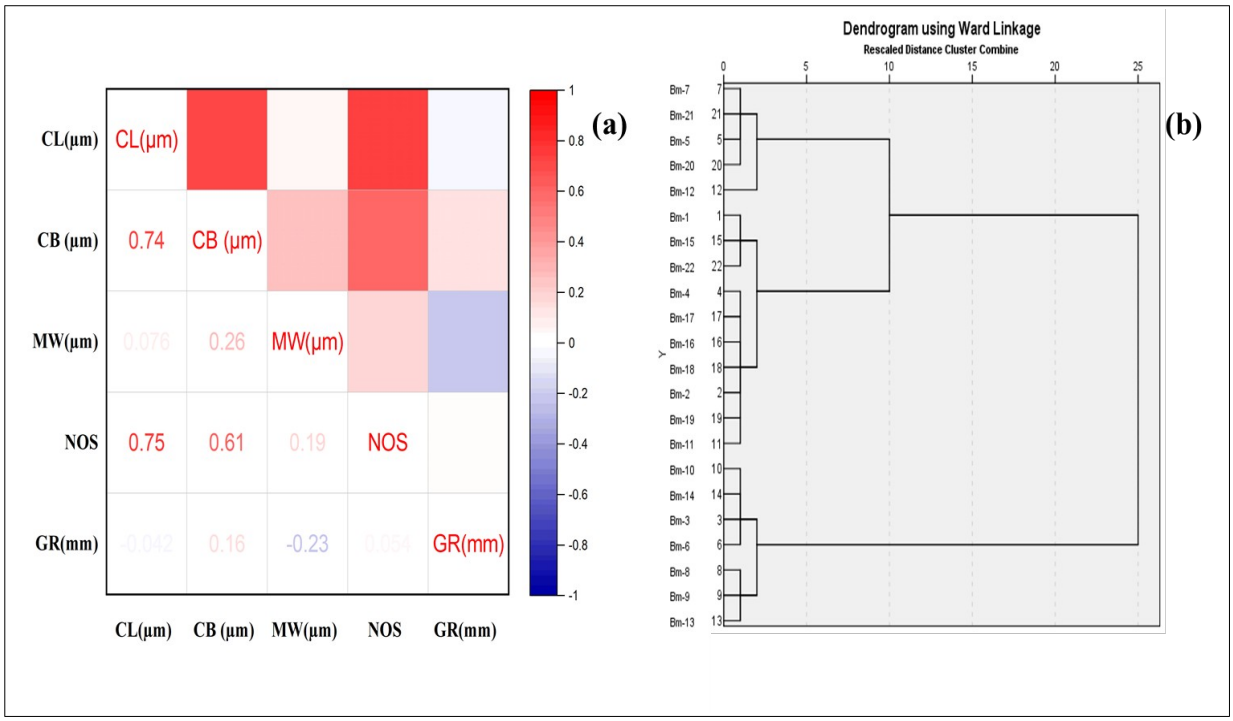



**Fig. 3.** a: Correlogram depicting correlation among morpho-cultural traits (** Co-relation is significant at 0.01 % level of significance); b: Clustering of *Bipolaris maydis* isolates on basis of cultural and morphological characters.

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### Lesion length, breadth and lesion colour

Lesion length (LL) and breadth (LB), both key components of pathogenic aggressiveness, also varied widely. Isolate Bm-7 again produced the largest lesions (19.35 mm length and 2.87 mm breadth), followed by Bm-10 and Bm-18, validating its classification as the most virulent isolate. In contrast, Bm-21 and Bm-17 produced smaller lesions, reflecting their weaker pathogenic ability. Among genotypes, HQPM-1 and HQPM-4 expressed the smallest lesion dimensions, indicating strong host-mediated restriction of pathogen invasion. HKI-327T and HM-8 developed the largest lesions, consistent with their high disease scores. Lesion colour ranged from light to dark brown, indicating differential degrees of tissue necrosis and phenolic accumulation. Darker lesions, typically associated with extensive colonisation, were predominantly produced by high-virulence isolates (Supplementary Table 4–6).

### Disease severity and identification of highly virulent isolates

Disease scores further highlighted the substantial pathogenic variability. Bm-7 emerged as the most virulent, producing susceptible reactions on eight of the ten maize genotypes and achieving the highest mean disease score (7.5). Bm-17 followed with a score of 7.0. The least virulent isolates, Bm-3 and Bm-6, recorded scores of 5.3. Among genotypes, HQPM-1 (mean score 2.8) and HQPM-4 (3.1) exhibited notable resistance, while HKI-536CBT (7.4) and HM-8 (7.3) were the most susceptible as shown in Supplementary Table 7. These responses demonstrate a wide spectrum of host resistance that can be effectively exploited for breeding programs.

### Association among pathogenicity parameters

Correlation analysis among pathogenicity parameters revealed distinct relationships between disease development traits (Fig. 4 a). Incubation period and LP exhibited a strong positive association ($r$ = 0.88***), indicating that isolates requiring longer time to initiate symptoms also tended to delay sporulation. Both IP and LP showed significant negative correlations with LL and LB, suggesting that isolates with shorter incubation and latent periods produced larger lesions. Lesion length and lesion breadth were positively correlated with each other, reflecting coordinated lesion expansion in both longitudinal and transverse directions. Disease severity exhibited a strong negative association with IP ($r$ = −0.57***) and LP ($r$ = −0.65***), while showing a positive relationship with lesion parameters, indicating that rapidly developing infections were associated with increased lesion expansion and higher disease severity. These results demonstrate that aggressiveness in *B. maydis* is primarily driven by faster infection processes and enhanced lesion development.

### Cluster analysis of *Bipolaris maydis* isolates based on pathogenic traits

Hierarchical cluster analysis using Ward's linkage method grouped the *B. maydis* isolates into distinct clusters based on pathogenicity-related traits (Fig. 4b, Supplementary Table 8). The dendrogram revealed the formation of two major clusters at a higher rescaled distance, indicating substantial variability in pathogenic behaviour among the isolates. One cluster comprised isolates characterised by shorter incubation and latent periods, larger lesion dimensions and higher disease severity, representing highly aggressive isolates. In contrast, the second cluster consisted of isolates exhibiting longer IP and LP, smaller lesions and comparatively lower disease severity, indicating reduced aggressiveness. Sub-clustering within the major groups further reflected intermediate levels of pathogenicity among certain isolates. The clustering pattern was independent of geographical origin, suggesting that pathogenic variability in *B. maydis* is not geographically structured but is likely governed by intrinsic biological differences among isolates.

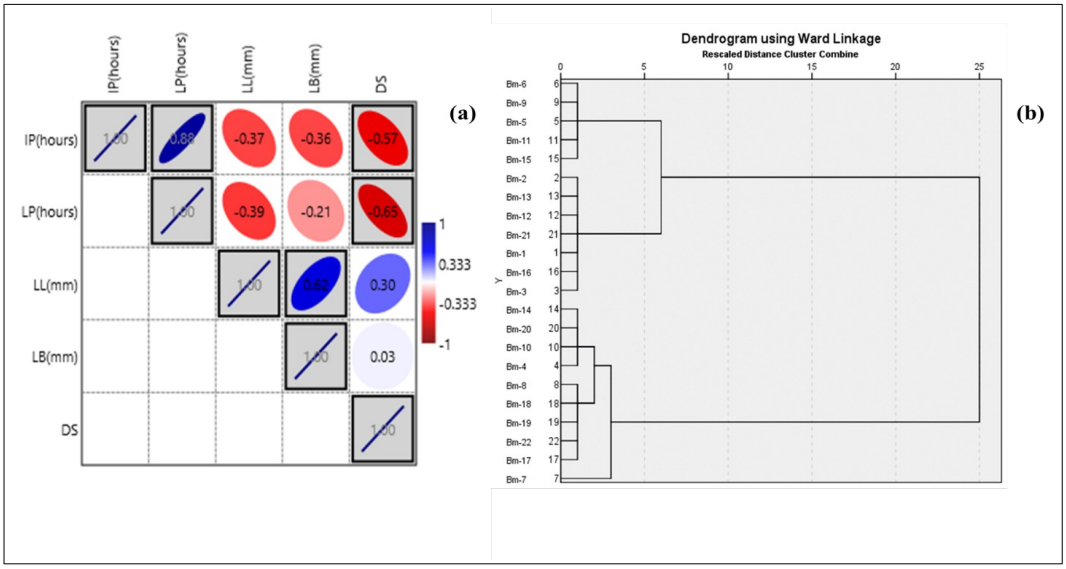



**Fig. 4.** a: Correlogram depicting correlation among pathogenic traits (** Co-relation is significant at 0.01% level of significance); b: clustering of *Bipolaris maydis* isolates on basis of pathogenic characters.

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### Molecular variability among isolates on basis of internal transcribed spacer sequencing

To access diversity among all *B. maydis* isolates ITS gene rDNA sequencing was used. Phylogenetic tree was constructed by using neighbor joining method and tamura nei model at 1000 bootstrap value. In tree construction 17 isolates were taken, four isolates of *B. maydis* from Argentine, China, Brazil and Japan were used along with one *Bipolaris zeicola* isolate for comparison. In phylogenetic tree two clusters were formed, cluster 1 indicating *Bipolaris maydis* isolates whereas cluster 2 depicts *B. zeicola.* In cluster 1, 6 groups were formed which further divided into subgroups.

Group 1 consist of one subgroup at 65 bootstrap values containing two isolates Bm-3 (Srinagar) and Bm-8 (Almora) isolate and one isolate of Brazil (KC005707) at 60 bootstrap value. Group 2 consist of 5 isolates Bm-18 (Sonipat-2, Manouli), Bm-5 (Hyderabad), Bm-12 (Kurukshetra), Bm-6 (Pantnagar-1) and Bm-15 (Jind-2, Sunderpur). Group 3 consist of two isolates Bm-1 (Motipur) and Bm-10 (Rusulpur Kalan, Karnal-1) at 59 bootstrap value. Group 4 at 64 bootstrap value divides into one subgroup at 86 bootstrap value consisting of two isolates Bm-9 (Kasganj), Bm- (china, AY372687) and one isolate Bm-16 (Bhotwala, Jind-3). Group 5 divides into subgroup 1 at 57 bootstrap value consisting of Bm (USA, NR 138224) and another subgroup 2 at 86 bootstrap value consisting of Bm (India, MT524327) and another subgroup 3 at 70 bootstrap value consist of Bm-7 (Pantnagar-2) and Bm- (Netherlands, MH864477). Group 6 at 44 bootstrap value divides into Bm-4 (Palampur) and subgroup 1 consisting of 4 isolates Bm-2 (Delhi), Bm-19 (Panipat), Bm-11 (Uchani, Karnal- 2) and Bm-20 (Ambala) at 63 bootstrap value. So, the phylogenetic tree clearly depicts variability among *B. maydis* isolates. Bm-7 (Pantnagar-2) isolate was observed to be the most diverse isolate as shown in Fig. 5a and b.

## Discussion

The present study revealed substantial variability among 22 *B. maydis* isolates collected from five agro-climatic zones of India, encompassing cultural, morphological, pathogenic and molecular traits. Considerable differences were observed in colony diameter, colour, texture, growth rate and conidial morphology, demonstrating the adaptive heterogeneity of the pathogen under diverse ecological conditions. The radial growth of isolates ranged from 49.0 to 90.0 mm, with corresponding growth rates varying from 4.9 mm day$^{-1}$ to 9.0 mm day$^{-1}$. Among them, isolate Bm-19 (Samalkha, Panipat) exhibited the fastest growth (9.0 mm day$^{-1}$), whereas Bm-7 (Pantnagar-2) grew slowest (4.9 mm day$^{-1}$). Colony colour varied widely from creamy white to black, while texture was either smooth or rough and colony margins ranged from regular to irregular. Most isolates produced raised colonies, while a few (Bm-2, Bm-4, Bm-6, Bm-9, Bm-15, Bm-16, Bm-17, Bm-19 and Bm-22) were appressed. Such variation is consistent with earlier findings of previous researchers who reported significant diversity among Indian *B. maydis* isolates in colony diameter, pigmentation and mycelial pattern (17–19).

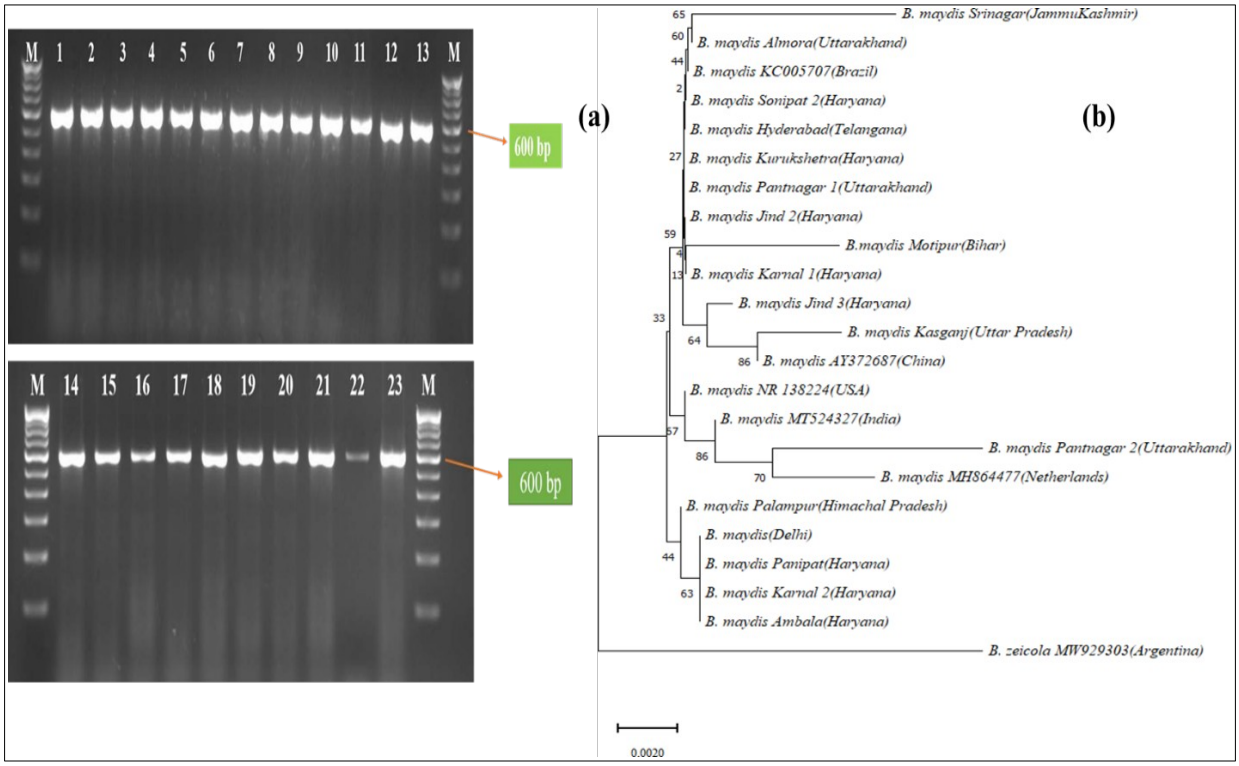



**Fig. 5.** Molecular characterisation and phylogenetic analysis of *Bipolaris maydis* isolates based on the internal transcribed spacer (ITS) region. a: polymerase chain reaction (PCR)-amplified product profile of *B. maydis* isolates based on the ITS region; b: phylogenetic tree constructed using the neighbour-joining method based on 589 bp rDNA ITS gene sequences of the isolates.

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The conidial dimensions also differed considerably, ranging from 36.62–72.12 µm in length and 9.45–14.45 µm in breadth, with 5–9 septa per conidium. The largest conidia were recorded in Bm-12 (Kurukshetra; 72.12 × 12.79 µm), while the smallest were in Bm-8 (36.62 × 9.45 µm). Mycelial width ranged from 3.58 µm to 7.51 µm, with Bm-16 showing the widest hyphae. Most isolates produced curved, brown to dark-brown conidia, whereas a few exhibited both curved and straight forms. These variations agree with classical descriptions of the genus *Bipolaris* by earlier researchers, who reported that conidia may be curved, obclavate, or fusoid, with 3–14 distosepta and colours ranging from pale to deep olivaceous brown (20–22). Positive correlations observed between conidial length, breadth and number of septa indicate an inherent association between morphological robustness and sporulation potential. Similar relationships were reported in previous studies (17, 23). Overall, the morpho-cultural heterogeneity detected among isolates in the present study highlights the genetic flexibility of *B. maydis* and its potential for adaptation to varying agro-ecological niches.

All isolates proved pathogenic on maize, though they differed markedly in aggressiveness. The incubation period ranged from 39.6 hr in the highly virulent isolate Bm-7 to 57.6 h in Bm-5 and Bm-11, while the LP varied between 67.2 hr (Bm-7) and 91.2 hr (Bm-11). Lesion length among isolates spanned 14.34–19.35 mm and LB 2.45–2.90 mm, with lesion colour varying from light to dark brown. The Bm-7 isolate from Pantnagar-2 was the most virulent, producing the shortest incubation and LPs and the highest mean disease score (7.5) across 10 maize genotypes. These findings are consistent with the previous findings which also documented wide pathogenic variation among Indian *B. maydis* populations, with Udaipur and Pantnagar isolates showing the greatest virulence (17, 20, 24). Comparable diversity in aggressiveness has also been demonstrated by previous researchers supporting the view that frequent monocropping and repeated use of resistant cultivars may impose strong selection pressure, promoting the emergence of new virulent races (14, 18, 19). The clustering of the present isolates into five distinct pathogenic groups further confirms the heterogeneity within the *B. maydis* population structure. Molecular analyses based on ITS gene sequencing provided complementary insights. The ITS-based phylogenetic tree differentiated *B. maydis* from *B. zeicola* and revealed six sub-groups within the *B. maydis* cluster, indicating moderate intraspecific variability. Isolate Bm-7 (Pantnagar-2) consistently appeared as the most divergent, clustering separately with reference isolates from the Netherlands and India at higher bootstrap support. These observations are in partial agreement with previous studies which found polymorphism among *B. maydis* isolates using random amplified polymorphic DNA (RAPD) markers but limited variation with ITS and restriction fragment length polymorphism (RFLP) analyses (25). Similarly, studies reported pronounced variability in *B. maydis* populations using RAPD and inter-simple sequence repeat (ISSR) markers, though ITS-based phylogeny alone failed to correlate with geographical origin (7, 26, 27). The absence of strong geographical clustering in the present study implies that gene flow or exchange of inoculum between maize-growing regions may contribute to homogenisation of the *B. maydis* population across India.

## Conclusion

Taken together, the results demonstrate that morphological, cultural and pathogenic traits exhibit significant phenotypic variability among *Bipolaris maydis* isolates, whereas ITS-based molecular markers reveal limited genetic divergence. The congruence between morpho-cultural and pathogenic dendrograms, but not with molecular phylogeny, suggests that phenotypic variation may be driven by epigenetic or environmental adaptation rather than large-scale genomic differentiation. Among all isolates, Bm-7 (Pantnagar-2) emerged as the most virulent and phenotypically distinct, exhibiting maximum conidial size, septation, lesion dimensions and disease severity. This isolate thus represents a valuable candidate for screening maize germplasm and for future host–pathogen interaction studies. Given the increasing incidence of maydis leaf blight (MLB) under changing climatic conditions, continued monitoring of *B. maydis* variability is essential for developing durable host resistance and for understanding pathogen evolution in Indian maize ecosystems.

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## Authors' contributions

HS designed the experiments. AK performed the experiments, analysed the data and wrote the initial draft. PB, P, ML and IR provided inputs and analysed the data. NS, NM and SY edited the manuscript. All authors read and approved the manuscript.

## Compliance with ethical standards

### Conflict of interest

Authors do not have any conflict of interests to declare.

### Ethical issues

None

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## Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work the authors used Quillbot to improve language editing, grammatical improvement, sentence restructuring and assistance in improving the clarity and readability of the manuscript. After using this tool, the authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

## References


1. FAOSTAT. Online database 2020. Rome: FAO; 2023. Available at: https://www.fao.org/faostat/en/data/QCL
2. Malik VK, Singh M, Hooda KS, Yadav NK, Chauhan PK. Efficacy of newer molecules, bioagents and botanicals against maydis leaf blight and banded leaf and sheath blight of maize. The Plant Pathology Journal. 2018;34(2):121. https://doi.org/10.5423/PPJ.OA.11.2017.0251
3. Aggarwal SK, Hooda KS, Kaur H, Gogoi R, Chauhan P, Bagaria PK, et al. Comparative evaluation of management modules against Maydis leaf blight disease in maize (*Zea mays*). European Journal of Plant Pathology. 2024;168(3):485–95. https://doi.org/10.1007/s10658-023-02777-x
4. Kumar B, Pushpendra, Kumar S, Kumar P, Singh R, Yankanchi S, et al. Understanding the genetic basis of resistance to maydis leaf blight and maturity-related traits in corn. Frontiers in Plant Science. 2025;16:1551940. https://doi.org/10.3389/fpls.2025.1551940
5. Kumar B, Choudhary M, Kumar K, Kumar P, Kumar S, Bagaria PK, et al. Maydis leaf blight of maize: Update on status, sustainable management and genetic architecture of its resistance. Physiological and Molecular Plant Pathology. 2022;121:101889. https://doi.org/10.1016/j.pmpp.2022.101889
6. Vignesh K, Vengadeskumar L, Sanjaygandhi S, Sabesan T. Morphological and molecular variation of *Bipolaris maydis* isolates causing maydis leaf blight in maize. Journals of Plant Disease Science. 2023;18(1):5–10. https://doi.org/10.48165/jpds.2023.1801.02
7. Karimishahari MR, Sharma RC. Genetic variation among isolates of *Bipolaris maydis* using RAPD-PCR. Italian Journal of Mycology. 2016;45:19–28.
8. Kashyap PL, Kumar S, Sharma A, Kumar RS, Mahapatra S, Kaul N, et al. Molecular diversity, haplotype distribution and genetic variation flow of *Bipolaris sorokiniana* fungus causing spot blotch disease in different wheat-growing zones. Journal of Applied Genetics. 2022;63(4):793–803. https://doi.org/10.1007/s13353-022-00716-w
9. Sinclair JB, Dhingra OD. Basic plant pathology methods. CRC Press; 2017. https://doi.org/10.1201/9781315138138
10. Ainsworth GC, Bisby GR. A dictionary of the fungi. Commonwealth Mycological Institute, Kew, England; 1961.
11. Alcorn JL. On the genera *Cochliobolus* and *Pseudocochliobolus*. Mycotaxon. 1983;16:353–79. https://doi.org/10.5962/p.417474
12. Sivanesan A. Graminicolous species of *Bipolaris*, *Curvularia*, *Drechslera*, *Exserohilum* and their teleomorphs. 1987;158:1–261.
13. Jobson JD. Applied multivariate data analysis: volume II: Categorical and multivariate methods. Springer Science & Business Media; 2012.
14. Sultana S, Adhikary SK, Islam MM, Rahman SM. Evaluation of pathogenic variability based on leaf blotch disease development components of *Bipolaris sorokiniana* in *Triticum aestivum* and agroclimatic origin. The Plant Pathology Journal. 2018;34(2):93. https://doi.org/10.5423/PPJ.OA.08.2017.0175
15. AICRP. Mass screening techniques for resistance to maize disease. 2019.
16. Gomez KA, Gomez AA. Statistical procedures for agricultural research. John Wiley & Sons; 1984.
17. Bunker RN, Rathore RS, Kumawat DK. Pathogenic and morphological variability of *Bipolaris maydis* incitant of maydis leaf blight in maize. Journal of Mycology and Plant Pathology. 2011;41(3):418.
18. Yadav RL, Bunker RN, Sharma SS. Morphological and pathogenic variability among isolates causing maydis leaf blight of maize. Journal of Mycology and Plant Pathology. 2013;43(4):401.
19. Ishar Pal IP, Vimla Singh VS, Robin Gogoi RG, Hooda KS, Namita Bedi NB. Characterization of *Bipolaris maydis* isolates of different maize cropping zones of India. 2015;68(1):63–66.
20. Lakshmi P. Differential interactions between *Helminthosporium maydis* Nisikado and Miyake incitant of maydis leaf blight and cultivars of *Zea mays* L. M.Sc. (Ag.) Thesis. IARI, New Delhi; 1984. p. 6–31.
21. Singh DV, Mathur SB, Neergaard P. Seed health testing of maize. Evaluation of testing techniques, with special reference to *Drechslera maydis*. 1974;2:349–65.
22. Manamgoda DS, Rossman AY, Castlebury LA, Crous PW, Madrid H, Chukeatirote E, et al. The genus *Bipolaris*. Studies in Mycology. 2014;79(1):221–88. https://doi.org/10.1016/j.simyco.2014.10.002
23. Kutawa AB, Ahmad K, Ali A, Hussein MZ, Wahab MA, Sijam K. State of the art on southern corn leaf blight disease incited by *Cochliobolus heterostrophus*: detection, pathogenic variability and novel control measures. Bulgarian Journal of Agricultural Science. 2021;27(1).
24. Misra AP, Singh RA. Comparative pathogenicity of different species of *Helminthosporium* on wheat in India. Proceedings of 59th Congress. 1972:567.
25. Gogoi R, Singh S, Singh PK, Kulanthaivel S, Rai SN. Genetic variability in the isolates of *Bipolaris maydis* causing maydis leaf blight of maize. African Journal of Agricultural Research. 2014;9:1906–13.
26. Esfahani MN. Genetic variability and virulence of some Iranian *Rhizoctonia solani* isolates associated with stem canker and black scurf of potato (*Solanum tuberosum* L.). Journal of Plant Protection Research. 2020;60(1).
27. Manzar N, Kashyap AS, Maurya A, Rajawat MVS, Sharma PK, Srivastava AK, et al. Multi-gene phylogenetic approach for identification and diversity analysis of *Bipolaris maydis* and *Curvularia lunata* isolates causing foliar blight of *Zea mays*. Journal of Fungi. 2022;8(8):802. https://doi.org/10.3390/jof8080802


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## Supplementary Files

**Supplementary Table 1.** Cluster means five clusters against their respective cultural and morphological characters

| Cluster/ Characters | Conidia length (µm) | Conidia breadth (µm) | Number of Septa (average) | Mycelia width (µm) | Growth rate (mm/day) |
|---|---|---|---|---|---|
| **Cluster–1** | 65.47 | 13.95 | 7.46 | 5.53 | 6.19 |
| **Cluster–2** | 58.25 | 12.56 | 6.7 | 4.76 | 6.41 |
| **Cluster–3** | 51.47 | 12.68 | 6.52 | 5.88 | 6.62 |
| **Cluster–4** | 43.53 | 11.86 | 5.97 | 5.43 | 6.03 |
| **Cluster–5** | 38.01 | 10.48 | 5.50 | 4.62 | 6.77 |

**Supplementary Table 2.** Incubation period (hr) of different *Bipolaris maydis* isolates on selected maize genotypes under poly house conditions

| Isolates/ Varities | Punjab sweet Corn composite | HKI–1105x HKI 488 | HKI–536 CBT | HKI–327 T | QPM–9 | HM–10 | HM–9 | HM–8 | HQPM–4 | HQPM–1 | Mean |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Bm–1 | 36 | 60 | 48 | 36 | 48 | 48 | 36 | 48 | 84 | 60 | 50.4 |
| Bm–2 | 48 | 36 | 60 | 48 | 60 | 36 | 48 | 36 | 60 | 60 | 49.2 |
| Bm–3 | 48 | 48 | 36 | 36 | 36 | 48 | 48 | 36 | 60 | 72 | 46.8 |
| Bm–4 | 36 | 48 | 36 | 48 | 48 | 48 | 36 | 36 | 48 | 72 | 45.6 |
| Bm–5 | 60 | 60 | 60 | 60 | 36 | 60 | 36 | 48 | 72 | 84 | 57.6 |
| Bm–6 | 60 | 48 | 48 | 60 | 48 | 60 | 48 | 48 | 72 | 60 | 55.2 |
| Bm–7 | 36 | 36 | 48 | 36 | 36 | 36 | 36 | 36 | 48 | 48 | 39.6 |
| Bm–8 | 48 | 36 | 36 | 48 | 36 | 36 | 48 | 48 | 60 | 60 | 45.6 |
| Bm–9 | 60 | 48 | 60 | 48 | 48 | 72 | 48 | 48 | 48 | 72 | 55.2 |
| Bm–10 | 48 | 36 | 48 | 36 | 48 | 60 | 60 | 36 | 60 | 48 | 48.0 |
| Bm–11 | 60 | 60 | 48 | 48 | 36 | 48 | 72 | 60 | 60 | 84 | 57.6 |
| Bm–12 | 48 | 60 | 60 | 36 | 60 | 60 | 48 | 48 | 48 | 60 | 52.8 |
| Bm–13 | 48 | 48 | 36 | 48 | 36 | 48 | 36 | 72 | 60 | 72 | 50.4 |
| Bm–14 | 48 | 36 | 60 | 36 | 48 | 60 | 48 | 36 | 48 | 48 | 46.8 |
| Bm–15 | 60 | 36 | 48 | 48 | 60 | 36 | 48 | 48 | 72 | 72 | 52.8 |
| Bm–16 | 48 | 36 | 36 | 60 | 36 | 60 | 60 | 48 | 60 | 60 | 50.4 |
| Bm–17 | 48 | 48 | 48 | 48 | 60 | 60 | 36 | 60 | 72 | 36 | 51.6 |
| Bm–18 | 60 | 48 | 36 | 36 | 48 | 60 | 36 | 36 | 60 | 48 | 46.8 |
| Bm–19 | 48 | 60 | 60 | 36 | 36 | 48 | 48 | 36 | 72 | 48 | 49.2 |
| Bm–20 | 36 | 36 | 36 | 48 | 36 | 48 | 36 | 48 | 84 | 60 | 46.8 |
| Bm–21 | 36 | 48 | 60 | 36 | 48 | 60 | 48 | 36 | 72 | 84 | 52.8 |
| Bm–22 | 48 | 48 | 48 | 36 | 48 | 36 | 60 | 48 | 60 | 60 | 49.2 |
| Mean | 48.6 | 46.4 | 48.0 | 44.2 | 45.3 | 51.3 | 46.4 | 45.3 | 62.7 | 62.2 | 50.0 |
| CD at 5 % | Isolate: 4.061, Variety: 2.738, Isolate × Variety: 12.842 | | | | | | | | | | |

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**Supplementary Table 3.** Latent period (hr) of different Bipolaris maydis isolates on selected maize genotypes under poly house conditions

| Isolates/Varities | Punjab sweet corn composite | HKI1105x HKI 488 | HKI–536 CBT | HKI–327 T | QPM–9 | HM–10 | HM–9 | HM–8 | HQPM–4 | HQPM–1 | Mean |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Bm–1 | 72 | 96 | 72 | 72 | 96 | 72 | 48 | 72 | 120 | 96 | 81.6 |
| Bm–2 | 96 | 96 | 72 | 96 | 96 | 48 | 72 | 72 | 96 | 96 | 84.0 |
| Bm–3 | 96 | 96 | 72 | 72 | 72 | 72 | 96 | 48 | 96 | 96 | 81.6 |
| Bm–4 | 72 | 72 | 48 | 72 | 72 | 72 | 48 | 72 | 72 | 96 | 69.6 |
| Bm–5 | 72 | 96 | 72 | 96 | 72 | 96 | 72 | 96 | 96 | 120 | 88.8 |
| Bm–6 | 72 | 96 | 72 | 96 | 96 | 96 | 72 | 72 | 120 | 96 | 88.8 |
| Bm–7 | 48 | 72 | 96 | 72 | 48 | 48 | 72 | 48 | 96 | 72 | 67.2 |
| Bm–8 | 72 | 72 | 72 | 72 | 48 | 72 | 72 | 72 | 96 | 96 | 74.4 |
| Bm–9 | 96 | 72 | 96 | 96 | 72 | 96 | 96 | 72 | 96 | 96 | 88.8 |
| Bm–10 | 72 | 48 | 72 | 72 | 72 | 96 | 72 | 48 | 96 | 72 | 72.0 |
| Bm–11 | 96 | 96 | 72 | 96 | 72 | 72 | 96 | 96 | 96 | 120 | 91.2 |
| Bm–12 | 72 | 96 | 96 | 72 | 96 | 96 | 72 | 72 | 72 | 96 | 84.0 |
| Bm–13 | 72 | 96 | 72 | 72 | 72 | 72 | 72 | 96 | 96 | 120 | 84.0 |
| Bm–14 | 72 | 72 | 96 | 48 | 72 | 96 | 72 | 48 | 72 | 72 | 72.0 |
| Bm–15 | 96 | 72 | 96 | 72 | 96 | 72 | 96 | 72 | 96 | 120 | 88.8 |
| Bm–16 | 72 | 48 | 72 | 96 | 72 | 72 | 96 | 72 | 96 | 96 | 79.2 |
| Bm–17 | 72 | 72 | 72 | 72 | 96 | 72 | 72 | 72 | 96 | 72 | 76.8 |
| Bm–18 | 96 | 72 | 48 | 72 | 96 | 96 | 48 | 48 | 96 | 96 | 76.8 |
| Bm–19 | 72 | 96 | 96 | 48 | 72 | 72 | 72 | 48 | 72 | 96 | 74.4 |
| Bm–20 | 48 | 48 | 72 | 72 | 48 | 72 | 72 | 72 | 120 | 96 | 72.0 |
| Bm–21 | 72 | 72 | 96 | 48 | 72 | 96 | 96 | 72 | 96 | 120 | 84.0 |
| Bm–22 | 96 | 72 | 72 | 72 | 72 | 48 | 72 | 72 | 96 | 96 | 76.8 |
| Mean | 77.5 | 78.6 | 77.5 | 75.3 | 76.4 | 77.5 | 75.3 | 68.7 | 94.9 | 97.1 | 79.8 |
| CD at 5 % | Isolate: 3.046, Variety: 2.054, Isolate × Variety: 9.632 | | | | | | | | | | |

**Supplementary Table 4.** Lesion length (mm) of different Bipolaris maydis isolates on selected maize genotypes under poly house conditions

| Isolates/ Varities | Punjab sweet corn composite | HKI–1105x HKI 488 | HKI–536 CBT | HKI–327 T | QPM–9 | HM–10 | HM–9 | HM–8 | HQPM–4 | HQPM–1 | Mean |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Bm–1 | 12.4 (5.5–16.4) | 11.5 (4.6–15.6) | 22.5 (7.2–28.5) | 24.2 (7.5–29.4) | 14.6 (6.5–19.4) | 10.6 (4.8–15.9) | 20.5 (6.2–27.5) | 20.2 (8.2–27.4) | 7.8 (3.4–13.6) | 8.5 (3.2–12.8) | 15.28 |
| Bm–2 | 15.2 (4.8–20.5) | 12.6 (5.5–15.9) | 21.4 (7.7–26.6) | 25.4 (6.8–30.5) | 12.8 (4.8–20.5) | 12.4 (5.1–16.1) | 23.5 (6.5–28.5) | 18.5 (6.7–24.8) | 7.4 (3.8–12.8) | 7.8 (4.1–11.7) | 15.70 |
| Bm–3 | 14.8 (4.5–18.5) | 10.9 (4.8–14.6) | 21.7 (7.4–28.2) | 24.7 (7.5–32.4) | 15.6 (5.5–20.5) | 11.8 (5.2–15.8) | 22.5 (7.8–30.1) | 22.8 (7.8–28.4) | 8.1 (3.2–13.9) | 7.5 (3.4–14.8) | 16.04 |
| Bm–4 | 14.5 (6.2–18.8) | 10.7 (5.5–14.2) | 24.4 (6.8–28.5) | 20.6 (5.6–27.4) | 16.4 (7.2–20.8) | 9.8 (6.1–15.7) | 22.8 (6.5–28.8) | 20.8 (7.5–25.6) | 7.5 (4.7–12.8) | 6.7 (3.5–11.4) | 15.42 |
| Bm–5 | 15.6 (5.1–21.4) | 11.5 (5.1–15.9) | 22.2 (6.2–28.5) | 25.4 (7.5–32.8) | 14.9 (5.1–18.8) | 13.5 (5.2–16.7) | 24.1 (6.5–30.5) | 21.4 (5.7–26.5) | 8.5 (4.5–14.2) | 8.1 (4.2–13.5) | 16.52 |
| Bm–6 | 12.8 (5.2–17.5) | 11.7 (5.5–16.6) | 20.1 (6.6–26.4) | 24.8 (7.4–29.5) | 11.8 (4.8–15.7) | 12.8 (5.5–15.9) | 22.5 (6.4–28.5) | 16.8 (5.6–22.4) | 6.9 (3.4–12.9) | 7.8 (3.5–12.7) | 14.80 |
| Bm–7 | 20.4 (5.7–24.8) | 11.8 (5.8–16.5) | 26.8 (9.2–32.8) | 25.2 (7.5–32.8) | 24.2 (6.5–30.5) | 13.5 (6.2–16.7) | 25.5 (7.2–31.5) | 28.2 (10.2–34.4) | 8.8 (5.8–15.1) | 9.1 (6.1–14.2) | 19.35 |
| Bm–8 | 15.8 | 12.8 | 22.8 | 23.5 | 12.8 | 11.9 | 20.6 | 20.2 | 7.8 | 7.2 | 15.54 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | (6.4–18.8) | (5.8–16.2) | (7.7–29.4) | (7.2–34.1) | (6.6–18.5) | (5.6–15.2) | (6.4–28.7) | (6.5–27.3) | (3.8–13.9) | (3.9–10.8) | |
| Bm–9 | 14.2 (4.8–18.5) | 11.4 (5.1–15.8) | 20.5 (6.5–25.7) | 21.8 (6.5–28.5) | 11.8 (4.5–15.8) | 10.2 (5.1–14.8) | 24.5 (7.5–28.6) | 17.6 (6.2–22.5) | 7.2 (3.7–12.8) | 6.7 (3.5–11.5) | 14.59 |
| Bm–10 | 18.5 (6.5–22.6) | 10.5 (5.5–14.2) | 27.5 (7.8–32.5) | 28.5 (7.2–34.2) | 20.7 (5.5–26.7) | 12.5 (5.8–16.1) | 30.4 (8.5–35.4) | 24.9 (7.5–30.5) | 8.5 (5.4–14.2) | 8.8 (5.8–13.7) | 19.08 |
| Bm–11 | 17.6 (5.2–21.6) | 12.4 (4.7–16.2) | 20.8 (5.4–26.5) | 20.8 (7.2–26.2) | 18.5 (4.5–23.7) | 11.9 (4.9–15.2) | 22.4 (6.5–28.5) | 22.8 (7.4–28.8) | 6.6 (3.5–11.9) | 7.6 (3.8–12.7) | 16.14 |
| Bm–12 | 18.9 (6.7–21.7) | 12.2 (5.2–16.1) | 24.4 (6.7–30.2) | 25.4 (6.7–34.2) | 21.7 (6.4–26.7) | 13.2 (6.2–16.4) | 22.5 (8.1–32.4) | 25.4 (6.5–32.4) | 8.5 (4.5–13.9) | 8.2 (4.2–14.2) | 18.04 |
| Bm–13 | 12.8 (4.5–16.5) | 11.5 (4.8–15.4) | 22.7 (6.7–28.8) | 24.5 (6.2–32.6) | 14.8 (4.8–18.5) | 10.8 (4.9–14.8) | 20.9 (6.5–30.7) | 21.5 (7.8–26.8) | 7.4 (3.8–12.6) | 6.8 (3.5–11.6) | 15.37 |
| Bm–14 | 18.6 (4.4–22.7) | 12.6 (6.2–16.5) | 21.4 (6.5–27.9) | 23.5 (7.5–30.4) | 16.6 (4.4–21.5) | 11.4 (5.2–14.8) | 22.8 (7.2–30.9) | 18.3 (6.5–24.7) | 7.6 (3.5–12.7) | 7.1 (4.5–12.4) | 15.99 |
| Bm–15 | 18.5 (5.6–22.4) | 12.4 (5.3–16.1) | 26.2 (6.4–30.2) | 24.5 (6.5–31.4) | 20.5 (5.6–25.7) | 12.5 (5.4–16.2) | 25.7 (7.4–32.5) | 24.4 (7.5–32.4) | 8.2 (4.2–13.7) | 7.4 (3.8–12.5) | 18.03 |
| Bm–16 | 12.8 (3.8–16.4) | 11.5 (5.2–15.9) | 20.6 (5.5–25.8) | 26.2 (8.5–34.2) | 11.5 (4.5–17.2) | 12.8 (5.2–16.2) | 24.5 (6.5–30.4) | 16.8 (5.4–22.8) | 7.8 (3.7–13.9) | 8.5 (4.5–14.5) | 15.30 |
| Bm–17 | 11.7 (4.5–16.4) | 12.5 (6.4–16.1) | 22.4 (7.2–27.4) | 22.6 (6.4–30.5) | 13.8 (5.5–18.4) | 12.2 (5.1–16.2) | 23.8 (6.5–28.8) | 21.8 (6.2–27.9) | 8.2 (4.1–13.7) | 7.4 (3.8–12.7) | 15.64 |
| Bm–18 | 14.8 (5.5–18.4) | 11.6 (5.6–15.8) | 24.2 (6.5–28.9) | 24.5 (6.2–32.2) | 14.8 (5.5–18.4) | 13.1 (6.6–15.9) | 22.5 (5.5–28.5) | 20.2 (6.1–25.7) | 7.6 (4.2–12.9) | 8.2 (4.2–13.8) | 16.15 |
| Bm–19 | 16.5 (5.8–20.4) | 12.5 (5.8–16.2) | 21.8 (7.4–28.2) | 24.8 (7.2–32.5) | 18.7 (4.8–22.4) | 11.9 (4.9–15.9) | 22.9 (7.5–28.5) | 22.9 (8.1–30.5) | 8.7 (5.4–14.2) | 8.4 (4.1–13.8) | 16.91 |
| Bm–20 | 18.5 (6.5–22.8) | 11.4 (5.8–15.8) | 25.4 (8.4–32.5) | 24.4 (7.8–30.2) | 21.5 (6.8–25.8) | 10.7 (4.8–14.8) | 26.5 (7.5–34.2) | 22.1 (7.5–28.8) | 7.2 (4.5–13.8) | 7.8 (3.8–13.5) | 17.55 |
| Bm–21 | 14.7 (4.5–18.7) | 10.8 (5.1–15.2) | 18.8. (5.7–25.7) | 20.9 (6.2–27.4) | 12.9 (4.5–19.5) | 12.6 (6.1–16.2) | 22.7 (6.7–28.5) | 20.2 (5.7–26.9) | 7.4 (4.1–13.2) | 6.9 (4.1–11.8) | 14.34 |
| Bm–22 | 15.4 (5.4–20.5) | 13.2 (5.9–16.5) | 26.4 (8.2–32.5) | 24.2 (6.8–31.8) | 18.8 (4.5–24.5) | 13.8 (5.8–16.2) | 25.9 (7.5–30.5) | 25.4 (6.5–32.5) | 8.5 (4.8–14.2) | 8.7 (4.6–12.7) | 18.03 |
| Mean | 15.68 | 11.81 | 23.1 | 24.10 | 16.35 | 12.08 | 23.63 | 21.50 | 7.82 | 7.78 | 16.3 |
| CD at 5 % | Isolate: 0.635, Variety: 0.428, Isolate × Variety: 2.007 | | | | | | | | | | |

**Supplementary Table 5.** Lesion breadth (mm) of different Bipolaris maydis isolates on selected maize genotypes under poly house conditions

| Isolates /Varities | Punjab sweet corn composite | HKI–1105x HKI 488 | HKI–536 CBT | HKI–327 T | QPM–9 | HM–10 | HM–9 | HM–8 | HQPM–4 | HQPM–1 | Mean |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Bm–1 | 2.8 (2.5–3.5) | 2.2 (2.0–2.8) | 3.1 (2.5–4.1) | 3.5 (2.6–4.0) | 2.6 (2.4–3.2) | 2.4 (2.2–3.0) | 3.3 (2.8–4.2) | 3.4 (2.7–4.5) | 1.8 (1.4–2.4) | 1.7 (1.4–2.4) | 2.68 |
| Bm–2 | 3.0 (2.8–4.0) | 2.0 (1.8–2.5) | 3.4 (2.7–4.0) | 3.3 (2.7–4.0) | 2.8 (2.6–3.4) | 2.2 (2.0–2.5) | 3.5 (2.5–4.5) | 3.2 (2.5–4.2) | 1.6 (1.2–2.5) | 1.5 (1.2–2.5) | 2.65 |
| Bm–3 | 2.6 (2.4–3.2) | 2.0 (1.6–2.8) | 3.7 (2.8–4.2) | 3.2 (2.8–3.8) | 2.5 (2.2–3.0) | 1.8 (1.5–2.5) | 3.5 (2.6–4.0) | 4.1 (2.5–4.5) | 1.4 (1.2–2.8) | 1.5 (1.2–2.8) | 2.63 |
| Bm–4 | 2.8 (2.5–3.0) | 2.4 (2.1–3.0) | 3.2 (2.6–4.2) | 3.4 (2.8–4.2) | 2.6 (2.2–3.2) | 2.5 (2.0–2.8) | 3.0 (2.5–3.8) | 3.5 (2.8–4.4) | 1.6 (1.4–2.5) | 1.6 (1.4–2.5) | 2.66 |
| Bm–5 | 2.8 (2.4–3.2) | 2.2 (2.0–2.8) | 2.8 (2.5–3.5) | 3.2 (2.9–4.4) | 2.6 (2.4–3.4) | 2.5 (2.0–2.8) | 3.0 (2.7–3.5) | 3.2 (2.4–3.8) | 1.8 (1.3–2.8) | 1.6 (1.3–2.8) | 2.57 |
| Bm–6 | 2.6 (2.5–2.8) | 2.5 (2.0–3.0) | 3.3 (2.7–3.8) | 3.0 (2.5–3.5) | 2.8 (2.5–3.4) | 2.4 (2.2–3.2) | 3.1 (2.8–3.9) | 3.5 (2.8–4.2) | 1.7 (1.0–2.2) | 1.4 (1.0–2.5) | 2.63 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| Bm–7 | 3.0 (2.8– 3.2) | 1.8 (1.5–2.5) | 4.0 (2.7– 4.5) | 4.1 (3.0– 4.5) | 3.2 (2.7– 3.5) | 2.0 (1.6–3.0) | 3.8 (2.7– 4.3) | 4.2 (2.9– 4.5) | 1.4 (1.0–2.2) | 1.2 (1.0–2.1) | 2.87 |
| Bm–8 | 2.8 (2.5–3.2) | 2.1 (1.8–2.8) | 3.2 (2.7–3.9) | 3.5 (2.7–3.9) | 2.7 (2.5–3.0) | 2.4 (2.0–2.8) | 3.0 (2.6–3.8) | 3.4 (2.9–3.8) | 1.7 (1.4–3.0) | 1.5 (1.2–2.6) | 2.63 |
| Bm–9 | 2.6 (2.2–3.0) | 2.0 (1.6–3.0) | 3.4 (2.9–4.1) | 3.5 (2.9–4.1) | 2.8 (2.5–3.4) | 2.1 (1.8–2.8) | 3.6 (3.0–4.4) | 3.2 (2.5–4.0) | 1.8 (1.5–2.8) | 1.6 (1.4–2.6) | 2.66 |
| Bm–10 | 2.7 (2.5–3.2) | 2.6 (2.2–3.1) | 3.5 (2.6–4.2) | 3.1 (2.5–4.3) | 3.0 (2.8–3.4) | 2.4 (2.0–3.0) | 3.4 (2.4–4.4) | 3.8 (2.9–4.2) | 1.5 (1.0–2.6) | 1.4 (1.2–2.4) | 2.74 |
| Bm–11 | 3.0 (2.8–3.4) | 2.4 (2.0–2.8) | 3.2 (2.7–3.8) | 3.4 (2.6–4.0) | 2.6 (2.4–3.2) | 2.6 (2.2–3.1) | 3.1 (2.8–4.0) | 3.5 (2.8–4.0) | 1.8 (1.4–2.5) | 1.5 (1.3–2.5) | 2.71 |
| Bm–12 | 2.8 (2.6– 3.4) | 2.5 (2.1–3.0) | 3.5 (2.5– 4.0) | 3.2 (2.8– 4.2) | 2.5 (2.4– 3.0) | 2.4 (2.2–2.8) | 3.5 (2.9– 4.5) | 3.7 (2.6– 4.2) | 2.0 (1.5–3.2) | 1.8 (1.5–2.8) | 2.79 |
| Bm–13 | 3.0 (2.8–3.2) | 2.4 (2.2–2.8) | 3.5 (2.6–3.9) | 3.4 (2.5–4.4) | 2.8 (2.6–3.2) | 2.2 (2.0–2.6) | 3.1 (2.5–4.0) | 3.4 (2.8–3.8) | 1.8 (1.5–2.8) | 1.4 (1.2–2.7) | 2.70 |
| Bm–14 | 3.2 (2.5–3.6) | 2.2 2.0–2.8) | 3.4 (2.8–4.1) | 3.5 (3.1–4.5) | 3.0 (2.8–3.4) | 2.0 (1.6–2.6) | 3.7 (3.0–4.5) | 3.5 (2.6–4.2) | 1.8 (1.4–3.2) | 1.5 (1.0–2.6) | 2.78 |
| Bm–15 | 3.2 (3.0–3.5) | 2.5 (2.0–3.0) | 3.8 (3.1–4.3) | 3.3 (2.6–4.0) | 3.0 (2.5–3.5) | 2.4 (2.0–2.8) | 3.5 (2.9–4.2) | 4.0 (3.4–4.5) | 1.6 (1.4–3.1) | 1.4 (1.2–2.4) | 2.87 |
| Bm–16 | 2.7 (2.2–3.O) | 2.0 (1.8–2.5) | 3.0 (2.5–3.8) | 3.4 (2.7–4.2) | 2.9 (2.6–3.4) | 2.4 (2.0–3.0) | 3.3 (2.7–4.0) | 3.5 (2.8–4.2) | 1.8 (1.5–2.8) | 1.6 (1.4–2.8) | 2.66 |
| Bm–17 | 2.6 (2.2–2.8) | 2.2 2.0–2.8) | 2.9 (2.4–3.7) | 3.0 (2.5–3.5) | 2.5 (2.2–3.0) | 2.0 (1.8–2.5) | 3.2 (2.7–3.9) | 3.2 (2.5–3.8) | 1.4 (1.2–2.8) | 1.5 (1.3–2.5) | 2.45 |
| Bm–18 | 3.0 (2.6–3.4) | 2.4 (2.1–3.0) | 3.4 (2.8–4.1) | 3.8 (3.2–4.4) | 3.1 (2.6–3.5) | 2.6 (2.4–3.0) | 3.5 (2.9–4.2) | 3.6 (2.7–4.2) | 1.9 (1.5–3.0) | 1.7 (1.4–3.1) | 2.90 |
| Bm–19 | 2.8 (2.5–3.0) | 2.3 (1.8–2.8) | 3.5 (2.8–4.4) | 3.2 (2.6–3.9) | 2.6 (2.3–3.0) | 2.5 (2.2–3.0) | 3.1 (2.7–3.8) | 3.6 (2.8–4.0) | 1.7 (1.4–2.8) | 1.4 (1.2–2.7) | 2.67 |
| Bm–20 | 2.8 (2.5–3.4) | 2.5 (2.1–3.0) | 3.1 (2.7–3.6) | 3.5 (2.5–4.4) | 3.0 (2.6–3.4) | 2.2 (2.0–3.2) | 3.4 (2.5–4.1) | 3.5 (2.5–3.8) | 1.5 (1.2–2.6) | 1.3 (1.0–2.6) | 2.68 |
| Bm–21 | 2.6 (2.2–3.0) | 1.8 (1.5–2.5) | 3.3 (2.6–3.9) | 3.3 (2.7–4.2) | 2.7 (2.4–3.0) | 2.0 (1.8–2.9) | 3.1 (2.5–4.0) | 3.4 2.7–4.1) | 1.5 (1.2–2.6) | 1.2 (1.0–2.8) | 2.49 |
| Bm–22 | 3.2 (3.0–3.4) | 2.5 (2.0–3.0) | 3.5 (2.8–4.2) | 3.4 (2.8–4.5) | 3.0 (2.6–3.5) | 2.6 (2.2–3.8) | 3.6 (2.8–4.4) | 3.8 (2.9–4.4) | 1.2 (1.0–2.1) | 1.5 (1.2–2.4) | 2.83 |
| Mean | 2.85 | 2.25 | 3.35 | 3.37 | 2.79 | 2.30 | 3.33 | 3.56 | 1.65 | 1.49 | 2.70 |
| CD at 5 % | Isolate: 0.127, Variety: 0.086, Isolate× Variety: 0.401 | | | | | | | | | | |

**Supplementary Table 6.** Lesion colour of different Bipolaris maydis isolates on selected maize genotypes under poly house conditions

| Isolates /Varities | Punjab sweet corn composite | HKI–1105x HKI 488 | HKI–536 CBT | HKI–327 T | QPM–9 | HM–10 | HM–9 | HM–8 | HQPM–4 | HQPM–1 |
|---|---|---|---|---|---|---|---|---|---|---|
| Bm–1 | Brown | Dark Brown | Light Brown | Brown | Brown | Brown | Light Brown | Brown | Dark Brown | Dark Brown |
| Bm–2 | Dark Brown | Light Brown | Brown | Dark Brown | Dark Brown | Brown | Light Brown | Brown | Light Brown | Brown |
| Bm–3 | Brown | Light Brown | Dark Brown | Light Brown | Brown | Brown | Light Brown | Brown | Dark Brown | Dark Brown |
| Bm–4 | Dark Brown | Brown | Dark Brown | Dark Brown | Brown | Light Brown | Dark Brown | Brown | Light Brown | Brown |
| Bm–5 | Dark Brown | Light Brown | Brown | Brown | Dark Brown | Brown | Brown | Light Brown | Dark Brown | Dark Brown |

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| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Bm–6 | Brown | Light Brown | Brown | Dark Brown | Brown | Dark Brown | Dark Brown | Brown | Dark Brown | Brown |
| Bm–7 | Dark Brown | Dark Brown | Dark Brown | Dark Brown | Dark Brown | Brown | Dark Brown | Dark Brown | Brown | Brown |
| Bm–8 | Light Brown | Brown | Light Brown | Brown | Brown | Dark Brown | Light Brown | Brown | Brown | Brown |
| Bm–9 | Brown | Brown | Light Brown | Light Brown | Brown | Dark Brown | Brown | Brown | Brown | Brown |
| Bm–10 | Brown | Brown | Light Brown | Brown | Brown | Light Brown | Dark Brown | Dark Brown | Light Brown | Brown |
| Bm–11 | Light | Brown | Light Brown | Dark Brown | Brown | Dark Brown | Light Brown | Dark Brown | Brown | Dark Brown |
| Bm–12 | Light Brown | Dark Brown | Dark Brown | Dark Brown | Light Brown | Dark Brown | Brown | Dark Brown | Dark Brown | Brown |
| Bm–13 | Brown | Dark Brown | Dark Brown | Dark Brown | Brown | Dark Brown | Dark Brown | Brown | Dark Brown | Dark Brown |
| Bm–14 | Dark Brown | Dark Brown | Light Brown | Dark Brown | Brown | Dark Brown | Brown | Dark Brown | Brown | Light Brown |
| Bm–15 | Light Brown | Dark Brown | Brown | Brown | Dark Brown | Dark Brown | Dark Brown | Brown | Brown | Dark Brown |
| Bm–16 | Brown | Light Brown | Dark Brown | Dark Brown | Light Brown | Brown | Dark Brown | Brown | Brown | Brown |
| Bm–17 | Light Brown | Brown | Dark Brown | Brown | Brown | Dark Brown | Light Brown | Brown | Light Brown | Dark Brown |
| Bm–18 | Light Brown | Brown | Dark Brown | Light Brown | Brown | Dark Brown | Light Brown | Dark Brown | Brown | Brown |
| Bm–19 | Brown | Brown | Dark Brown | Dark Brown | Brown | Dark Brown | Dark Brown | Brown | Brown | Dark Brown |
| Bm–20 | Light Brown | Light Brown | Brown | Dark Brown | Dark Brown | Dark Brown | Dark Brown | Brown | Brown | Dark Brown |
| Bm–21 | Dark Brown | Brown | Dark Brown | Brown | Light Brown | Dark Brown | Dark Brown | Brown | Brown | Brown |
| Bm–22 | Brown | Dark Brown | Dark Brown | Brown | Brown | Dark Brown | Dark Brown | Dark Brown | Brown | Dark Brown |

**Supplementary Table 7.** Disease score of different Bipolaris maydis isolates on selected maize genotypes under poly house conditions

| Isolates /Varities | Punjab sweet corn composite | HKI–1105x HKI 488 | HKI–536 CBT | HKI–327 T | QPM–9 | HM–10 | HM–9 | HM–8 | HQPM–4 | HQPM–1 | Mean |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Bm–1 | 6.4 | 5.5 | 8.5 | 6.7 | 6.0 | 5.0 | 6.6 | 7.2 | 2.6 | 2.8 | 5.7 |
| Bm–2 | 7.0 | 5.0 | 6.8 | 5.9 | 6.0 | 4.5 | 6.7 | 8.0 | 3.0 | 2.7 | 5.5 |
| Bm–3 | 5.8 | 5.2 | 6.5 | 6.0 | 6.3 | 5.2 | 5.6 | 6.5 | 2.9 | 2.0 | 5.3 |
| Bm–4 | 6.5 | 6.3 | 8.5 | 8.5 | 6.4 | 4.8 | 8.1 | 7.5 | 3.8 | 3.0 | 6.1 |
| Bm–5 | 6.3 | 6.2 | 6.8 | 6.1 | 6.0 | 5.3 | 6.7 | 6.5 | 2.9 | 2.5 | 5.5 |
| Bm–6 | 5.8 | 5.0 | 6.2 | 6.0 | 7.7 | 5.1 | 6.0 | 6.2 | 2.6 | 2.7 | 5.3 |
| Bm–7 | 8.5 | 7.2 | 8.4 | 9.0 | 8.1 | 7.2 | 8.8 | 9.0 | 4.6 | 4.2 | 7.5 |
| Bm–8 | 6.5 | 6.2 | 7.7 | 6.5 | 6.3 | 6.0 | 6.9 | 6.7 | 3.2 | 3.0 | 5.9 |
| Bm–9 | 6.0 | 5.6 | 6.8 | 6.3 | 6.1 | 5.4 | 6.5 | 6.8 | 3.1 | 2.7 | 5.5 |
| Bm–10 | 6.4 | 5.7 | 7.0 | 6.3 | 6.3 | 5.6 | 6.5 | 7.2 | 3.0 | 3.2 | 5.7 |

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| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Bm–11 | 5.6 | 4.5 | 6.3 | 5.9 | 5.2 | 4.0 | 6.0 | 5.8 | 2.6 | 2.5 | 4.8 |
| Bm–12 | 5.9 | 5.7 | 6.5 | 6.5 | 6.3 | 5.8 | 6.8 | 7.5 | 2.9 | 3.2 | 5.7 |
| Bm–13 | 6.5 | 6.4 | 7.5 | 6.8 | 6.5 | 5.3 | 7.0 | 6.7 | 3.2 | 2.5 | 5.8 |
| Bm–14 | 6.7 | 5.4 | 8.5 | 7.1 | 6.7 | 6.2 | 6.9 | 7.8 | 3.2 | 3.2 | 6.1 |
| Bm–15 | 5.7 | 5.5 | 6.8 | 6.4 | 5.9 | 5.3 | 6.2 | 6.4 | 2.9 | 2.5 | 5.3 |
| Bm–16 | 6.5 | 6.3 | 7.0 | 6.5 | 6.4 | 5.5 | 6.9 | 8.2 | 3.0 | 3.0 | 5.9 |
| Bm–17 | 7.8 | 7.1 | 9.0 | 7.4 | 7.4 | 7.5 | 8.5 | 9.0 | 3.9 | 3.1 | 7.0 |
| Bm–18 | 6.1 | 5.4 | 7.0 | 6.3 | 6.0 | 5.3 | 6.5 | 6.5 | 2.9 | 2.5 | 5.4 |
| Bm–19 | 6.5 | 5.5 | 7.7 | 6.9 | 6.5 | 4.1 | 6.9 | 8.2 | 3.3 | 3.0 | 5.8 |
| Bm–20 | 6.1 | 5.5 | 7.4 | 6.3 | 6.1 | 5.7 | 6.2 | 6.5 | 2.5 | 2.7 | 5.5 |
| Bm–21 | 6.5 | 6.3 | 7.5 | 6.5 | 6.3 | 5.5 | 6.7 | 7.6 | 2.9 | 2.5 | 5.8 |
| Bm–22 | 6.7 | 6.9 | 8.5 | 7.5 | 6.7 | 5.4 | 7.8 | 9.0 | 3.5 | 3.1 | 6.5 |
| Mean | 6.4 | 5.8 | 7.4 | 6.7 | 6.4 | 5.4 | 6.8 | 7.3 | 3.1 | 2.8 | 5.8 |
| CD at 5 % | Isolate: 0.254, Variety: 0.171, Isolate × Variety: 0.803 | | | | | | | | | | |

**Supplementary Table 8.** Cluster means five clusters against their respective pathogenic characters under study

| Clusters/Characters | Latent period (hr) | Incubation period (hr) | Lesion length (mm) | Lesion breadth (mm) | Disease score |
|---|---|---|---|---|---|
| Cluster 1 | 89.28 | 55.68 | 16.01 | 2.68 | 5.28 |
| Cluster 2 | 82.62 | 50.4 | 15.71 | 2.65 | 5.67 |
| Cluster 3 | 71.4 | 46.8 | 17.01 | 2.71 | 5.85 |
| Cluster 4 | 78.72 | 48.48 | 16.45 | 2.69 | 6.12 |
| Cluster 5 | 67.2 | 39.6 | 19.35 | 2.87 | 7.5 |

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