JETIR.ORG ISSN: 2349-5162 | ESTD Year : 2014 | Monthly Issue
JOURNAL OF EMERGING TECHNOLOGIES AND INNOVATIVE RESEARCH (JETIR)
An International Scholarly Open Access, Peer-reviewed, Refereed Journal

Host Range Variability, Infection Dynamics and Relative Abundance of *Alternaria alternata* Across Diverse Plant Species from Amravati Division

Shilanand V. Hiwarale
Vinayak Vidnyan Mahavidyalaya, Nandgaon Khandeshwar, Amravati – 444708,
Maharashtra, India
Corresponding Author: svhiwarale@gmail.com

Abstract : Alternaria alternata is a cosmopolitan phytopathogenic fungus exhibiting broad host range and remarkable ecological adaptability. The present study investigates its host range variability, infection dynamics and relative abundance across twenty-two naturally infected plant species belonging to eighteen families collected from different localities within the Amravati Division of Maharashtra, India. Field-based observations, host-specific symptomatology, and herbarium-supported documentation reveal significant variations in susceptibility, lesion morphology, and ecological associations. The results highlight the wide natural host spectrum of A. alternata in the region from fruit trees and forest species to ornamentals and cultivated crops emphasizing its epidemiological significance and potential impact on local biodiversity and agriculture. The study contributes to understanding host-pathogen interactions and provides baseline data for disease monitoring and management strategies in the Amravati Division.

Key words: *Alternaria alternata,* Amravati, Abundance.

1. Introduction

Most widely distributed, economically significant, and ecologically adaptable phytopathogenic fungi known worldwide is *Alternaria alternata* (Fr.) Keissl. Characterized by its darkly pigmented, septate conidia and ability to produce an array of host-specific and non-host-specific toxins, *A. alternata* is capable of infecting more than 400 plant species across diverse climatic zones (1,18). Its pathogenic versatility is attributed to multiple factors, including rapid asexual reproduction, adaptability to varied humidity and temperature regimes, and the ability to survive as both a saprophyte and pathogen on plant debris, leaves, seeds, and fruits. As a result, the fungus is consistently reported as a causal agent of leaf spot, blight, defoliation, fruit rot, and post-harvest losses in numerous crops, ornamentals, forest species, and medicinal plants (12).

In India, especially in the semi-arid to sub-tropical regions such as the Amravati Division of Maharashtra, *A. alternata* forms an integral part of the mycoflora associated with agricultural fields, forest ecosystems, and urban vegetation. The Amravati Division encompasses varied ecological landscapes including the Satpuda hill ranges, dry deciduous forests, agricultural plains, and peri-urban green belts offering ideal microhabitats for fungal proliferation. Despite this ecological heterogeneity, systematic documentation of the natural host range of *A. alternata* in this region remains limited. Previous studies have largely focused on agricultural crops such as cotton, tomato, and groundnut, leaving a significant knowledge gap regarding its occurrence on wild, ornamental, and non-traditional hosts within forested and urban settings.

Host range studies are essential not only for understanding the pathogen's epidemiology but also for determining its potential to act as a reservoir for disease spread across landscapes. Broad-spectrum pathogens such as *A. alternata* can serve as bridges connecting different ecological zones transmitting inoculum from forest species to agricultural systems, or from ornamentals to fruit trees. Variation in symptom morphology across hosts also provides insights into differential host susceptibility, tissue physiology, and environmental influences (19). Moreover, climate-linked fluctuations in humidity and temperature further modify infection dynamics, allowing *A. alternata* to thrive in both dry and moist periods of the year.

2. Materials and Methods

2.1 Study Area

The Amravati Division, located in the Vidarbha region of Maharashtra, India, encompasses a diverse landscape that includes agricultural plains, dry deciduous forests, undulating hill ranges, and semi-urban ecosystems. The study area spans the districts of Amravati, Akola, Yavatmal, and Washim each representing a unique combination of climatic and ecological conditions conducive to fungal diversity. The region typically experiences a tropical monsoon climate characterized by hot summers (temperatures often exceeding 42°C), a humid monsoon season with annual rainfall ranging between 800–1100 mm, and mild to moderately cool winters, with minimum temperatures occasionally falling below 12°C. Relative humidity varies seasonally, reaching up to 85–90% during monsoon months and dropping below 40% in peak summer. Such fluctuating environmental conditions strongly influence the sporulation, dispersal, and infection potential of *Alternaria alternata*, which thrives in warm, humid, and moderately dry atmospheres (1). The microclimatic variation across forested zones like Chikhaldara, urban pockets such as Yavatmal City, and agricultural belts like Akot and Telhara provides suitable niches for pathogen survival and host interactions.

2.2 Collection and Documentation

Naturally infected leaves showing typical symptoms of *Alternaria* infection were collected from 2014 to 2025. Collections were performed systematically across different seasons to capture the temporal and ecological variability of the pathogen. Each specimen was photographed in situ, and field notes were recorded, including GPS coordinates, altitude, habitat type, and associated environmental conditions. Immediately after collection, samples were stored in sterile paper envelopes to prevent moisture accumulation and transported to the laboratory for further examination. Herbarium accession numbers were assigned following standard mycological curation protocols described by (6) and deposited in institutional repositories for long-term preservation. The meticulous documentation ensures traceability, aids in future comparative studies, and maintains taxonomic integrity.

2.3 Identification

Identification of *Alternaria alternata* was conducted through a combination of macroscopic and microscopic diagnostic features. Symptom-based identification involved assessing lesion morphology such as concentric rings, necrotic spread, chlorotic halos, and tissue collapse following criteria outlined by (19). Microscopic examination included preparing lactophenol cotton blue mounts to observe conidial characteristics, including color, septation, beak length, and branching pattern of conidiophores. Conidial morphology was compared with authoritative identification manuals such as (18) and other taxonomic keys. Where necessary, sporulating cultures were obtained on Potato Dextrose Agar (PDA) to study cultural traits like colony texture and pigmentation. morphological identification remains an accepted method for *Alternaria* species determination, particularly in ecological field surveys (14). Naturally infected living leaves exhibiting characteristic *Alternaria* symptoms were collected by Mr. Shilanand Hiwarale between 2014 and 2025. Each specimen was assigned a collection number and deposited in the herbarium.

3.Results

A comprehensive survey across the Amravati Division revealed twenty-two distinct plant species naturally infected by *Alternaria alternata*, illustrating its exceptionally broad host range. The detailed are given in table no.3.1 below.

Sr. No.	Host Plant (Scientific Name)	Host Plant Family	Location	Date of Collection	Accession No.
1	*Aloe vera*	Asphodelaceae	Pohara, Dist. Amravati	10-Sep-17	SVH/SGBAU 022
2	*Arachis hypogaea*	Fabaceae	SGBAU Campus, Dist. Amravati	13-Jan-16	SVH/SGBAU 018
3	*Azadirachta indica*	Meliaceae	Karanja Lad, Dist. Washim	15-Dec-16	SVH/SGBAU 010
4	*Bougainvillea spectabilis*	Nyctaginaceae	Walgaon Road, Dist. Amravati	14-Sep-19	SVH/SGBAU 078
5	*Cajanus cajan*	Fabaceae	Morshi, Dist. Amravati	19-Nov-18	SVH/SGBAU 052
6	*Capsicum annuum*	Solanaceae	Dattapur, Dist. Amravati	12-Mar-23	SVH/SGBAU 171
7	*Carica papaya*	Caricaceae	Tivsa, Dist. Amravati	6-Sep-20	SVH/SGBAU 124
8	*Catharanthus roseus*	Apocynaceae	Morshi Road, Dist. Amravati	27-Jul-17	SVH/SGBAU 020
9	*Citrus limon*	Rutaceae	Dhamangaon Railway, Dist. Amravati	5-Aug-20	SVH/SGBAU 126
10	*Coriandrum sativum*	Apiaceae	Chandur Bazar, Dist. Amravati	9-May-25	SVH/SGBAU 196
11	*Ficus benghalensis*	Moraceae	Wari, Telhara, Akola	31-Dec-19	SVH/SGBAU 100
12	*Ficus carica*	Moraceae	Balegaon, Akot, Dist. Akola	15-Jan-14	CBECH0082
13	*Hibiscus rosa-sinensis*	Malvaceae	Rajapeth, Dist. Amravati	17-Feb-22	SVH/SGBAU 158
14	*Holoptelea integrifolia*	Ulmaceae	Pohara, Dist. Amravati	29-Jul-20	SVH/SGBAU 130
15	*Mangifera indica*	Anacardiaceae	Rahatgaon, Dist. Amravati	22-Jun-18	SVH/SGBAU 033
16	*Mimusops elengi*	Sapotaceae	Chikhaldara Forest, Dist. Amravati	17-Jul-18	SVH/SGBAU 040
17	*Pongamia pinnata*	Fabaceae	Ner, Dist. Yavatmal	19-Jan-20	SVH/SGBAU 103

18	*Ricinus communis*	Euphorbiaceae	Ner, Dist. Yavatmal	18-Nov-17	SVH/SGBAU 025
19	*Solanum lycopersicum*	Solanaceae	Talegaon Bazar, Dist. Amravati	28-Oct-19	SVH/SGBAU 082
20	*Tecoma stans*	Bignoniaceae	Yavatmal City, Dist. Yavatmal	12-Oct-19	SVH/SGBAU 081
21	*Tectona grandis*	Lamiaceae	Akot road, Dist. Akola	11-Aug-16	SVH/SGBAU 014
22	*Ziziphus jujuba*	Rhamnaceae	Pusad Road, Yavatmal	21-Dec-15	SVH/SGBAU 009

Table 3.1: Showing list of hosts infected by *A. alternata*

3.2 Relative Abundance of Host Plant Families Infected by *A. alternata:*

The results illustrate the relative abundance of plant families hosting *Alternaria alternata* across the Amravati Division, based on twenty-two confirmed field records. The distribution clearly indicates that infections are not confined to a narrow taxonomic group but instead span across eighteen different plant families, highlighting the pathogen's pronounced polyphagous nature. Fabaceae emerged as the most frequently infected family (13.6%), represented by multiple hosts such as *Pongamia pinnata*, *Arachis hypogaea*, and *Cajanus cajan*. Moraceae and Solanaceae followed as the next most represented families (each 9.1%), reflecting the susceptibility of widely distributed species like *Ficus spp.* and *Solanum lycopersicum*. These families are ecologically and economically important, suggesting that *A. alternata* has established itself in key vegetation components of both natural and cultivated landscapes.

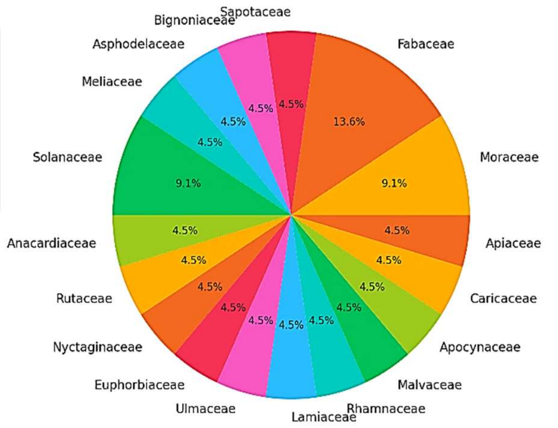

Fig. 3.1 Showing relative abundancy of host plants infected by *A. alternata*

The remaining plant families including Anacardiaceae, Rutaceae, Malvaceae, Euphorbiaceae, Lamiaceae, Apocynaceae, Caricaceae, Apiaceae, and others each accounted for 4.5% of the documented infections, indicating sporadic but widespread occurrence. The broad yet moderately even distribution across these families demonstrates that *A. alternata* does not rely on specialized host associations but can colonize diverse anatomical and physiological leaf types. Such taxonomic breadth signifies high ecological adaptability of the pathogen and suggests a persistent risk of cross-host transmission in mixed cropping systems, home gardens, and forest edges. Overall, observations underscore the importance of continuous surveillance across varied plant groups to understand shifting host preferences and emerging disease dynamics in the region.

4. Discussion

The present study documents a remarkably broad host range of *Alternaria alternata* across agricultural, horticultural, forest, and urban ecosystems of the Amravati Division. The identification of twenty-two host species spanning eighteen plant families underscores the highly polyphagous nature of this pathogen. The wide taxonomic diversity, as revealed by the abundance analysis, indicates that *A. alternata* does not exhibit strict host specificity but instead demonstrates strong ecological flexibility and opportunistic infection behavior. This is consistent with global reports suggesting that *A. alternata* thrives in environments characterized by fluctuating humidity, moderate temperatures, and host plant stress conditions commonly prevailing in semi-arid regions such as Vidarbha. The high representation of Fabaceae, Moraceae, and Solanaceae in the infection records may be attributed to their prevalence in cultivated systems and their physiological susceptibility to necrotrophic pathogens.

The infection dynamics observed in the study also highlight the pathogen's capacity to colonize both dicotyledonous tree species and economically important crops. The presence of infections in forest ecosystems (e.g., *Mimusops elengi*, *Tectona grandis*, *Holoptelea integrifolia*) demonstrates that natural vegetation can act as a reservoir for inoculum, facilitating spillover into agricultural fields. Conversely, horticultural and urban plantings may sustain infections that cycle back to wild hosts, creating a continuous inoculum network across landscapes. This interconnectivity has significant epidemiological implications, as it promotes year-round survival of the pathogen, especially through conidia dispersed by wind, rain splash, and mechanical transmission. The recent detection of infections up to May 2025 further signifies that *A. alternata* is actively spreading and adapting to a broad set of environmental conditions in the region, potentially intensifying disease pressure under climate variability.

5. Conclusion

The study conclusively demonstrates that *Alternaria alternata* is a widespread and ecologically versatile pathogen within the Amravati Division, infecting an extensive array of twenty-two host plant species representing eighteen families. Its broad host spectrum, coupled with its ability to thrive in diverse habitats, underscores its significance as a persistent phytopathogen with potential impact on both natural vegetation and economically important crops. The distribution patterns revealed through the abundance analysis highlight key plant families especially Fabaceae, Moraceae, and Solanaceae as more frequently affected, indicating potential hotspots for disease emergence.

These findings emphasize the need for continuous surveillance, early detection, and integrated disease management strategies that consider both cultivated and wild host reservoirs. Future research should focus on pathogenic variability, environmental drivers of disease outbreaks, and molecular characterization of isolates to better understand host–pathogen interactions. Overall, the results contribute valuable baseline information that can aid in predicting disease risks and formulating mitigation strategies for sustainable crop and forest health management in the region.

Acknowledgement

The authors thank the Head of the Department of Botany at Sant Gadge Baba Amravati University in Amravati and Head of the Department of Botany, Vinayak Vidnyan Mahavidyalya, Nandgaon Khandeshwar for providing required facilities for this work.

References

1. Agrios, G. N. (2005). Plant Pathology (5th ed.). Elsevier Academic Press.
2. Chaudhary, P., Singh, V., & Kumar, A. (2019). Alternaria diseases: Biology, ecology and management. Journal of Plant Pathology, 101(3), 567–580.
3. Chaudhary, R., Sharma, S., & Deep, S. (2017). Morphological and pathogenic variability in *Alternaria alternata* causing leaf spot in different hosts. International Journal of Current Microbiology and Applied Sciences, 6(9), 1121–1130.
4. Dugan, F. M. (2008). The Identification of Fungi: An Illustrated Introduction with Keys, Glossary, and Guide to Literature. APS Press.
5. Eschevarria-Cerda, J., & Butler, E. E. (2016). Host range and infection biology of *Alternaria alternata* in solanaceous crops. Plant Disease, 100(2), 325–332.
6. Hawksworth, D. L. (2011). A new dawn for the taxonomy of fungi? *IMA Fungus*, 2(1), 1–12.
7. Ismail, A. M., Johnson, R., & Sainsbury, J. (2016). Environmental influences on sporulation and infection efficiency of *Alternaria alternata*. Phytopathology, 106(5), 566–575.
8. Jain, P., & Kharbikar, L. L. (2018). Occurrence and pathogenic variability of *Alternaria alternata* infecting fruit crops in India. Indian Phytopathology, 71(2), 267–275.
9. Kaul, J. L. (2012). Plant Diseases in India. Scientific Publishers, Jodhpur.
10. Krishna, R., & Prasad, R. (2020). Ecology and epidemiology of Alternaria spp. under changing climatic conditions. Environment and Ecology, 38(4), 1301–1309.
11. Meena, P. D., Chattopadhyay, C., & Awasthi, R. P. (2010). Disease progression and host range of Alternaria alternata in oilseed crops. Journal of Oilseed Research, 27(1), 99–105.
12. Misra, A. K., & Horn, B. W. (2015). *Alternaria* species: Taxonomy, pathogenicity and host range. *Journal of Plant Pathology*, 97(1), 45–56.
13. Neergaard, P. (1979). Seed Pathology (Vol. 1 & 2). Macmillan Press.
14. Pryor, B. M., & Michailides, T. J. (2002). Morphological, pathogenic, and molecular characterization of *Alternaria* isolates associated with *Alternaria* late blight of pistachio. *Phytopathology*, 92(4), 406–416.
15. Ranjan, R., & Verma, K. S. (2017). *Alternaria alternata*: A ubiquitous pathogen with diverse host associations. International Journal of Agricultural Sciences, 9(2), 483–489.
16. Rotem, J. (1994). The Genus *Alternaria*: Biology, Epidemiology, and Pathogenicity. APS Press.
17. Sharma, N., Saxena, R., & Sharma, S. (2015). *Alternaria* leaf blight in vegetable crops: Host susceptibility and disease dynamics. International Journal of Vegetable Science, 21(4), 367–377.
18. Simmons, E. G. (2007). Alternaria: An Identification Manual. CBS Biodiversity Series 6, CBS Fungal Biodiversity Centre.
19. Thomma, B. P. H. J. (2003). Pathogenicity of *Alternaria* spp.: The role of host-specific toxins. Molecular Plant Pathology, 4(2), 83–91.
20. Yadav, S. S., & Ghuse, S. (2021). Fungal foliar diseases affecting forest vegetation in Melghat region of Maharashtra. Journal of Forestry Research, 32(5), 1681–1693.
21. Yellareddygari, S. K., Taylor, R. J., & Gossen, B. D. (2016). Weather-based disease forecasting models

for *Alternaria* leaf spot. Plant Disease, 100(10), 1980–1990.

22. Zhang, C., Wang, Z., & Bai, J. (2020). Diversity and host adaptability in *Alternaria* species: A comprehensive review. Mycological Progress, 19, 213–230