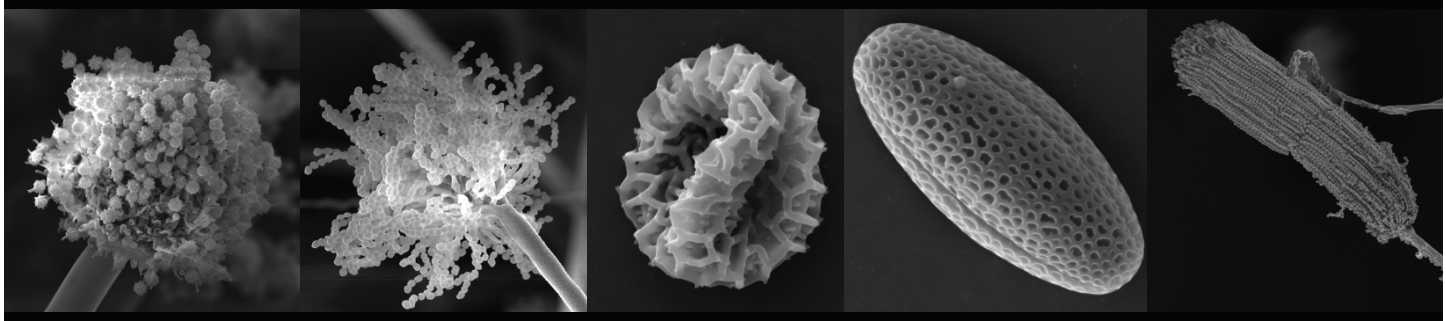
Volume 39, Number 1, 2026 ISSN No. 0971-1546



INDIAN JOURNAL OF AEROBIOLOGY



An Official Publication of

Indian Aerobiological Society

(Registration No. S/32742)

INDIAN JOURNAL OF AEROBIOLOGY

[Official Peer Reviewed Journal of Indian Aerobiological Society]

ISSN No. 0971-1546

[Website: www.indianaerobiologicalsociety.org]

Editorial Board

Editor-in Chief

Prof. Swati Gupta Bhattacharya

Bose Institute, Kolkata, West Bengal

Associate Editors

Pampa Chakraborty, Howrah

Gaurav Sircar, Kolkata

Dola Boral, Berhampore

Partha Karak, Kolkata

International Advisory Board

R. Valenta, Austria

Carmen Galan, Spain

P. Comtoise, Canada

F. Th. M. Spieksma, The Netherlands

R. Panzani, France

C. H. Katelaris, Australia

Jean Emberlin, UK

Bernard Clot, Switzerland

Roberto Albertini, Italy

S. Hasnain, S. Arabia

A. Rantio-Lethtimaki, Finland

G. Frenguelli, Italy

Jae-Won OH, S. Korea

G. Peltre, France

National Editorial Board

A. H. Rajasab, Bangalore

B. N. Pande, Pune

K. L. Tiwari, Bilaspur

S. K. Jadhav, Raipur

Subrata Raha, Purulia

A. H. Munshi, Kashmir

Debajyoti Ghosh, USA

Rajib Sahay, USA

A. B. Singh, Delhi

N. I. Singh, Imphal

U. K. Talde, Parbhani

S. B. Jogdand, Pune

Y. B. Gaikwad, Ahmednagar

J. A. Tidke, Amravati

K. S. Ramchander Rao, Muscat

D. R. More, Nanded

K. Bhattacharya, Santiniketan

Mahesh Roy, Vaishali

Surekha Kalkar, Nagpur

G. V. Patil, Amravati

Subrata Mondal, Santiniketan

Manju Sahney, Allahabad

Uday Prakash, Chennai

B. K. Nayak, Pondicherry

A. K. Jain, Gwalior

K. B. Mishra, Patna

A. A. Saoji, Nagpur

K. Manjunath, Bangalore

S. R. Patil, Pune

B. E. Rangaswamy, Davangere

Anima Nanda, Chennai

T. N. More, Pune

Editorial Office

Division of Plant Biology, Bose Institute

93/1 Acharya Prafulla Chandra Road, Kolkata - 700009, India

E-mail: swati@jcbose.ac.in, swatigb29@rediffmail.com

Contents

Obituary **1**

Dietrich Kraft : Physician, Scientist, Mentor and Architect of Molecular Allergology 1-4

Debajyoti Ghosh, Pampa Chakraborty and Swati Gupta Bhattacharya

Review Articles **5**

Application of Aerobiology, Bioinformatics and Artificial Intelligence in Health and Environmental Sciences 5-18

T. N. More and Swapnaja R. More

Palynology in Archaeology: Methods, Applications and Insights into Past Environmental Change and Human-Environment Interactions 19-31

Anusha Jadhav, Shubhra Tiwari and Shailesh Kumar Jadhav

Research Articles **33**

Seasonal Variations and Allergenic Significance of Airborne Pollen Grains in the Hilly rural areas of Purulia District, West Bengal, India 33-44

Poulami Ojha and Subrata Raha

Morphological characterization, Floral Biology and Pollen Productivity of some species of Malvaceae. 45-52

Nikita Arvind Sontakke, Kamlakar Chandar More and Prashant Ashokrao Gawande

Aerobiological insights into Airborne Fungal Spores and Soybean Disease Management in India 53-63

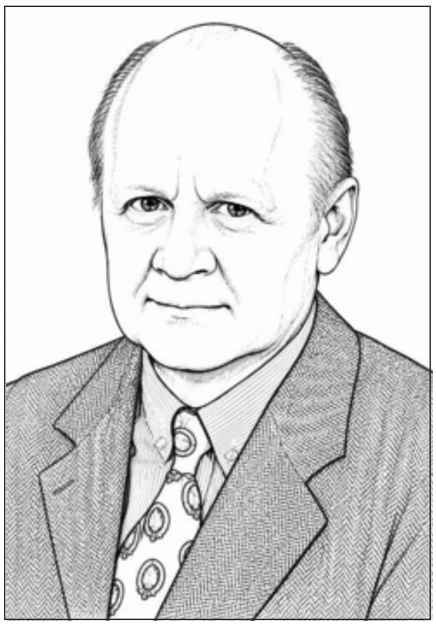
Deepali Sawant and Vaishali Thakur

Author's Guidelines **64**

Ind. J. Aerobiol., Vol. 39, No. (1), pp. 1-4 [2026] ISSN No. 0971-1546

OBITUARY

Dietrich Kraft: Physician, Scientist, Mentor and Architect of Molecular Allergology



Dietrich Kraft

(January 6, 1937 – February 28, 2026)

Professor Dietrich Kraft (1937–2026) was among the pioneering scientists who transformed allergology from a primarily descriptive clinical discipline into a mechanistically defined molecular science. His passing earlier this year marks not only the loss of a physician-scientist of exceptional originality and rigor but also the end of a formative era in which the conceptual foundations of modern allergy research were established. Through groundbreaking work in molecular allergen characterization, the introduction of recombinant allergen technology, and the creation of a globally influential scientific environment in Vienna, Professor Kraft fundamentally reshaped both the understanding and clinical management of IgE-mediated disease. His legacy is reflected in advances in allergy diagnostics, the development of allergen-specific immunotherapy, and the global community of researchers he trained and inspired.

Education and Early Career

Professor Kraft received his medical degree in 1965 from the University of Vienna, where he also began his clinical training in internal medicine. Early in his career as a physician-scientist, he developed a strong interest in immune-mediated disease mechanisms, which led him to pursue

advanced postdoctoral training in allergic inflammation in the Department of General and Experimental Pathology at the University of Vienna. Subsequently, during 1969 to 1974, he worked in the university's Department of Dermatology II, with a clinical residency in dermatology in 1973 under the supervision of Professor Herwig Ebner.

A formative period of his early career was his fellowship at the University of Cambridge, United Kingdom, in the laboratory of Professor Robin Coombs, where he received rigorous training in immunological methodology and experimental disease models. This experience provided him with a strong conceptual and technical foundation in immune effector mechanisms and solidified his commitment to hypothesis-driven translational research. Upon returning to Vienna, he integrated clinical responsibilities with laboratory investigation, establishing a dual academic trajectory that bridged bedside observation with molecular experimentation. This integrative training became the intellectual framework for his later contributions to allergen molecular characterization and recombinant allergen development.

From Clinical Observation to Molecular Precision

At the beginning of Professor Kraft's career, allergology relied predominantly on crude allergen extracts with limited molecular characterization. Although these preparations were clinically useful, their heterogeneous composition obscured the molecular basis of IgE recognition and limited mechanistic insight into allergic sensitization. Professor Kraft was among the first to recognize that advancing the field required defining allergens at the molecular level. His seminal contributions to the cloning and recombinant expression of allergens, particularly the characterization of Bet V 1, established a molecular framework for allergen specificity. These advances enabled the development of component-resolved diagnostics and laid the groundwork for precision allergy medicine. The transition from extract-based to molecule-defined allergology fundamentally changed both diagnostic strategies and therapeutic design.

Scientific Foundations and Early Contributions

Professor Kraft's early research reflected a sustained engagement with fundamental immunology. His research on complement pathways, natural killer cell biology, and drug hypersensitivity—particularly penicillin allergy—consistently sought to elucidate the immune mechanisms underlying clinical phenomena. These studies established a conceptual foundation that informed his later leadership in molecular allergology and translational immunology.

The Vienna School and the Development of a Scientific Collective

A defining feature of Professor Kraft's career was the establishment of a highly integrated scientific environment that became known as the Vienna School of Allergology. In 1976, he assumed leadership of the Allergy and Immunology Research Group at the University of Vienna, which evolved into a leading international center for molecular allergy research. From the early 1980s onward, he built a multidisciplinary research team that integrated clinical allergology with molecular biology and protein chemistry. The group brought together internationally trained scientists and investigators, including Michael Breitenbach, Christof Ebner, Otto Scheiner, and later Heimo Breiteneder,

Rudolf Valenta, Erika Jensen-Jarolim, and others who would become leading figures in allergy research. Within this collaborative environment, the research focus shifted decisively toward the molecular identification of allergens, recombinant allergen expression, and mechanistic studies of IgE-mediated cross-reactivity.

A landmark achievement of this group was the molecular characterization of Bet V 1 and its homologous proteins, along with the elucidation of their role in pollen-food cross-reactivity. These studies provided the first structural basis for clinically observed allergen cross-reactivity and contributed directly to the conceptual development of component-resolved diagnostics. The Vienna group subsequently became one of the world's leading centers in allergology, distinguished by its scientific output and legacy through the training of researchers who continue to advance the field.

Leadership and Institutional Influence

Professor Kraft's influence extended far beyond his laboratory through leadership roles at the Medical University of Vienna and membership in the Austrian Academy of Sciences. He played a central role in advancing standardized allergen characterization and integrating molecular approaches into clinical allergy research. His efforts contributed to the emergence of a more unified international framework for allergology, enabling reproducibility and comparability across research settings. This global harmonization reflected his broader vision of science as a collaborative, transnational enterprise grounded in shared methodological rigor.

Philosophy of Science, Innovation and Art

Central to Professor Kraft's legacy was a coherent philosophy of scientific inquiry that guided both his research and institutional leadership. He was known for his conviction that one must do the right thing without fear of authority or convention, a principle that shaped his scientific independence throughout his career. Deeply influenced by Karl Popper's philosophy of critical rationalism, he regarded scientific knowledge as inherently provisional, always subject to refinement, and empirical testing. This epistemological stance provided the intellectual foundation for his transition from descriptive allergology to mechanistic, hypothesis-driven molecular research. This philosophy was most clearly reflected in his early advocacy of recombinant allergen technology. During the early 1980s, such approaches received minimal institutional or industrial support and were often considered speculative. Despite this, Professor Kraft pursued the concept with sustained determination.

A pivotal moment occurred during a scientific banquet of the Austrian Society of Allergology and Immunology, where he discussed his vision with Jörg Mayrhofer, owner of the Schutzengel Apotheke in Linz. Recognizing the scientific and translational potential of recombinant allergens, Mayrhofer and his father, Theodor Mayrhofer, agreed to support the initiative. This collaboration led to the founding of Biomay in 1984, providing essential financial and organizational support for the early development of recombinant allergen technology and establishment of molecular allergology as a distinct scientific discipline. Beyond science, Professor Kraft maintained a deep engagement with the arts and humanities, reflecting a broad intellectual sensibility that enriched his

scientific perspective. His appreciation of art, literature, and philosophy informed a worldview that valued creativity alongside analytical rigor.

Mentorship and Scientific Lineage

Professor Kraft was widely regarded as an exceptional mentor who fostered intellectual independence, critical thinking, and scientific rigor. He cultivated an environment in which trainees were encouraged to challenge assumptions and develop independent lines of inquiry. The global distribution of his trainees and collaborators has created a scientific lineage that continues to influence allergology and immunology. Through this network, his intellectual legacy remains actively embedded in ongoing research and innovation.

Transforming Clinical Practice

The clinical impact of Professor Kraft's work has been profound. His contributions enabled the molecular definition of allergens, significantly improving diagnostic precision and facilitating the development of safer and more effective immunotherapies. This transformation extended across multiple allergen sources, including pollen, molds, and food allergens, replacing poorly standardized extracts with recombinant molecular reagents. The shift toward personalized, component-resolved allergy diagnosis continues to shape contemporary clinical practice and guideline development.

Importance of the knowledge about the contribution of Prof. Kraft in Indian Perspective

Allergy is a major public health concern in India, affecting more than 25% of the country's approximately 1.4 billion population. Allergic disorders are complex, multifactorial conditions that require a comprehensive understanding of their epidemiology, clinical manifestations, and management strategies. Allergen research in India dates back to 1873, when the renowned British physician D. D. Cunningham conducted microscopic examinations of air samples in Calcutta, documenting airborne pollen and fungal spores. After nearly a century-long gap, systematic allergen research in independent India was revived through the pioneering efforts of physicians such as Dr. D. N. Shivpuri and scientists including Prof. S. Chanda, Prof. S. T. Tilak, Prof. S. N. Agashe, and their students.

Today, India requires a paradigm shift toward modern clinical allergology, advancing into the molecular era through the use of purified and recombinant allergens and their clinical applications. In this context, the visionary contributions and scientific philosophy of Prof. Dr. Dietrich Kraft serve as a lasting inspiration for Indian allergy researchers. The allergy research community in India will remember Prof. Dietrich Kraft as a pioneering figure who helped usher in the era of molecular allergen biology and established a globally influential research legacy. His contributions remain milestones that have shaped modern allergy research, clinical practice, and translational innovation, leaving an enduring impact on the field.

Debajyoti Ghosh
Pampa Chakraborty
Swati Gupta Bhattacharya
On behalf of Indian Aerobiological Society

Ind. J. Aerobiol., Vol. 39, No. (1), pp. 5-18 [2026] ISSN No. 0971-1546

Review Article

APPLICATION OF AEROBIOLOGY, BIOINFORMATICS AND ARTIFICIAL INTELLIGENCE IN HEALTH AND ENVIRONMENTAL SCIENCES

T. N. MORE[1*] AND SWAPNAJA R. MORE[2]

[1]*MAEER'S MIT GROUP OF INSTITUTIONS, PUNE, INDIA*

[2]*DR. OMICS RESEARCH LABS, NEW DELHI*

[*]*CORRESPONDING AUTHOR:*

Aerobiology is an interdisciplinary branch of life sciences concerned with the study of biological particles suspended in the atmosphere, including bacteria, fungi, viruses, pollen grains and other bioaerosols. These airborne components play a vital role in ecosystem functioning, atmospheric processes, agricultural productivity and human health. Conventional aerobiological investigations have largely depended on microscopic identification and culture-based methods, which are constrained by low sensitivity, limited taxonomic resolution and inability to detect non-culturable microorganisms.

Recent advancements in molecular biology, bioinformatics and artificial intelligence (AI) have fundamentally transformed aerobiological research. High-throughput sequencing and metagenomic approaches now enable comprehensive characterization of airborne microbial communities, functional genes, allergenic determinants and antimicrobial resistance markers. Bioinformatics pipelines support large-scale data integration and interpretation, while AI-based systems facilitate automated pollen and spore recognition, predictive modeling and real-time environmental surveillance.

This review critically summarizes recent developments in aerobiology with emphasis on bioinformatics-driven and AI-enabled analytical frameworks. The manuscript provides a consolidated scientific reference for researchers aiming to explore aerobiology using emerging computational technologies, highlighting applications in public health, environmental monitoring, agriculture and climate-sensitive disease prediction.

Key Words: Aerobiology, Bioinformatics; Artificial Intelligence, Metagenomics, Public Health Surveillance.

Received: 25.02.2026 Revised: 20.03.2026 Accepted:26.03.2026

INTRODUCTION

Aerobiology is a multidisciplinary branch of life sciences concerned with the study of biological particles suspended in the atmosphere, commonly referred to as bioaerosols. These particles include pollen grains, fungal spores, bacteria, viruses, algae, protozoa, fragments of plants and animals, and other biologically derived organic matter that may remain airborne for periods ranging from minutes to several weeks depending on their size, density, morphology and prevailing meteorological conditions[1–3]. The discipline encompasses the investigation of the sources, release mechanisms, atmospheric transport, transformation, deposition, and biological effects of these airborne components on ecosystems, agriculture, and human health.

The atmosphere is now recognized as a dynamic reservoir and long-range transport pathway for biological material at local, regional, and intercontinental scales, with profound implications for biogeography, ecosystem connectivity, and disease ecology[2, 4].

Airborne biological particles exert major influences on public health, particularly in relation to allergic rhinitis, asthma, hypersensitivity pneumonitis, and other inflammatory and infectious respiratory diseases[5–7]. Pollen grains and fungal spores represent the most important outdoor aeroallergens worldwide, while airborne bacteria and viruses contribute to the transmission of infectious diseases and shape the composition of indoor and outdoor microbiomes[8, 9]. In parallel, aerobiology plays a central role in agriculture and plant pathology, as numerous economically important crop diseases are initiated and disseminated through airborne spores and propagules, often over long distances and across political boundaries[2, 4].

Beyond their biological and medical relevance, bioaerosols also participate in fundamental atmospheric and Earth system processes. They contribute to cloud formation, ice nucleation, and precipitation dynamics, and they interact with atmospheric chemistry, thereby linking biological activity with climate processes through complex feedback mechanisms[2, 10, 11]. Ongoing global changes, including urbanization, industrialization, land-use transformation, and climate change, are altering the Aerobiology is a fundamentally multidisciplinary scientific field positioned at the interface of atmospheric, biological, environmental, agricultural, and health sciences. Airborne biological particles, collectively termed bioaerosols, include bacteria, fungi, pollen, spores, and virus-containing particles that can remain suspended in the atmosphere over variable spatial and temporal scales depending on their physical properties and meteorological conditions[1, 2]. Understanding their sources, atmospheric transport, ecological roles, and impacts forms the core of contemporary aerobiological research.

In health sciences, aerobiology provides critical insight into the environmental drivers of allergic diseases, asthma, and respiratory infections. Airborne pollen and fungal spores remain among the dominant outdoor aeroallergens worldwide, and epidemiological studies consistently demonstrate associations between bioaerosol exposure and respiratory morbidity[2, 6]. The COVID-19 pandemic further accelerated interest in airborne pathogen dynamics and environmental surveillance, reinforcing the importance of molecular approaches for monitoring viral aerosols[13, 14].

Microbiology and mycology are central to characterizing the atmospheric microbiome, or aerobiome, which exhibits substantial taxonomic and functional heterogeneity shaped by source environments, transport processes, and atmospheric stressors[3, 12]. Aerobiological studies continue to document allergenic and pathogenic taxa in airborne particulate matter, while advances in automated image analysis and molecular identification are improving the standardization and scalability of fungal spore and microbial detection[15, 16].

In agriculture, aerobiology underpins plant disease epidemiology and biosecurity, as airborne dispersal of fungal spores and other

propagules plays a pivotal role in initiating and intensifying crop disease outbreaks. Aerobiological monitoring combined with meteorological and landscape data supports spatial risk assessment and outbreak forecasting[17].

Aerobiology also intersects closely with climate science, as biological particles can act as cloud condensation nuclei and ice-nucleating particles, linking biospheric processes to atmospheric feedbacks and climate variability. At the same time, land-use change, urbanization, and climate change are altering the production, distribution, and seasonality of bioaerosols, with implications for ecosystem and human health[2, 10, 11].

Given its inherently interdisciplinary scope, modern aerobiology increasingly relies on computational and data-driven approaches to integrate molecular, meteorological, and environmental datasets. High-throughput sequencing and metagenomic methods enable comprehensive characterization of aerobiomes, while advanced analytical frameworks support the synthesis of complex, multi-dimensional data into ecologically and clinically meaningful information[2, 3].

Together, these perspectives underscore aerobiology's role as a bridge between environmental systems and health sciences and highlight the necessity of integrative computational frameworks capable of processing large and heterogeneous biological and environmental datasets.

LIMITATIONS OF TRADITIONAL AEROBIOLOGICAL APPROACHES

Classical aerobiological investigations have historically relied on volumetric air sampling followed by microscopic identification and, in some cases, culture-based isolation of airborne microorganisms[1, 5]. While these approaches have provided invaluable baseline data on pollen and spore seasonality, long-term trends, and exposure patterns, they suffer from several inherent limitations.

First, morphological identification of pollen grains and fungal spores is often hindered by strong structural similarity among taxa, leading to limited taxonomic resolution and observer-dependent bias. Manual counting and identification are labor-intensive, time-consuming, and poorly suited for high-frequency or large scale monitoring programs. Second, culture-based methods detect only a small fraction of airborne microorganisms, as a substantial proportion of atmospheric microbes are viable but non-culturable or require highly specific growth conditions[3, 12].

Third, traditional approaches provide little or no information on the functional properties of airborne biological particles, such as allergenicity, pathogenic potential, virulence factors, or antimicrobial resistance. They also lack the capacity to resolve complex microbial communities or to track fine-scale temporal and spatial variability in the aerobiome[2]. The main methodological and analytical differences between traditional and data-driven aerobiological approaches are summarized in Table 1.1.

In the context of rapidly changing environmental conditions, urbanization, and climate variability, these methodological constraints increasingly limit the ability of classical aerobiology to support real-time surveillance, early warning systems, and predictive risk assess-

Table 1.1: Comparative Analysis of Traditional and AI-Based Aerobiological Approaches

Aspect	Traditional Aerobiology Methods	AI-based Modern Aerobiology Approaches
Identification technique	Manual microscopic examination of pollen and spores	Automated image recognition using machine learning and deep learning algorithms.
Taxonomic resolution	Limited; dependent on morphological similarity	High-resolution classification using trained AI models and genomic data.
Observer dependency	High observer bias and subjectivity	Minimal bias; reproducible and standardized analysis.
Throughput	Low throughput; time-consuming manual counting	High-throughput processing of large datasets.
Detection capability	Primarily culturable and morphologically identifiable particles	Detection of culturable and non-culturable organisms through omics-based approaches.
Data handling	Limited dataset analysis	Big-data analytics integrating biological and environmental variables.
Predictive capability	Descriptive analysis only; no forecasting	Predictive modeling of pollen load, bioaerosol dynamics and health risk.
Temporal resolution	Delayed results (daily or weekly analysis)	Near real-time monitoring and continuous surveillance.
Scalability	Restricted to local or small-scale studies	Scalable from local to regional and global monitoring networks.
Application scope	Primarily academic and observational studies	Public health surveillance, environmental monitoring and decision support systems.

ment. Recent studies have explicitly highlighted the need for automated, high-throughput, and data-integrative approaches for pollen, spore, and bioaerosol monitoring, including image-based recognition systems, molecular profiling, and computational modeling frameworks[15,16].

These limitations have driven the transition of aerobiology from a predominantly descriptive discipline toward a technology-enabled, data-rich science, in which molecular methods, bioinformatics, and data-driven analytical tools are increasingly used to achieve higher taxonomic resolution, functional insight, automation, and predictive capability[2,3,12].

BIOINFORMATICS IN AEROBIOLOGICAL RESEARCH

The rapid development of molecular biology and high-throughput sequencing technologies has fundamentally transformed aerobiological

research, enabling a shift from predominantly morphology-based observations toward sequence-driven, data-intensive analysis of airborne biological communities. Modern aerobiology increasingly relies on bioinformatics to process, integrate, and interpret large volumes of genomic data derived from air samples, allowing comprehensive characterization of the atmospheric microbiome (aerobiome) and its functional potential[2,3,12].

Genomic and Metagenomic Analysis

High-throughput sequencing platforms such as Illumina, PacBio, and Oxford Nanopore have enabled the direct analysis of airborne DNA and RNA without the need for cultivation. These technologies have made it possible to explore the diversity of airborne microbial, fungal, and plant-derived communities at unprecedented depth and resolution. Metabarcoding approaches targeting standard genetic markers, including 16S rRNA for bacteria, ITS and ITS2 for fungi, and rbcL for plant pollen, are now widely applied for taxonomic profiling of complex bioaerosol assemblages[18,19].

Recent studies have demonstrated that DNA metabarcoding and metagenomic sequencing significantly outperform classical microscopy in terms of taxonomic resolution, detection sensitivity, and reproducibility, particularly for morphologically similar pollen types and cryptic fungal taxa[18,19]. In addition to taxonomic composition, metagenomic approaches provide insights into the structure, diversity, and spatio-temporal dynamics of airborne microbial communities in both indoor and outdoor environments[9,20]. The application of these approaches has led to the emergence of the concept of the "aerobiome" as a complex and dynamic microbial ecosystem shaped by source environments, atmospheric transport, and environmental stressors[3,12].

As illustrated in the systematic workflow of modern aerobiological research (Fig. 1.1), bioinformatics now forms the central analytical bridge between air sampling, molecular laboratory analysis, and applied domains such as environmental monitoring, public health surveillance, agricultural risk assessment, and climate impact studies. This integrated pipeline allows researchers to move from raw airborne biological material to high-resolution taxonomic, functional, and ecological interpretation.

Functional and Resistome Profiling

Beyond taxonomic identification, shotgun metagenomics enables the functional characterization of airborne biological communities by directly analyzing their genetic content. This approach allows the detection and annotation of virulence-associated genes, antibiotic resistance genes (ARGs), stress tolerance mechanisms, and metabolic pathways, providing direct insight into the ecological and health relevance of airborne microorganisms[21,22]. Such functional profiling has demonstrated that the atmosphere is not merely a passive carrier of inert biological particles, but a reservoir of genetically diverse and potentially metabolically active microorganisms with implications for public health, ecosystem functioning, and atmospheric processes[23,24].

Several recent studies have documented the widespread presence of clinically relevant antibiotic resistance genes in urban and industrial air environments, highlighting the role of

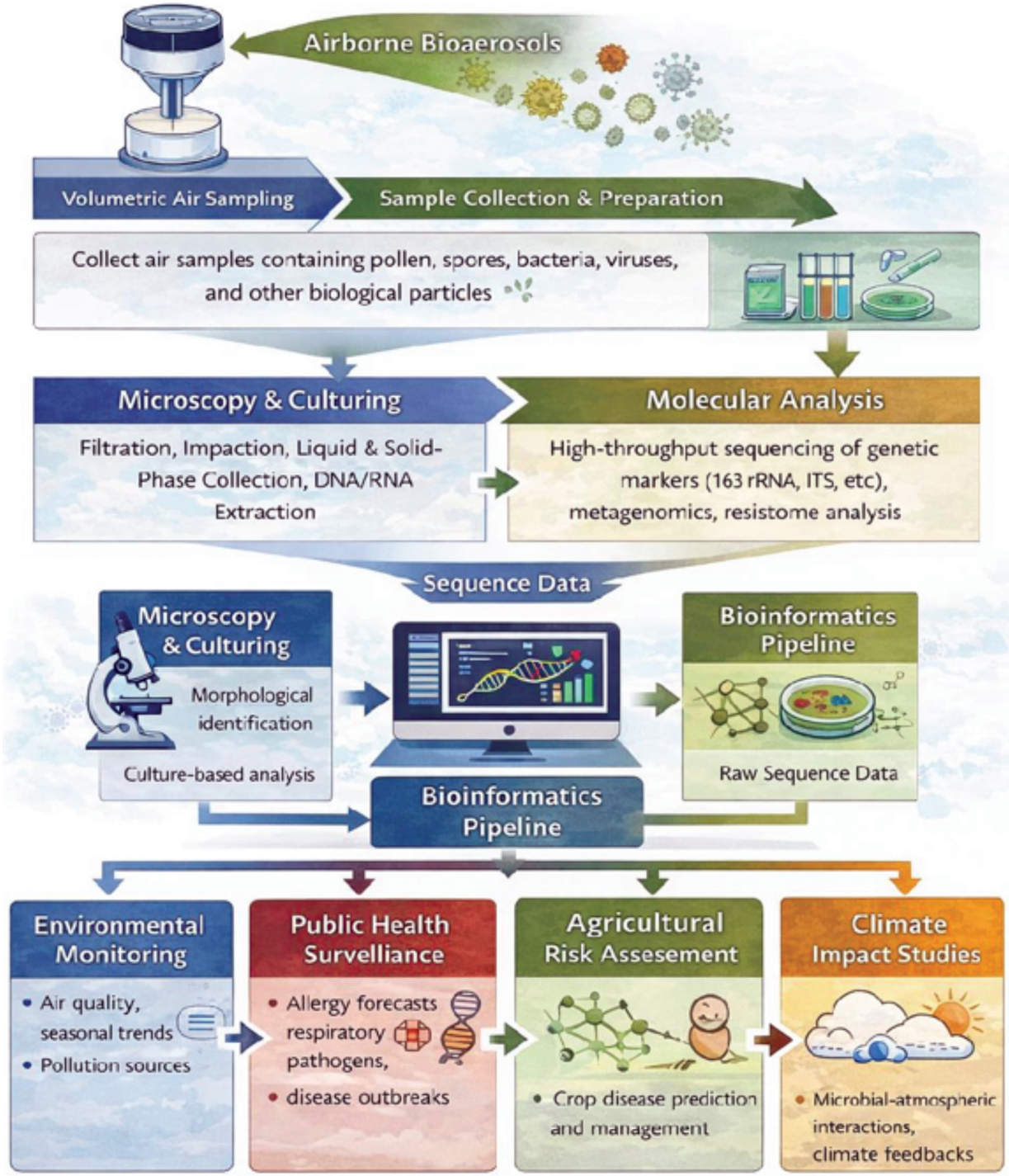


Fig. 1.1: Systematic pipeline of modern aerobiological research integrating air sampling, molecular analysis, bioinformatics processing, and applied domains including environmental monitoring, public health surveillance, agriculture, and climate studies.

airborne transmission in the global dissemination of antimicrobial resistance[25,26]. In particular, analyses of environmental and global resistomes have shown that the airborne resistome

reflects both local anthropogenic pressures and long-range atmospheric transport processes, underscoring the importance of routine aerobiome monitoring within a One Health framework[25,26].

In addition, functional metagenomics provides insights into microbial survival strategies under atmospheric stress conditions, including UV radiation, desiccation, temperature extremes, and oxidative stress, thereby linking aerobiology with atmospheric ecology, cloud microphysics, and climate-related processes[23,27,28].

Bioinformatics Pipelines and Data Processing Frameworks

The massive datasets generated by high-through put sequencing require robust, standardized, and reproducible bioinformatics workflows for data processing, analysis, and interpretation. Several bioinformatics platforms have become central to sequence-based aerobiological research by enabling standardized analysis of airborne microbial and pollen DNA datasets. QIIME2 is widely used for processing amplicon sequencing data from aerobiome studies, supporting quality control, taxonomic assignment, and diversity analysis[29]. Mothur remains a robust framework for comparative analysis of airborne microbial communities based on marker-gene sequencing[30]. For shotgun metagenomic data, Kraken2 and MetaPhlAn enable rapid and accurate taxonomic profiling of complex airborne microbial assemblages[31,32], while MG-RAST provides an automated platform for taxonomic and functional annotation of environmental and aerobiome sequencing datasets[33].

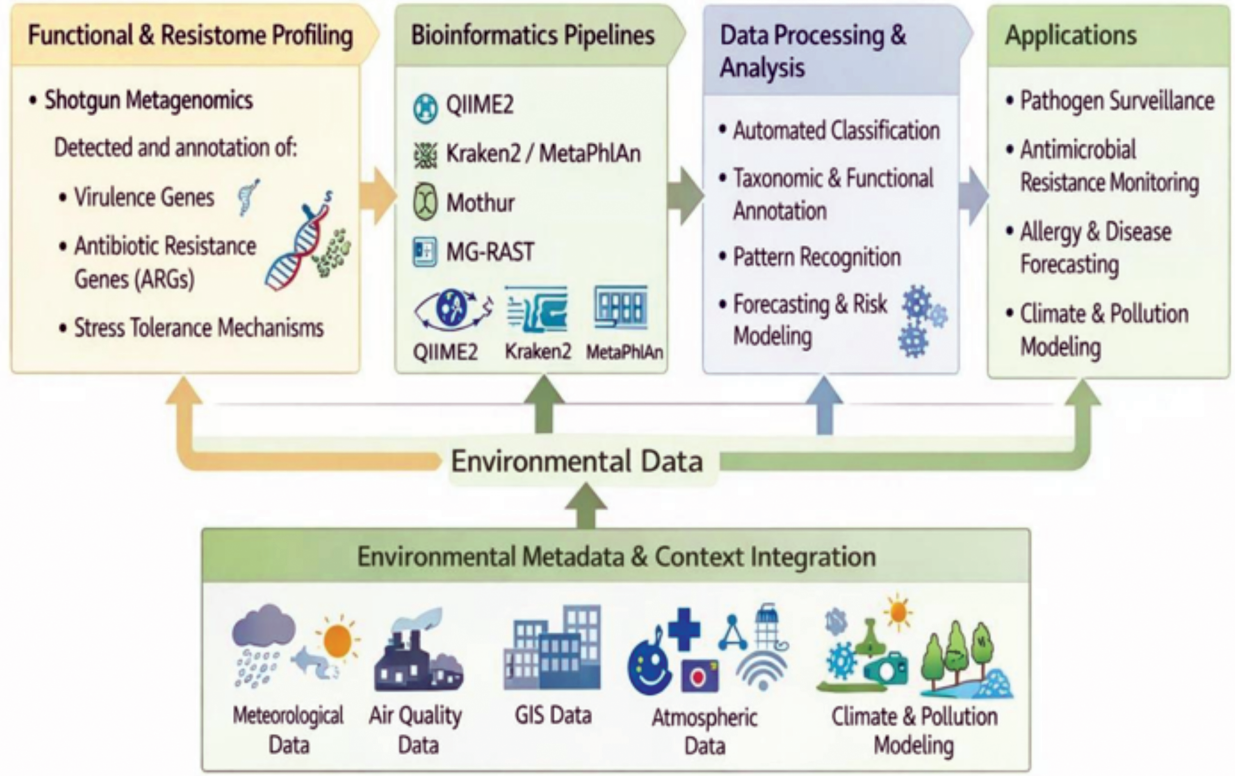


Fig. 1.2: Systematic bioinformatics pipeline for aerobiological data analysis and environmental integration

These pipelines support essential analytical steps such as quality control, sequence filtering, taxonomic assignment, alpha and beta diversity analysis, community comparison, and functional annotation, and they enable cross-study comparisons and large-scale meta-analyses across different geographical regions and environmental contexts[21,22,34].

Within the systematic pipeline of modern aerobiological research (Fig. 1.2), bioinformatics represents the core analytical engine integrating molecular data with environmental metadata, meteorological parameters, and spatiotemporal information. This integration transforms raw sequence data into ecologically and clinically meaningful knowledge, supporting applications in air quality assessment, allergy forecasting, pathogen surveillance, crop disease prediction, and climate-sensitive risk modeling[35–39].

Overall, the incorporation of bioinformatics has elevated aerobiology from a primarily descriptive discipline to a data-rich, quantitative, and mechanistically informative science, providing the essential foundation for subsequent integration with artificial intelligence and advanced computational modeling approaches[38–41].

INTEGRATED COMPUTATIONAL AND ARTIFICIAL INTELLIGENCE FRAMEWORKS FOR AEROBIOLOGICAL ANALYSIS

Modern aerobiology increasingly relies on integrated computational frameworks that combine bioinformatics, image-based analysis, and data-driven modeling to support automated monitoring, quantitative interpretation, and predictive assessment of airborne biological particles. These approaches enable the systematic integration of biological data with meteorological and environmental variables such as temperature, humidity, wind velocity, precipitation, and particulate matter concentration, thereby facilitating a systems-level understanding of bioaerosol dynamics across spatial and temporal scales[22,23].

The principal application domains of aerobiology, corresponding data types, computational and molecular methodologies, analytical objectives, and their scientific and practical relevance are summarized in Table 1.2. The table highlights how bioinformatics, artificial intelligence, and data-driven modeling approaches collectively support automated identification, functional and taxonomic profiling, spatiotemporal analysis, and predictive risk assessment across public health, environmental, and agricultural contexts.

Computational Modeling and Spatiotemporal Analysis

Computational modeling approaches are widely used in aerobiology to analyze time-series patterns of pollen and spore concentrations, to map spatial distributions of bioaerosols using geographic information systems (GIS), and to investigate source–receptor relationships through trajectory and dispersion modeling. These methods support the identification of seasonal trends, long-range transport events, and meteorological drivers of bioaerosol variability, and they provide a quantitative basis for exposure and risk assessment[22,23].

Automated Identification and Monitoring Systems

Automated analysis of pollen and fungal spores using image-based classification methods has

Table 1.2: Integrated applications, data types, and computational approaches in modern aerobiological research

Application Domain	Data Type	Computational/ Molecular Approaches	Analytical Objectives	Scientific and Practical Relevance
Microbial aerobiology	Metagenomic sequencing (16S rRNA, shotgun)	Bioinformatics pipelines (QIIME2, Kraken2, MetaPhlAn, MG-RAST), statistical learning	Taxonomic and functional profiling of airborne microbial communities	Assessment of airborne microbiome diversity, environmental exposure, and ecological dynamics
Fungal aerobiology	ITS sequencing, microscopy images	Metabarcoding, supervised ML and deep learning classifiers	Detection and identification of allergenic and pathogenic fungal spores	Respiratory health risk evaluation and early warning of fungal outbreaks
Pollen monitoring	Microscopy images, optical sensor data	CNN-based image recognition, automated monitoring systems	Automated pollen identification, quantification, and trend analysis	High-throughput, real-time pollen surveillance with reduced observer bias
Public health aerobiology	Bioaerosol, meteorological, and GIS data	Machine learning, predictive analytics, spatio-temporal modeling	Exposure modeling disease risk prediction, and outbreak forecasting	Public health preparedness, allergy and asthma risk mitigation
Environmental aerobiology	Bioaerosol data integrated with climate and GIS variables	Bioinformatics–AI integration, trajectory and dispersion modeling	Spatiotemporal distribution and source-receptor analysis	Air quality assessment, ecosystem health monitoring, climate-sensitive risk evaluation
Agricultural aerobiology	Bioaerosol, pathogen, and meteorological	AI-driven predictive modeling and disease forecasting systems	Long-range transport and dispersion of plant pathogens	Crop disease surveilance, sustainable agriculture, and biosecurity management

significantly improved the efficiency, consistency, and scalability of aerobiological monitoring. Deep learning–based classifiers have been shown to achieve identification accuracies comparable to or exceeding those of manual microscopy, enabling high-throughput and standardized processing of large sample volumes[24,25]. These methods form the core of modern automated pollen and spore monitoring systems that integrate optical sensors, digital imaging, and computational classification to generate near real-time aerobiological data streams.

Data-Driven Forecasting and Risk Assessment

Data-driven modeling approaches are increasingly applied to forecast pollen concentrations, assess allergy risk, and evaluate climate-sensitive changes in aerobiological patterns. Models based on machine learning algorithms, including random forests and deep neural networks, have demonstrated improved predictive performance compared to traditional statistical approaches, particularly when combining biological observations with meteorological and land-use data[26].

APPLICATIONS IN HEALTH AND ENVIRONMENTAL SCIENCES

The integration of molecular, bioinformatics, and computational approaches has substantially expanded the applied scope of aerobiology,

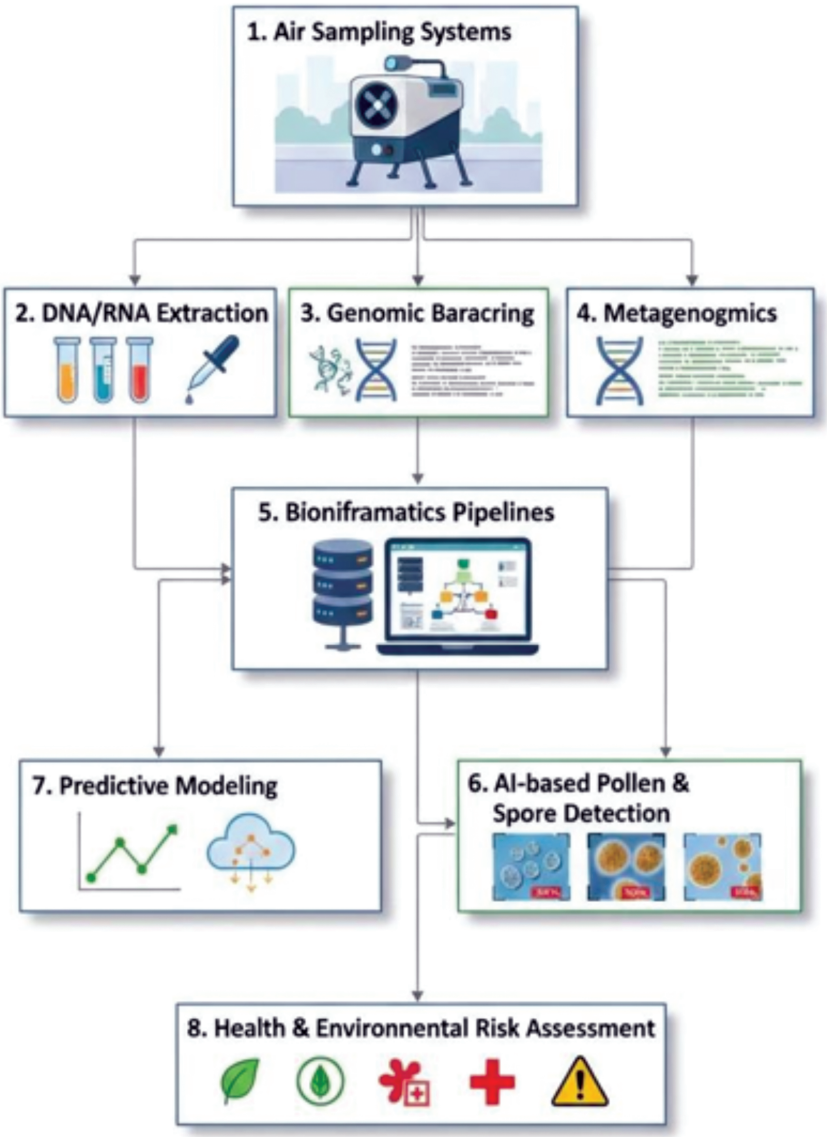


Fig. 1.3: Conceptual workflow illustrating the transition from bioinformatics-based analysis to integrated computational and artificial intelligence–driven aerobiological frameworks.

enabling its use in public health surveillance, environmental assessment, and agricultural risk management.

Such predictive frameworks support the development of early warning systems and decision-support tools for public health, agriculture, and environmental management. The conceptual transition from sequence-based analysis to integrated computational and data-driven workflows is illustrated in Fig. 1.3.

Public Health

Aerobiological monitoring provides critical information for allergy and asthma surveillance by supporting the assessment and forecasting of airborne pollen and fungal spore loads. In addition, sequence-based and automated detection systems enable early warning of airborne pathogens and contribute to environmental surveillance of antimicrobial resistance genes, strengthening public health preparedness and preventive healthcare planning[6,22,23].

Environmental Monitoring

In environmental sciences, aerobiology is increasingly applied to assess ecosystem health, evaluate urban air quality, and investigate the biological impacts of climate variability and climate change. The integration of aerobiome data with meteorological and land-use information enables the detection of long-term trends, source–receptor relationships, and climate-sensitive shifts in airborne biological communities[12,23].

Agriculture and Biosecurity

In agriculture, aerobiological surveillance plays a key role in crop disease forecasting and the detection of long-distance transport of plant pathogens. Sequence-based identification and automated monitoring systems enhance early warning capabilities and support biosecurity strategies aimed at reducing the spread of economically important plant diseases[22,19].

FUTURE PERSPECTIVES

Future advances in aerobiology are expected to be driven by the integration of high-throughput molecular monitoring, sensor-based sampling networks, and advanced computational analysis. The development of real-time or near–real-time sequencing and automated sampling platforms will substantially improve the temporal resolution of bioaerosol surveillance and early warning capabilities. Increasing emphasis will be placed on the integration of biological, meteorological, and environmental datasets within unified analytical frameworks, enabling more robust and transferable predictive models. In parallel, coordinated regional and global aerobiome mapping initiatives, supported by standardized protocols and open data infrastructures, will be essential for assessing long-term trends, climate-driven changes, and emerging biological risks. Together, these developments will strengthen the role of aerobiology in environmental monitoring, public health preparedness, and agricultural biosecurity.

CONCLUSION

The integration of aerobiology with molecular biology, bioinformatics, and computational analysis has transformed the discipline from a largely descriptive science into a quantitative and predictive field. High-throughput molecular methods enable high-resolution characterization

of airborne biological diversity, while automated and data-driven analytical frameworks support large-scale monitoring, forecasting, and risk assessment. This interdisciplinary convergence reinforces the role of aerobiology in addressing major challenges related to public health, environmental sustainability, agricultural biosecurity, and climate change.

ACKNOWLEDGMENTS

We wish to Acknowledge MAEER's MIT Group of Institutions, Pune for their invaluable support and collaboration, which significantly contributed to the success of this review.

AUTHORS DECLARATION

T.M. contributed primarily to aerobiology-focused conceptual development, methodology formulation, literature review, data curation, formal analysis, and also provided overall supervision, critically reviewed the analysis, and contributed to validation and final interpretation of the manuscript. S.M. contributed to the development of the bioinformatics and computational framework, including analytical conceptualization, workflow design, and preparation of figures and tables, and participated in manuscript drafting and technical refinement.

REFERENCES

1. Gregory PH. 1973. The Microbiology of the Atmosphere. 2nd ed. London: Leonard Hill.
2. Fröhlich-Nowoisky J, Kampf C. J, Weber B, *et al*. 2022. Bioaerosols in the Earth system: climate, health, and ecosystem interactions. Atmos Res. 268:105986. https://doi.org/10.1016/j.atmosres.2021.105986.
3. Smets W, Moretti S, Denys S. & Lebeer S.2021. Airborne bacteria in the atmosphere: presence, purpose, and potential. Atmos Environ. 139:214-221. https://doi.org/10.1016/j.amosenv.2016.05.038.
4. Barberán A, Henley J, Fierer N. & Casamayor EO. 2020. Structure, inter-annual recurrence, and global-scale connectivity of the atmospheric microbiome. Sci Total Environ. 724:138161. https://doi.org/10.1016/j.scitotenv.2020.138161.
5. Tilak S. T. 1989. Aerobiology in India. New Delhi: Today & Tomorrow's Printers and Publishers.
6. D'Amato G, Cecchi L, Bonini S, *et al*. 2007. Allergenic pollen and pollen allergy in Europe. Allergy. 62:976-990. https://doi.org/10.1111/j.1398-9995.2007.01393.
7. World Health Organization. 2024. Air quality and health. WHO. https://www.who.int.
8. Pal C, Bengtsson-Palme J, Kristiansson E. & Larsson DGJ. 2020. The structure and diversity of human, animal and environmental resistomes. Microbiome.8:54. https://doi.org/10.1186/s40168-020-00836-4.
9. Li H, Zhou X, Wang X, *et al*. 2022. Airborne resistome in urban environments reveals widespread antibiotic resistance genes. Environ Int.158:106906.
10. Ervens B, Baumgardner D, Cziczo D. J., *et al*. 2025. Bioaerosols in the Earth system: climate, clouds, and health interactions. Atmos Chem Phys. 25:123-158. https://doi.org/10.5194/acp-25-123-2025.
11. Péguilhan R, et al. 2025. Clouds influence the functioning of airborne microorganisms. Biogeosciences. 22(5): 1257-1275.
12. Behzad H, Gojobori T & Mineta K. 2020. Challenges and opportunities of airborne metagenomics. Genome Biol Evol. 12:121-135. https://doi.org/10.1093/gbe/evz284
13. Morawska L & Milton D.K.2020. It is time to address airborne transmission of COVID-19. Clin Infect Dis. 71:2311-2313.https://doi.org/10.1093/cid/ciaa939.
14. Prather K.A., Wang C.C. & Schooley R.T.2020. Reducing transmission of SARS-CoV-2. Science. 368:1422-1424. https://doi.org/10.1126/science.abc6197.

15. Oteros J, Sofiev M, Smith M, *et al*. 2020. Automatic pollen monitoring: advances, challenges, and perspectives. Sci Total Environ.714:136763. https://doi.org/10.1016/j.scitotenv.2020.136763.

16. Buters J.T.M., Antunes C, Galveias A, *et al*. 2022. Pollen and spore monitoring: advances in automation and standardization. Aerobiologia. 38:593-609. https://doi.org/10.1007/s10453-022-09754-9.

17. van der Heyden M, Madden L.V. & Jeger M.J. 2021. Climate change and plant disease epidemiology. Annu Rev Phytopathol. 59:183-206. https://doi.org/10.1146/annurev-phyto-020620-113501.

18. Banchi E, Ametrano C.G., Greco S, *et al*. 2020. Environmental DNA metabarcoding for airborne plant biodiversity monitoring. Mol. Ecol. Resour. 20: 356-368. https://doi.org/10.1111/1755-0998.13108.

19. Kraaijeveld K, de Weger L.A., Ventayol García M, et al. 2021.Efficient and sensitive identification of airborne pollen using NGS. Mol. Ecol. Resour. 21:224-236. https://doi.org/10.1111/1755-0998.13229.

20. Woo C, An C, Xu S, *et al*. 2021. Metagenomic analysis of airborne microbial communities. Sci Total Environ. 748:141359. https://doi.org/10.1016/j.scitotenv.2020.141359.

21. Behzad H, Gojobori T & Mineta K.2020. Airborne metagenomics: challenges and opportunities. Genome Biol Evol. 12:121-135.

22. Smets W, Moretti S, Denys S & Lebeer S. 2021. Airborne bacteria in the atmosphere. Atmos Environ.139:214-221.

23. Fröhlich-Nowoisky J, *et al*. 2022. Bioaerosols in the Earth system. Atmos Res. 268:105986.

24. Ervens B, *et al*. 2025. Ideas and perspectives: Microorganisms in the air through the lenses of atmospheric chemistry and microphysics. Biogeosciences. 22, 243-256. DOI: 10.5194/egusphere-egu25-17716.

25. Pal C, *et al*. 2020. Global resistome structure. Microbiome. 8:54.

26. Li H, *et al*. 2022. Airborne resistome. Environ Int.158:106906.

27. Péguilhan, R., Besaury, L., Rossi, F., Enault, F., Baray, J. L., Deguillaume, L., and Amato, P. 2021. Rainfalls sprinkle cloud bacterial diversity while scavenging biomass, FEMS Microbiol. Ecol., 97, fiab144, https://doi.org/10.1093/femsec/fiab144.

28. Ervens, B. 2022. Average cloud droplet size and composition: Good assumptions for predicting oxidants in the atmospheric aqueous phase?, J. Phys. Chem. A, 126, 8295-8304. https://doi.org/10.1021/acs.jpca.2c05527.

29. Bolyen E, Rideout J.R., Dillon M.R., *et al*. 2019. QIIME 2. Nat Biotechnol. 37:852-857. https://doi.org/10.1038/s41587-019-0209-9.

30. Schloss P.D., Westcott S.L., Ryabin T, *et al*. 2009. Appl Environ Microbiol. 75: 7537-7541. https://doi.org/10.1128/AEM.01541-09.

31. Wood D.E., Lu J, Langmead B. Kraken 2. 2009. Genome Biol. 20:257. https://doi.org/10.1186/s13059-019-1891-0.

32. Beghini F, McIver L.J., Blanco-Míguez A, *et al*. 2021. MetaPhlAn 3. Nat Biotechnol. 39:921-929. https://doi.org/10.1038/s41587-020-0603-7.

33. Meyer F, Paarmann D, D'Souza M, *et al*. 2008. MG-RAST. BMC Bioinformatics. 9:386. https://doi.org/10.1186/1471-2105-9-386.

34. Barberán A, *et al*. 2020. Atmospheric microbiome. Sci. Total Environ. 724:138161.

35. Oteros J, *et al*. 2020. Automatic pollen monitoring. Sci Total Environ. 714:136763.

36. Buters J, Clot B, Galán C, *et al*. 2024. Automatic detection of airborne pollen: an overview. Aerobiologia. 40:13-37.

37. Nicolas Bruffaerts *et al*. 2025. Advancing automated identification of airborne fungal spores: guidelines for cultivation and reference dataset creation. Aerobiologia. 41:505-525.

38. Singh N.I. 2024. Integrating AI and bioinformatics for automated detection of airborne pollen grains and fungal spores. Ind. J. Aerobiol. 37, No. (1):1-12.

39. Zhang Y, Zhang L, Chen X, *et al*. 2023. Machine learning-based pollen concentration forecasting. Sci. Total Environ. 858: 159833. https://doi.org/10.1016/j.scitotenv.2022.159833.

40. Kour D, Sharief Khan S, Harpreet Kaur et al. 2025. Airborne fungal communities: diversity, health impacts and AI applications in aeromycology. 3(4), 10. https://doi.org/10.3390/aerobiology3040010.
41. Justin Y.Y. Lee, Yanhao Miao, Ricky L.T. Chau, Mark Hernandez & Patrick K.H. Lee. 2023. Artificial intelligence–based prediction of indoor bioaerosol concentrations from indoor air quality sensor data. Environmental International. 173: :107900, DOI:10.1016/j.envint.2023.107900.

Ind. J. Aerobiol., Vol. 39, No. (1), pp. 19-31 [2026] ISSN No. 0971-1546

Review Article

PALYNOLOGY IN ARCHAEOLOGY: METHODS, APPLICATIONS, AND INSIGHTS INTO PAST ENVIRONMENTAL CHANGE AND HUMAN–ENVIRONMENT INTERACTIONS

ANUSHA JADHAV, SHUBHRA TIWARI* AND SHAILESH KUMAR JADHAV

SCHOOL OF STUDIES IN BIOTECHNOLOGY, PT. RAVISHANKAR SHUKLA UNIVERSITY, RAIPUR, 492 010, CHHATTISGARH, INDIA

**CORRESPONDING AUTHOR: shubhratiwari77@gmail.com*

In archaeology, the main aim of palynology is to interpret, reconstruct, and comprehend changes in prehistoric environments. Analyses of pollen and spores serve as crucial instruments for reconstructing ancient environments and understanding long-term ecological dynamics. This review, drawing on pollen analytical studies from areas like Italy, Egypt, the Indus Valley Civilization, and the Narmada Basin, emphasizes pollen's role as a proxy for identifying historical vegetation patterns, shifts in vegetation, deforestation events, climatic changes, interactions between humans and the environment, biodiversity, hydrological alterations, and fire regimes. Archaeopalynology offers a comprehensive framework for understanding ancient environments and their connections with human societies. Additionally, this article provides a historical overview of the evolution of pollen analysis and examines the methodologies used in pollen extraction and preservation, which continue to present significant challenges to researchers. Recent advancements in analytical techniques have enhanced the precision and reliability of palynological studies, thereby deepening our understanding of past environmental interactions. The integration of palynology with archaeology is increasingly contributing to modern environmental management by offering insights into ecosystem resilience, vulnerability, and responses to environmental changes. Such interdisciplinary approaches are valuable for tackling contemporary ecological challenges and promoting sustainable resource management.

Key Words: Archaeopalynology,Pollen Extraction, Paleoenvironmental reconstruction, Sporopollenin,

Received: 05.03.2026 Revised: 28.03.2026 Accepted: 06.04.2026

INTRODUCTION

The field of palynology plays a crucial role in archaeological studies. Examining fossil pollen serves as a potent and adaptable method, offering significant insights into historical environmental and cultural settings. The development of pollen analysis from an archaeological viewpoint is chronicled in its history. Pollen grains (Fig. 2.1), which are the microscopic reproductive elements of various plants, are studied scientifically under the discipline of palynology. Each grain is encased in a durable outer layer known as the exine, made of a resilient natural biopolymer called sporopollenin, which aids in the preservation of pollen in sediments over extensive geological periods. Sites where pollen is transported by human activity enhance our understanding of plant life and vegetation areas. Comprehending pollination helps researchers

decipher how pollen becomes embedded in archaeological layers. Wind-pollinated plants, such as oak, pine, and alder, release large quantities of pollen that can travel long distances and are commonly found in sediment records. In contrast, insect-attracting plants like *Rosa*, *Capparis* and *Brassica* produce heavier pollen grains, which tend to indicate more localized vegetation[1]. Some plant species have uncertain or mixed pollination methods, making their pollen transport patterns less distinct. The article further details the step-by-step extraction and analysis of samples from excavation sites, which reveal prehistoric practices[2]. Although identifying pollen can sometimes be challenging, modern tools have improved the description of pollen samples. The surrounding pollen community significantly affects the shape and type of pollen. Its analysis demonstrates its application in archaeology. This article employs case studies to illustrate various plant habitats, which reflect differences in vegetation, agricultural areas, fire regimes, and human impact.

History of archaeological palynology[3]

Palynology for archaeology, chronological arrangement is essential because it allows for accurate connection of pollen sequences with stratified site strata, creating timelines for environmental changes and human activity.

METHODOLOGY USED IN PALYNOLOGICAL ANALYSIS

Preparing palynological samples requires a series of technical steps. The extraction phase is notably challenging due to risks of contamination and sample degradation, necessitating oversight by skilled professionals. The following outlines the primary stages in sample extraction and processing[1].

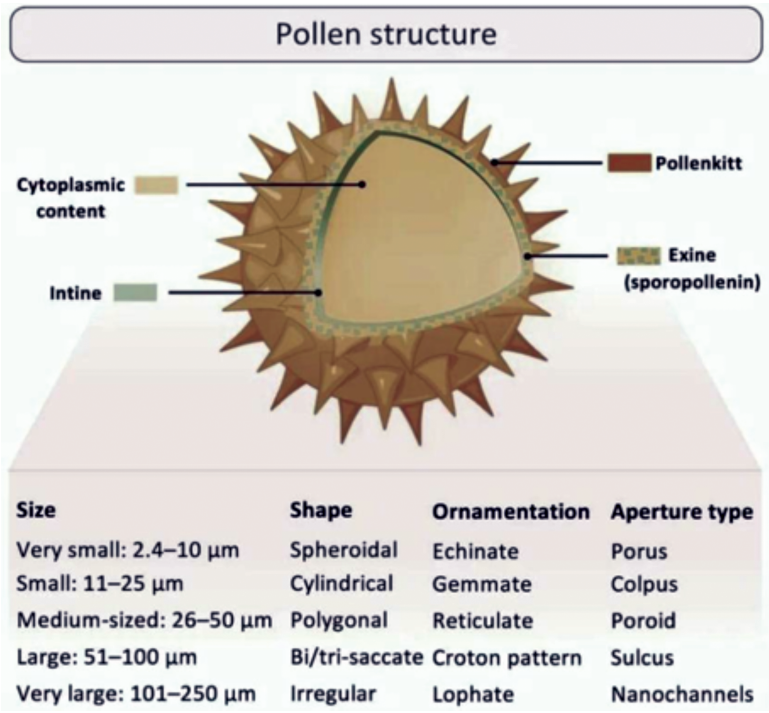


Fig. 2.1: Structure of pollen

Table 2.1: Historical Development and Major Milestones in Archaeopalynology

Sl. No.	Year	Contributions	Significance
1.	1905	Conducted the first attempt to calculate pollen percentages from peat deposits in Sweden.	Considered the earliest application of pollen analysis in palaeoenvironmental studies.
2.	1916	Introduced the first systematic pollen percentage calculations.	Enabled quantitative reconstruction of past vegetation and climatic conditions.
3.	1932-37	Proposed that climatic changes favorable to maize cultivation may have influenced the expansion of the Hopewell culture and conducted pioneering pollen studies in the American Southwest.	Represented one of the earliest attempts to relate pollen evidence to archaeological and cultural processes.
4.	1941	Used the decline of Ulmus (elm) pollen and the increase in herbaceous and weed pollen to date the onset of the Neolithic period in Denmark.	Demonstrated the use of pollen analysis in detecting forest clearance and early agricultural activities.
5.	1944-56	Provided pollen evidence for anthropogenic vegetation changes associated with agriculture across Europe.	Confirmed the role of humans in shaping prehistoric landscapes.
6.	1955	Investigated pollen preserved in cave sediments within archaeological contexts.	Expanded palynological sampling to cave deposits.
7.	1960	Examined plant macrofossils and pollen from the Muldbjerg Neolithic site in Denmark.	Reconstructed local ecology and demonstrated the influence of animal domestication on vegetation.
8.	1960	Demonstrated that pollen records could reveal changes in forest composition resulting from prehistoric agriculture and pastoral activities.	Improved understanding of human-induced landscape modification.
9.	1963	Developed a method to estimate total pollen grains per gram of soil at a Mesolithic site in Kent, England.	Enabled quantitative assessment of cultural impacts on vegetation.
10.	1963	Established a systematic palynological research program in the American Southwest using lake, peat, and ancient sediment records.	Marked the institutionalization of archaeopalynological research.
11.	1960-70	Expanded pollen analysis to numerous archaeological sites across North America and Europe.	Established palynology as a routine tool in archaeological and paleoenvironmental linvestigations.

1. Sampling from archaeological contexts

During archaeological excavations, sediments are gathered for palynological study from well-defined stratigraphic layers. These layers represent different periods of human activity and environmental conditions. It is vital to collect samples from these undisturbed layers to ensure chronological accuracy and avoid contamination.

2. Laboratory chemical processing

In the lab, sediments are subjected to various chemical processes to extract pollen grains. Dispersing agents such as sodium pyrophosphate are applied to the sediments, and hydrochloric acid (HCl) is used to remove carbonates. Acetolysis is performed to eliminate organic matter and improve the visibility of pollen exine. Pollen grains are concentrated through heavy liquid separation and centrifugation. Hydrofluoric acid (HF) is then used to dissolve silicates before the samples are preserved with glycerol.

3. Microscopic identification

The processed samples are examined using light microscopy. Pollen grains are identified by comparing features like size, aperture type, and exine ornamentation.

4. Pollen counting and classification

After identification, pollen grains are counted, and their relative proportions are calculated. This helps in distinguishing various pollen types, which are classified into arboreal, non-arboreal, and anthropogenic pollen, potentially indicating agricultural or pastoral activities.

5. Data representation and interpretation

Data interpretation is carried out using pollen percentage diagrams and graphical displays (Fig. 2.2). Statistical analysis can be employed to assess pollen diversity, preservation conditions, and the relationship between vegetation changes and influencing factors. Numerical analysis is beneficial for interpreting archaeological sites, enabling the identification of pollen distribution patterns and the reconstruction of ancient settlement activities. Detrended Correspondence Analysis is frequently used in palynological research to explore relationships between pollen types and identify ecological gradients, with minimal impact from rare species. Spatial modelling can also recreate the distribution of specific pollen types, such as Cerealia-type pollen, which may suggest crop cultivation. These analyses can be performed using specialized software like PAST and Rock

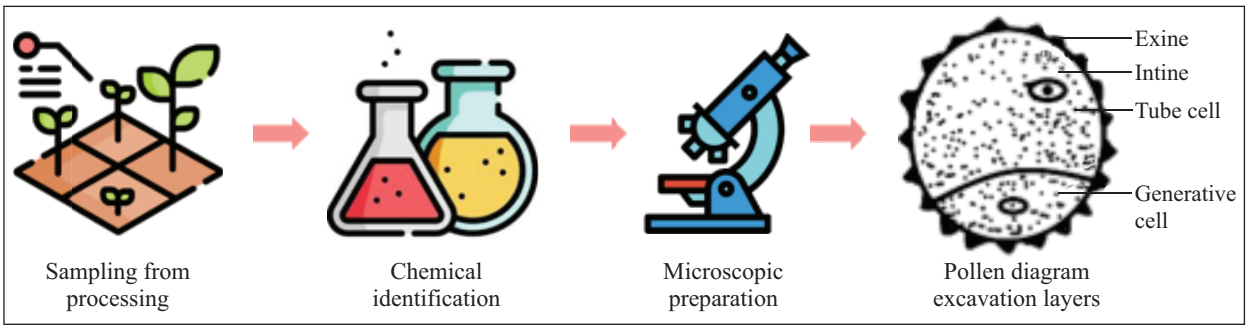


Fig. 2.2: Methods of extraction of pollen

Works, offering detailed visualizations and interpretations of vegetation and activity areas within archaeological sites.

APPLICATIONS OF ARCHAEOPALYNOLOGY

1. Climate reconstruction

Pollen analysis is crucial for deciphering historical climate variations by examining shifts in vegetation patterns at archaeological sites. Variations in pollen types reflect transitions from forested areas to grasslands and steppes, often linked to climatic factors like temperature fluctuations, rainfall changes, and monsoon intensity. For instance, at the Neolithic site of Burzahom in Kashmir, a shift from dense Himalayan forest species such as Abies, Pinus, and Cedrus to steppe species like Artemisia and Chenopodiaceae suggests a period of climatic aridity[4]. Research on pollen from the Narmada Basin reveals a transition[5], from arid grassland vegetation during the Pleistocene to more humid forest vegetation in the early Holocene.

2. Origin of agriculture

Palynological research has significantly advanced our understanding of agriculture's beginnings. Crop pollens like *Oryza sativa, Triticum spp*., and *Hordeum*, along with weed pollens such as *Chenopodium* and *Amaranthus*, suggest that early humans engaged in farming[6]. Sites like Rakhigarhi[7] and Harappa, part of the Indus Valley Civilization, reveal a mixed farming system. Similarly, pollen evidence from Mehrgarh indicates that the initial stages of plant domestication involved cultivating barley, wheat, pulses like Lens and *Cicer*, and fruits such as *Ficus*. These findings highlight the transition from gathering wild plants to agricultural practices among early human communities.

3. Human Landscape Modification

Pollen records also provide insights into how human activities have altered natural landscapes over time. For instance, changes in pollen composition, such as reduced arboreal pollen and increased grasses, weeds, and cultivated plant pollen, suggest activities like deforestation, grazing, and agriculture. Studies of pollen from regions like the Bradano Valley in Italy have demonstrated that grassland environments dominated by Poaceae and other herbaceous species emerged around human settlements due to human influence1. Additionally, indicators of disturbance, grazing, and burning activities, such as Centaurea, Asteraceae, and fire-related fungal spores, point to practices like pastoralism and farming. These changes illustrate how human populations have impacted the natural environment through settlement expansion, agriculture, and resource use.

CASE STUDIES

1. Bradano Valley, Italy

Palynological research carried out on two archaeological sites located in the Bradano Valley in Southern Italy, namely Difesa San Biagio (DSB) and Altojanni (ALJ)1, has given us information about past vegetation and its relationship with past human activities. Indeed, the archaeological site of Difesa San Biagio has revealed archaeological features from the Bronze Age and Iron Age to the Late. Hellenistic Period, including archaeological material such as houses, pottery, flour millstones, storage vessels, and an olive press. Pollen analysis from this site has

revealed that the surrounding environment was dominated by open and relatively dry grassland vegetation dominated by Poaceae associated with Asteraceae, Chenopodiaceae, and Brassicaceae[1]. Palynological assemblages from the ALJ site showed an increased number of different types of pollen compared to the DSB site. There were arboreal and herbaceous species of plants such as *Quercus, Pinus, Ulmus, Corylus*, and *Alnus*, which indicated the presence of mixed woodland vegetation[8]. The presence of *Olea europaea, Juglans, Brassica*, and cereal types of plants indicated agricultural activities related to the settlement of humans. Comparison of the two sites indicated that the landscape has undergone significant changes due to the activities of humans. There was an indication of an increase in humidity during the Roman and Medieval periods at the ALJ site due to the presence of Cyperaceae types of plants.

2. Neolithic landscape at La Draga, Northeastern Spain

Palynological analysis of the Neolithic settlement site of La Draga in northeastern Spain indicates a complex mosaic landscape with Mediterranean shrub land, woodland, wetlands, and freshwater habitats. The pollen record at the site indicates the dominance of *Erica* sp., suggesting the presence of Mediterranean heath or maquis vegetation which is characteristic of open shrub land habitats with disturbance or grazing pressures. The evidence of past agricultural activities is indicated by the presence of Cerealia-type pollen. Pastoral activities are indicated by the presence of coprophilous fungal spores of the type of *Sordaria* and *Sporormiella*. The spores of these types of fungi grow on the dung of herbivores and thus imply the presence of these animals around the settlements[9]. Additional signals of disturbance in the landscape are represented by the high frequencies of herbaceous species, especially those belonging to the Asteraceae family. These are often linked to grazed and anthropogenically modified landscapes. Fire history in the surrounding landscape is represented by the presence of fungal taxa associated with charcoal. Wetland and freshwater habitats are represented by the presence of hygrophilous species such as Cyperaceae, *Typha*, and aquatic algae such as *Spirogyra* and *Pediastrum*[9]. The overall palynological record points to a landscape that was affected by a combination of natural ecological processes and the early impacts of humans through practices such as farming, grazing, and burning.

3. Indus valley civilization

The palynological data from important Indus Valley Civilization sites, such as Rakhigarhi in Haryana, India, and Harappa in present-day Pakistan, have greatly helped to shed light on past agricultural practices[7]. Archaeological excavations at these sites have yielded various cultural materials such as pottery, mud floors, hearths, storage pits, from which plant remains have been collected. The pollen record indicates that *Oryza sativa* (rice), *Triticum* sp. (wheat), *Hordeum* (barley), and other crops indicate a diversified agricultural system. The occurrence of *Phoenix dactylifera* (date palm) suggests that plant introduction or exchange could have been achieved through trade routes from the west. Moreover, pollen from cultivation-related weed plants like *Chenopodium* and *Amaranthus* indi-

cate that agriculture was highly developed at this time. The shift from forest pollen to grassland and cereal pollen indicates that there was a gradual process of deforestation[10]. Overall, the palynological evidence demonstrates that Indus communities practiced organized agriculture and significantly modified their surrounding landscapes through systematic cultivation and land management.

4. Climatic change at the Burzahom Neolithic Site, Kashmir

Palynological records from the Neolithic archaeological site of Burzahom in the Kashmir Valley throw light on past climatic changes and their impact on human societies. Pollen records in the lower layers of the site show a predominance of arboreal species such as *Abies*, and *Pinus*[11]. These records point towards a thick cover of Himalayan coniferous forest in earlier periods of site occupation. On the other hand, pollen records in the upper layers of the site show an increased abundance of *Artemisia* and Chenopodiaceae pollen. These species are generally associated with dry steppe or semi-arid habitats. The increase in charcoal particles in these two layers indicates that there were instances of burning in the region, possibly as a result of vegetation stress under dry conditions. Archaeological data from Burzahom indicates that these environmental changes impacted human subsistence strategies and settlement patterns, including pastoral activities and the use of storage sites and seasonal occupation. On the whole, the palynological data indicate that Neolithic climatic drying has been an important factor in influencing not only vegetation patterns but also human adaptive strategies in the Kashmir region.

5. Early agricultural development at Mehrgarh, Pakistan

The Mehrgarh settlement, in present-day Pakistan, is believed to be one of the earliest agricultural settlements in South Asia, dating back to around 7000 BCE[12]. Palynological research on artifacts like pottery, bricks, and soil has helped in gaining useful information about early agriculture and plant usage in Mehrgarh. The record also shows cultivated plant species such as *Hordeum vulgare* (barley) and *Triticum monococcum* (wheat), which indicate that there was early cultivation at this settlement site. The record of pulses such as *Lens* and *Cicer* indicates that there was also legume farming at this site. Apart from that, the record of wild grass indicates that at this time, the inhabitants of this site had already started utilizing natural plant resources as well. The record of *Ficus* sp. (Fig. 2.…) indicates that there was a possible use of fruit-bearing trees by the inhabitants of this site[13]. Therefore, on the whole, the palynological data, in addition to other archaeological evidence, suggests that Mehrgarh was an early centre for the development of agriculture in the Indian subcontinent, where a system of mixed farming and gradual domestication was in vogue.

6. Floral Offerings in Ancient Egyptian Burial Rituals

The plant taxa identified from the wrappings and burial chambers of the mummy are significant, and among these, the pollen of *Nymphaea*, also known as the lotus, is particularly significant, as it is linked with the idea of rebirth and afterlife[14]. The identification of date palm and *Acacia* pollen also suggests

that these plants may have been possibly used in the preparation of floral garlands with the deceased during the funeral rites. In addition, the identification of *Centaurea cyanus*, also known as cornflower, pollen suggests the use of other flowers, possibly for adornment, and these flowers may have been possibly obtained from distant regions. Thus, the palynological evidence from the Egyptian burials gives clue about the religious symbolism and rituals, ceremonial practices, and the exchange of botanical goods in the ancient Egyptian civilization. Palynological evidence also highlights the importance of plants in the rituals.

7. Chirand—Son River System (Bihar): Human occupation, Agriculture & River migration

A specific chronology of environmental and cultural changes from the Neolithic period to the Iron Age can be identified through pollen analysis in the Son River sediments at the Chirand archaeological site, located near the confluence of the Ganga and Son rivers. Moist deciduous forests are represented by the presence of *Shorea, Madhuca*, and *Terminalia* pollen in the Neolithic layer. A pre-agricultural environment is represented by the low amounts of Poaceae pollen and the absence of any crop pollen[15]. Higher amounts of Poaceae, *Oryza sativa, Setaria, Panicum*, along with weed species like *Chenopodium, Amaranthus*, and *Polygonum*, indicate an increase in agricultural activity during the Chalcolithic period. Along with the aquatic plants such as *Typha* and Cyperaceae, tree pollen reduction and the prevalence of crop pollen can be observed. This indicates the impact of floods and river migration on the settlement. This marked the beginning of rice-millet cultivation around 2000 BCE.

8. Monsoon variability and Human occupation in the Narmada Basin, Central India

Evidence of human and climate interaction found from the sediment cores in the Narmada Basin - especially near Hoshangabad, Mandla, and Bargi. Poaceae, Chenopodiaceae and *Artemisia* were commonly present[5]. The augmentation in *Tectona, Boswellia,* and *Anogeissus* pollen during the early Holocene period (10,000–7,000 BP) reflects the strengthening monsoon and tropical dry deciduous forests. An increase of arboreal pollen and aquatic taxa, including *Nymphaea* and *Typha* during Mid-Holocene period (7,000-4,000 BP) suggests humid climatic conditions and relatively stable fluvial environment. The decline in forest pollen and increase in grasses, weeds, and cereal plants like rice, wheat, and barley from 4000 BP indicates the expanding of agriculture, vegetation clearance and intensified human activity corresponding broadly with later archaeological evidence of Iron Age settlements[16].

9. Ganga Plain

This area provides evidence for reconstructing past climatic condition of late-Quaternary and Holocene period. Poaceae (grasses), *Artemisia* and Chenopodiaceae/Amaranthaceae present in high frequencies indicates open grassland vegetation and relatively dry or semi- arid conditions[17], *Madhuca indica, Acacia, Bombax ceiba, Terminalia,* and *Emblica officinalis* suggesting tropical deciduous forest, indicating warmer

and more humid monsoon phases. Fossil pollen records indicate the presence of *Oryza sativa* pollen as a major indicator of rice-based farming systems. Cereal taxa such as *Hordeum vulgare* (barley) and *Triticum aestivum* or *Triticum sphaerococcum* (wheat) indicate diversified crop cultivation. Millets such as *Paspalum scrobiculatum* and *Sorghum bicolor*, along with pulses such as *Vigna radiata, Cicer arietinum,* and *Lens culinaris,* demonstrate the gradual expansion of mixed farming practices and crop diversification.

COMPARATIVE ANALYSIS OF DOMINANT POLLEN TAXA, VEGETATION DYNAMICS, CLIMATE VARIABILITY, AND HUMAN INFLUENCE ACROSS SELECTED ARCHAEOLOGICAL AND PALAEOENVIRONMENTAL SITES

Comparative pollen analysis indicates that vegetation history across the selected sites was influenced by both climatic variability and anthropogenic disturbance. Burzahom exhibits evidence of declining arboreal vegetation accompanied by increasing aridity, whereas Rakhigarhi reflects intensified human influence associated with agricultural expansion and vegetation disturbance. Bradano Valley records shifts between relatively drier and more humid environmental conditions, while the Narmada Basin demonstrates vegetation changes linked to fluctuations in monsoonal intensity. Collectively, these pollen records highlight the complex interactions among climate change, vegetation dynamics, and human activities in shaping past landscapes across Europe and South Asia. The case studies from different regions provide representative dominant pollen taxa that are useful for interpreting vegetation patterns and climatic conditions, as summarized in Table 2.2.

Preservation challenges

Preservation of pollen is a complex process and at times hindered by mechanical, biological, and chemical processes.

1. *Mechanical degradation*: Transport and sedimentation, human activities at archaeological sites, temperature changes, and alternating wet–dry cycles cause abrasion of pollen grains and can alter the pollen exine or damage pollen[18].
2. *Chemical degradation*: Pollen survival is significantly influenced by the chemical conditions in sediments. Certain chemical compounds—especially alkaline compounds containing chlorine, magnesium, sodium, potassium, and carbonates—cause severe pollen wall degradation. It is also depends on oxidation reduction potential (Eh). Low Eh (reducing, anaerobic environment) favours preservation. High Eh (oxidizing conditions) accelerates pollen destruction.
3. *Biological agents and pollen degradation*: Fungi and bacteria attack pollen grains for instance Phycomycetes, a class of fungi preferentially infect certain pollen types, especially conifer pollen[19]. Certain bacteria (e.g., Actinomycetes) degrade pollen walls in characteristic patterns[20]. Biological degradation may occur even after pollen has been preserved for long periods. Identifica-

Table 2.2: Comparative Summary of Dominant Pollen Taxa and Inferred Climate Signals

Site	Dominant Pollen Taxa	Arboreal Vegetation Trend	Anthropogenic Influence	Climatic Interpretation
Burzahom (Kashmir)	*Pinus, Abies, Betula* → *Artemisia*, Chenopodiaceae	Forest decline and expansion of open vegetation	Increasing agriculture and settlement activity	Humid forest phase followed by increasing aridity
Rakhigarhi (Indus Valley)	Poaceae, Cerealia, Chenopodiaceae, cultivated taxa	Reduction in natural vegetation	Strong agricultural expansion and land-use modification	Progressive drying and increased human influence
Chirand–Son River (Bihar)	*Shorea, Madhuca, Terminalia, Oryza, Setaria, Panicum*	Moist deciduous forest with increasing agri-cultural landscape	Expansion of rice-millet cultivation	Humid conditions with periodic flooding
Narmada Basin (Central India)	Poaceae, Chenopodiaceae, *Artemisia* → *Tectona, Boswellia, Anogeissus* → Cerealia	Grassland → forest expansion → vege-tation clearance	Increasing agricultural activity and landscape modification	Strengthening monsoon → humid Mid-Holocene → later monsoon weakening
Bradano Valley (Italy)	*Olea*, Cerealia, Poaceae, anthro-pogenic indicators	Open woodland and cultivated landscape	Grazing, cultivation, and settlement impact	Dry phases alter-nating with relatively humid conditions
Mehrgarh (Pakistan)	Wheat, barley, pulses, cultivated taxa	Transition from natural vegetation to agroecosystems	Early farming and domestication practices	Favourable semi-arid conditions supporting agriculture

tion is often limited to the genus or family level. Different pollen types degrade at different rates in the same sediment.

Despite of all these difficulties there are various chemicals and modern techniques developed to preserve pollen for study. For instance,

- At the Rhoades Site (Illinois), pollen was absent in most soils but preserved near copper artifacts. Decaying copper produced cupric salts that acted as fungicides, preventing the microbial destruction of the pollen grains.
- Automated pollen identification systems and advanced imaging techniques have revolutionized the field by enabling large-scale, high-resolution investigations that were previously unfeasible.
- Confocal and Scanning Electron Micro-scopy (SEM) imaging provide high-resolution data on pollen morphology.
- DNA-based palynology—including environ-mental DNA (eDNA) and metabarcoding—allows for precise taxonomic identification.

- Quantitative climate reconstruction models utilize pollen data to track historical environmental changes.
- Integrating pollen data with Geographic Information Systems (GIS) and remote sensing enables advanced spatial vegetation analysis.

Discrepancies between local pollen data and regional vegetation records, along with difficulties in separating anthropogenic signals from taphonomic biases, limit interpretative accuracy. Methodological constraints in pollen representation and preservation, combined with weak integration into archaeological contexts, further restrict reliable reconstructions[1]. Additionally, the dearth of detailed spatial and diachronic analyses—alongside the difficulty of distinguishing depositional from post-depositional processes—reduces the precision of palaeoenvironmental reconstructions[9]. However, the development of modern analytical techniques is rapidly mitigating these limitations. Recent methodological advances assist not only in locating but also in precisely identifying fossil pollen. Because the visual classification of pollen remains a challenging problem, it provides a valuable framework and model for visual representation across other biological domains.

Modern advances

Advanced analytical tools, including deep learning and digital morphometric large analysis allow researchers to study pollen morphology quantitatively and examine large ecological and evolutionary datasets. Machine- learning in low- and high-density tropical systems are in development which tells how deep learning can be used in automate pollen identification[21]. Convolutional neural network (CNN) are able to classify 48 fossil *Striatopollis* specimens from the Paleocene, Eocene, and Miocene, helped improve taxonomic fossil pollen[22]. For automated pollen identification researchers are developing a web-accessible palynology image analysis platform for hosting published computerised tool to advance palynological community[23].

To reduce time consuming process of counting pollen under microscope slide-scanning microscopes like the Hamamatsu Nano Zoomer, Zeiss Axioscan, and many others have been developed in the last decade for pathology research and these are capable of scanning entire slides with multiple focal planes.

CONCLUSION

Palynology has become an indispensable tool in archaeological and palaeoecological research, providing unique insights into past vegetation, agricultural practices, climate variability, and long-term human–environment interactions. Despite challenges related to taphonomy and the need for careful archaeological contextualization, interdisciplinary collaboration between archaeologists and palynologists remains crucial for reliable interpretations. Recent advances in digital microscopy, automated image analysis, neural network–based identification, and molecular techniques are expanding the scope and accuracy of palynological studies. The integration of palynological evidence with other environmental proxies will further strengthen reconstructions of past landscapes and ecologi-

cal change. By combining traditional approaches with emerging technologies, palynology is well positioned to enhance our understanding of the dynamic relationships among humans, vegetation, and climate through time.

REFERENCES

1. Mercuri, A.M., Florenzano, A., Massamba N'Siala, I., Olmi, L., Roubis, D. & Sogliani, F. 2010. Pollen from archaeological layers and cultural landscape reconstruction: case studies from the Bradano Valley (Basilicata, southern Italy). Plant Biosystems 144(4):888-901.
2. Aylanc, V., Peixoto, A., Vale, N., Freire, C. & Vilas-Boas, M. 2023. Sporopollenin-based biomicrocapsules as green carriers for controlled delivery of pharmaceutical drugs. Applied Materials Today 33:101860.
3. Halbritter, H. *et al*. 2018. Palynology: history and systematic aspects. In Illustrated Pollen Terminology, pp. 3-21. Springer International Publishing, Cham.
4. Sharma, A.K. 1969. Excavations at Burzahom (1960-61). Memoirs of the Archaeological Survey of India. New Delhi: Archaeological Survey of India.
5. Murthy, K.P.N. & Kurian, S. 1990. Quaternary pollen records from the Narmada Valley. Gondwana Geological Magazine 5:115-130.
6. Singh, G., Joshi, K.M. & Agrawal, D.P. 1974. Pollen evidence for vegetational and climatic changes in the Indus Valley during the Harappan civilization. Proceedings of the Indian Academy of Sciences 80:1-37.
7. Meadow, R.H. 1996. The origins and spread of agriculture in the Indus Valley region. In The Origins and Spread of Agriculture and Pastoralism in Eurasia (Ed. D.R. Harris), pp. 390-412. UCL Press.
8. Osanna, M., Roubis, D. & Sogliani, F. 2007. Ricerche archeologiche ad Altojanni (Grottole-MT) e nel suo territorio. Rapporto preliminare. SIRIS 8:137-156.
9. Revelles, J. 2021. The role of palynology in archaeoecological research: reconstructing human-environment interactions during the Neolithic in the Western Mediterranean. Applied Sciences 11(9):4073.
10. Madella, M. & Fuller, D.Q. 2006. Palaeoecology and the Harappan Civilisation of South Asia: a reconsideration. Quaternary Science Reviews 25(11-12):1283-1301.
11. Chauhan, M.S. 1993. Palynological evidence for Holocene climatic changes in the Kashmir Valley. The Palaeobotanist 41:329-337.
12. Costantini, L. 1984. The first farmers of western Pakistan: the palaeoethnobotanical evidence from Mehrgarh. In South Asian Archaeology (Eds. J. Schotsmans & M. Taddei), pp. 305-321. Istituto Universitario Orientale, Naples.
13. Madella, M. & Fuller, D.Q. 2006. Palaeoethnobotanical investigations at Mehrgarh. Man and Environment 31(2):1-10.
14. Azzazy, M.F. 2018. Exploratory palynological studies at the Tell el-Daba'a-Avaris archaeological site. PLoS ONE 13(2):e0180770.
15. Agrawal, D.P. & Sood, R.K. 1982. Pollen analysis of Ganga Plains and its archaeological implications. Current Science 51(12):658-660.
16. Sharma, C. & Joachimski, M. 2006. Palaeoenvironmental reconstruction of Holocene sediments from central India. Quaternary International 133-134:84-96.
17. Chauhan, M.S., Pokharia, A.K. & Bhandari, Y. 2018. Quaternary vegetation, climate, farming and human habitation in the Ganga Plain, based on pollen and macro-botanical remains from lakes and archaeological sites. Indian Journal of Archaeology 3:1-65.
18. Bryant, V.M. Jr. & Holloway, R.G. 1983. The role of palynology in archaeology. In Advances in Archaeological Method and Theory, pp. 191-224. Academic Press.
19. Holloway, R.G. 1981. Preservation and experimental diagenesis of the pollen exine. Texas A&M University.
20. Elsik, W.C. 1971. Microbiological degradation of sporopollenin. In Sporopollenin, pp. 480-511. Academic Press.

21. Johnsrud, S., Yang, H., Nayak, A. & Waduge Punyasena, S. 2013. Semi-automated segmentation of pollen grains in microscopic images: a tool for three imaging modes. Grana 52(3):181-191.

22. Romero, I.C., Kong, S., Fowlkes, C.C., Jaramillo, C., Urban, M.A., Oboh-Ikuenobe, F., D'Apolito, C. & Punyasena, S.W. 2020. Improving the taxonomy of fossil pollen using convolutional neural networks and super-resolution microscopy. Proceedings of the National Academy of Sciences 117(45):28496-28505.

23. Punyasena, S.W., Haselhorst, D.S., Kong, S., Fowlkes, C.C. & Moreno, J.E. 2022. Automated identification of diverse Neotropical pollen samples using convolutional neural networks. Methods in Ecology and Evolution 13(9):2049-2064.

Ind. J. Aerobiol., Vol. 39, No. (1), pp. 33-44 [2026] ISSN No. 0971-1546

Research Article

SEASONAL VARIATIONS AND ALLERGENIC SIGNIFICANCE OF AIRBORNE POLLEN GRAINS IN THE HILLY RURAL AREAS OF PURULIA DISTRICT, WEST BENGAL, INDIA

POULAMI OJHA AND SUBRATA RAHA *

DEPARTMENT OF BOTANY, SIDHO-KANHO-BIRSHA UNIVERSITY, PURULIA, WEST BENGAL, INDIA

CORRESPONDING AUTHOR: subrata-raha@skbu.ac.in

Atmospheric pollen grains are a major cause of respiratory allergies worldwide. The present study aims to measure the aero-pollen load in the study areas and, for the first time in the rural sites of Purulia district, prepare a pollen calendar, followed by the clinical identification of allergy-causing pollen grains. One-year air sampling was conducted from July 2024 to June 2025 in some rural villages on the hilly slopes of the Ajodhya Hills, surrounded by dry deciduous forests. During the study period, a total of 75 types of airborne pollen from 32 plant families were recorded. Meteorological parameters, including temperature, rainfall, wind speed, and relative humidity, were also monitored in the study areas, and their influence on pollen concentration was evaluated using Pearson's correlation analysis. The prevalence of pollen allergy was assessed through Skin Prick Tests (SPT) among patients with respiratory allergies, and blood sera from SPT-positive patients were collected to estimation total IgE levels using an ELISA kit. The study revealed that pollen from Poaceae and Shorea robusta were the most dominant in the rural atmosphere, followed by *Alternanthera sessilis, Amaranthus spinosus, Ricinus communis, Syzygium cumini, Borassus flabellifer, Saraca asoca, Alstonia scholaris, Madhuca indica, Eclipta prostrata, Phyllanthus emblica,* and *Argemone mexicana*. Antigenic extracts from 35 selected pollen types were used for SPT, out of which 23 pollen types elicited positive reactions. In Shorea robusta, pollen-sensitized patients' total IgE levels showed wide variation (range approx. 252–546 IU/mL), and Specific IgE values (P/N ratios) measured by ELISA ranged from approximately 3.11 to 5.45. In Ricinus communis pollen-sensitized patients' total IgE levels showed 275–526 IU/mL. Pollen of Shorea robusta and Ricinus communis caused the maximum allergenicity. This study provides a comprehensive pollen calendar and allergen profile for the rural hilly region of Purulia, offering valuable insights for allergy diagnosis, prevention, and management among the local population.

Key Words: Airborne pollen grain, Pollen calendar, Respiratory allergy, Skin prick test (SPT), IgE estimation, ELISA, Purulia, West Bengal, India.

Received: 15.03.2026 Revised: 05.04.2026 Accepted:16.04.2026

INTRODUCTION

Aerobiology is a branch of biology that studies the nature and impact of airborne biological material, such as pollen grains, fungal spores, viruses, and bacteria, on the spread of airborne diseases like allergies, asthma, etc.[1,2]. According to estimates from the World Allergy Organization (WAO), allergies affect approximately 20–30% of the global population[3]. Respiratory allergy is the major form of allergy in India, which includes bronchial asthma as a common

disease phenotype, and in most cases, it is due to inhalant airborne allergens such as pollen grains and spores[4]. One of the most important sensitising aeroallergens is pollen[5]. Pollen distribution mainly depends on meteorological conditions, micro- and macro- topography of a particular area[6,7]. Climate change has a major impact on the pollen season and increased respiratory allergy[8,9,10,11,12]. Pollen calendars must be established to accurately characterize the onset, duration, and intensity of the pollen season, thereby facilitating the prevention and diagnosis of allergic diseases. Pollen calendars in a particular area are particularly useful since they offer easily readable visual data on the different kinds of airborne pollen that occur throughout the year[13,14].

The aim of the current work is (i) to determine the concentration, seasonal periodicity of some dominant pollen grains in the partially explored rural atmosphere of Purulia district, West Bengal, India. (ii) to prepare the pollen calendar for the hilly rural areas of the Ajodhya hills, (iii) to observe the prevalence of sensitization to *Shorea robusta* and *Ricinus communis* pollen among the respiratory allergic patients in rural areas of Purulia district.

MATERIALS AND METHODS

Study area

Purulia is the westernmost district of West Bengal, situated on the eastern edge of the Chota Nagpur Plateau. Its boundaries are 85.750° and 86.65° east longitudes and 22.40°

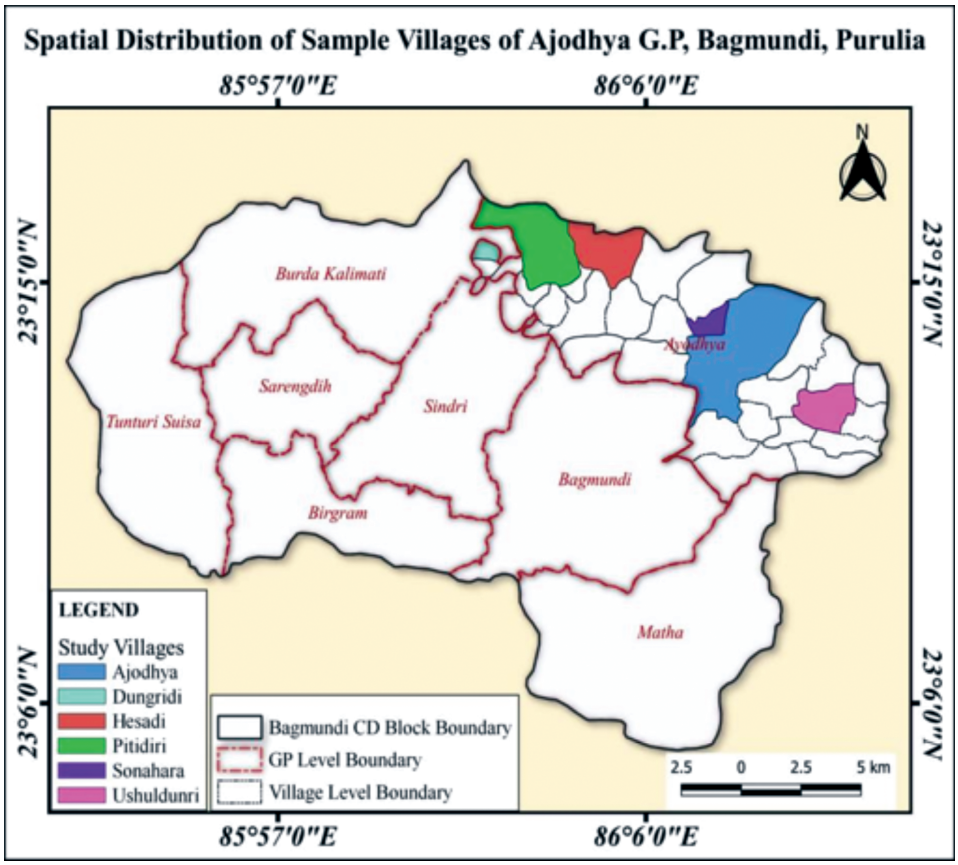


Fig. 3.1: Location map of study areas

and 23.50° north latitudes. Pollen grains were trapped from six rural villages (Fig. 3.1), namely Usuldungri, Ajodhya, Sonahara, Hesadi, Pitidiri, and Dungridi, located in Ajodhya GP of Bagmundi CD Block, Purulia district, West Bengal. All the villages are located in the hilly slopes of Ajodhya hills (altitude almost 430-700 msl) amidst of dry deciduous forests. The hilly areas have subtropical weather, with summer temperatures of 38°C and chilly winters of 7°C, and an average rainfall of 1355.20 mm.

Aerobiological Sampling

In the present study, the seasonal periodicity of airborne pollen flora was done with the help of "Burkard portable volumetric sampler" (Burkard Man. Co. Ltd., Rickmansworth, UK). The sampling was conducted from July, 2024 to June, 2025. The sampler was positioned at the height of two meters above the ground in the selected locations. To capture the pollen grains, a 1 cm thick microslide coated with a tiny layer of glycerine jelly was inserted through the slide slit of the sampler. At the end of the sampling, the slide was removed by rotating the upper ring using forceps. The sampler pulled air through the top slit, depositing a 2 × 14 mm sample on the glass slide. The particles formed a thin band on the microslide covered with glycerine jelly. The cover slip was placed over the exposed slides, which were then mounted using DPX and left to dry for two to three days. A high-resolution light microscope was used to scan the slides[15,16,17,18].

Collection of pollen sample and Meteorological data

Pollen samples were taken from mature anthers of fresh flowers during the peak flowering time. They were dried at 37°C, mildly crushed, and passed through different sieves (50, 105, 150, 250, and 300 mesh/cm^2) successively to remove the other floral impurities. The purity of the isolated pollen material was checked under the microscope. Pollen grains were stored at –22°C for further use. The pollen analysis was done by the standard acetolysis methods[18]. Two methods were used to study the amount of pollen produced per anther in order to evaluate counting error. In the first method, the anther was burst open on a glass slide by heating a little and then mounting in 3-4 drops of glycerine jelly with safranin. In the other method the anther was thoroughly smashed in 10-20 drops of safranin stained 50% glycerine, and then mounting a drop on the slide and counting pollen grains under the microscope[19].

The detailed weekly meteorological data, such as maximum and minimum temperature (°C), rainfall (mm), wind speed (km/h), relative humidity (%), were collected form the Agriculture office block seed farm, Bagmundi, Purulia, respectively, for monitoring rural weather status.

Preparation of Pollen extract

The pollen grains were defatted with diethyl ether, and then one gram of the pollen was extracted in phosphate buffer saline (PBS: 0.1 M Na-phosphate 150 mM, pH 7.2) by continuous stirring at 4°C for 16 h in a 1:10 (w/v) ratio. After centrifugation at 14,000g for 20 min, the clear supernatant was dialyzed and passed through a 0.22 μm Millipore filter. The filtrate was then lyophilized and stored at -35°C in sterile vials containing aliquots of known volume.

Study group, skin prick tests (SPT) and sera collection

Patient population and skin tests: Skin tests were performed with some pollen allergen extracts on 180 adult respiratory allergic patients (Age range: 18-55 years), attending the Shakti Sangha Allergy Unit, Purulia, during 2024-2025. Skin tests were performed with some dominant pollen allergen extracts such as *Acacia* sp., *Shorea robusta, Cassia* sp., *Eucalyptus* sp., *Lantana camara, Tridax procumbens, Butea monosperma, Cyanthillium cinereum*, *Alternanthera sessilis, Amaranthus spinosus, Ricinus communis, Syzygium cumini, Borassus flabellifer, Albizia lebbeck, Bombax ceiba, Saraca asoca, Alstonia scholaris, Madhuca indica, Eclipta prostrata, Phyllanthus emblica, Argemone mexicana*. After antigen preparation, a 26G disposable hypodermic needle was used to apply 20μl of allergen solution to the ventral side of the forearm in order to conduct the tests. Histamine phosphate (1 mg/ml) and PBS (1 mg/ml) were used as positive and negative controls, respectively. After 20 minutes, the reaction was measured. According to International guidelines, positivity was defined as a mean wheal diameter ≥ 3 mm compared with a negative control[20]. The reaction was graded from +1 to +3 level[21]. Control sera were collected from 4 non-sensitized healthy patients having no history of previous allergic reactions. Serum of each patient was separated and stored at –20°C for future use. The study was approved by the Ethics Committee of the Sidho-Kanho-Birsha University, Purulia.

Estimation of Total IgE and Specific IgE

ELISA was performed to measure the levels of specific IgE against the whole antigenic extract of the pollen grain[22]. The wells of the microtiter plates were coated with 50 μl/well of the pollen extract (protein) in 0.1 M PB, 150 mM NaCl, pH 7.2 and were kept overnight at 4°C. After blocking at room temperature for 1.5 h in 0.1 M PBS (pH 7.2) containing 0.05% (v/v) Tween 20, the plate was incubated with 50 μl of individual/pooled patient sera (1:10, v/v) overnight at 4°C, followed by incubation (2 h at 25°C) with antihuman IgE alkaline phosphatase conjugate diluted (1:1,000, v/v) in blocking solution. Each incubation step was followed by 3 times washing with PBST. The 4-nitrophenyl phosphate (pNPP) was used as substrate dissolved in PBS (1 mg/ml). After incubating in the dark for 30 min at 25°C, the reaction was stopped by adding 3 N NaOH. The absorbance was measured with an ELISA reader at 405nm. The results were expressed as P/N values. A P/N ratio (patient vs. non-allergic participants) of more than 3.5 for a given serum sample was considered as in vitro "positive" with noticeably higher IgE levels against the study antigen.

Statistical analysis

Pearson's correlation coefficients were performed to evaluate the strength and direction of linear associations between pollen concentrations and each meteorological variable. Pollen calendar was conducted using Python (v3.x) within the Jupyter Notebook environment.

RESULTS

Aerobiological survey

In the one-year aerobiological survey in rural villages of Ajodhya hill, a total of 75 airborne pollen types belonging to 32 plant families were

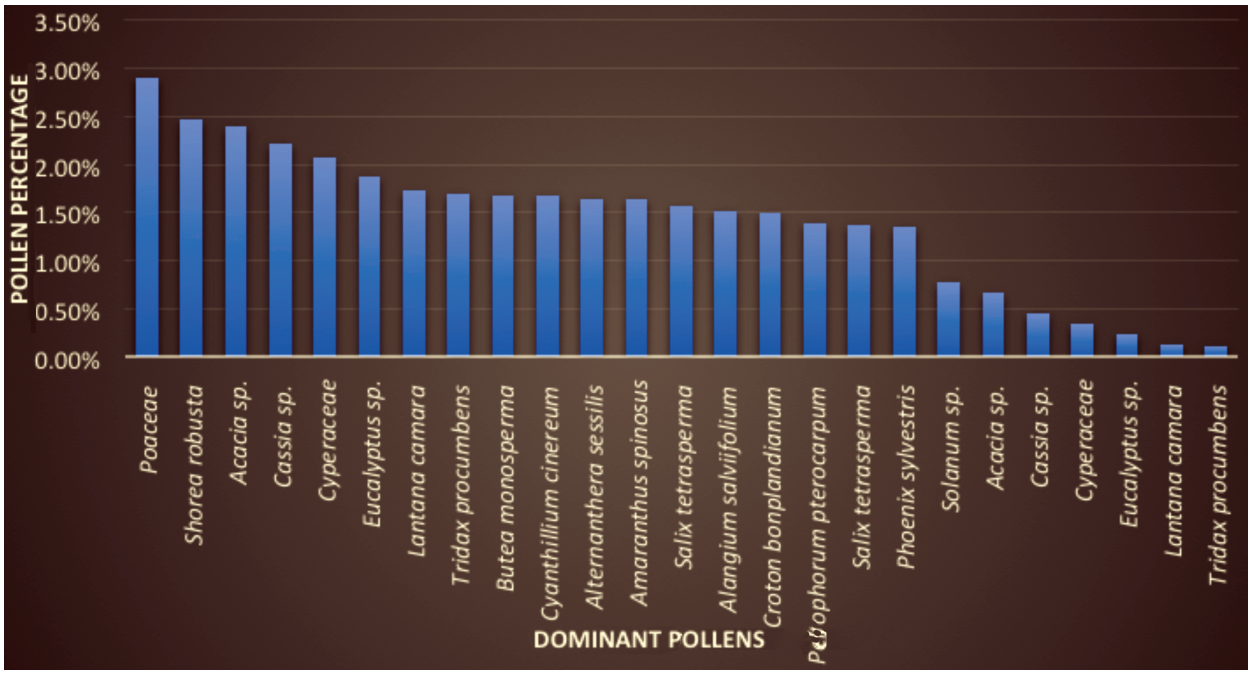


Fig. 3.2: Airborne pollen spectra of dominant pollen grains in rural areas of Purulia district, West Bengal

recorded (Fig. 3.2). During this one year of study periods, the maximum monthly concentration of pollens was observed in April (7837 /m^3), followed by March (7641/m^3), May (4796 /m^3), and February (4790 /m^3). The most dominant pollen grains include *Shorea robusta* (2.23%), *Acacia auriculiformis* (2.3%), *Cassia* sp. (2.14%), *Alangium salviifolium* (1.41%), *Butea monosperma* (1.68%), *Albizia lebbeck* (1.28%), *Peltophorum pterocarpum* (1.21%), *Delonix regia* (1.2%), *Eucalyptus citriodora* (1.87%), *Phoenix sylvestris* (1.36%), *Syzygium cumini* (1.28%), *Ricinus communis* (1.33%). A monthly pollen calendar was prepared for the rural study areas (Fig. 3.3).

Recording of Meteorological data

The one-year weekly meteorological data were collected from six sampling sites. The maximum temperature (38°C) was observed in the month of May, and the minimum temperature (7°C) was observed in January. The maximum rainfall (378.87 mm) & maximum relative humidity (99%) was observed in July. The correlation analysis (Fig. 3.4) revealed that pollen count exhibited strong negative correlations with maximum relative humidity (r = –0.81), minimum and average relative humidity (r = 0.99). Pollen count has a strong inverse relationship with relative humidity (RH). As RH increases, pollen count decreases significantly. Temperature variables were highly interrelated, with maximum and minimum temperatures showing a strong positive correlation (r = 0.93). These results suggest that higher humidity and rainfall conditions are associated with reduced pollen levels, whereas temperature has a weaker effect.

Clinical study

Skin prick tests were performed with *Shorea robusta* pollen extracts in a population of 180 allergic patients (age range 18-55), 50 showed

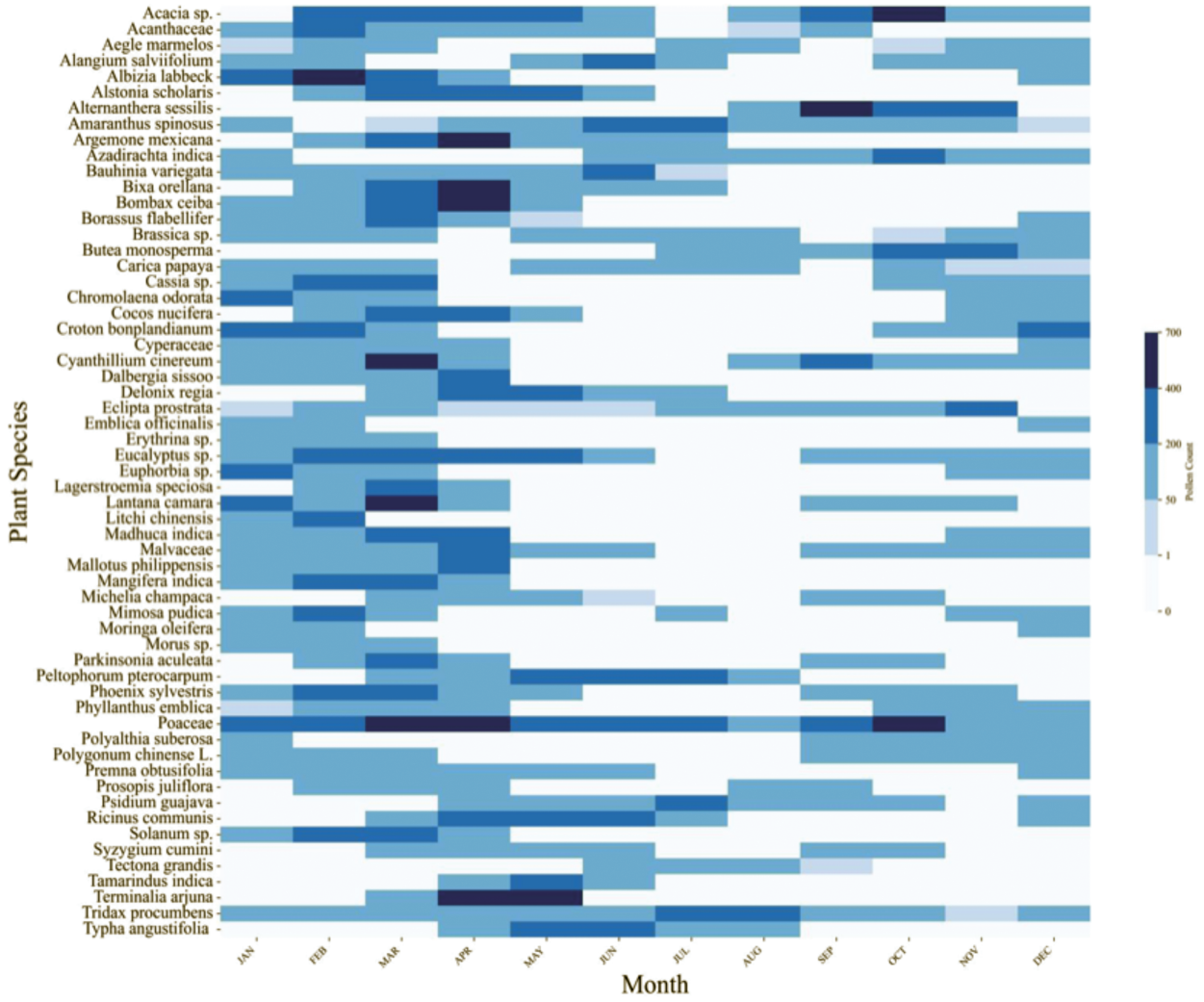


Fig. 3.3: Monthly pollen calendar for rural sites of Purulia district

a positive skin reaction (SPT) to three pollen allergens, which namely *Shorea robusta* and *Ricinus communis*. Most of the sensitive patients showed a +3 grade of positivity, followed by +2 and +1.

SPT report of *Shorea robusta* antigen

Out of the 180 patients, 64% patients showed a positive reaction to Shorea robusta antigen (Fig. 3.5). Among them, 43% of patients showed ≥ 2+ grade in SPT and were considered clinically significant. A +3/+4 grade of positivity was found to be most predominant, followed by +2. Only 50 patients with marked positive reactions in SPT agreed to donate blood, and the collected serum samples were analysed for specific IgE by indirect ELISA.

SPT report of *Ricinus communis* antigen:

Out of 180 patients 67% patients, showed a positive reaction to *Ricinus communis* antigen (Fig. 3.6). Among them, 41% patients showed ≥2+ grade in SPT and were considered to be clinically significant. A +3/+4 grade of positivity

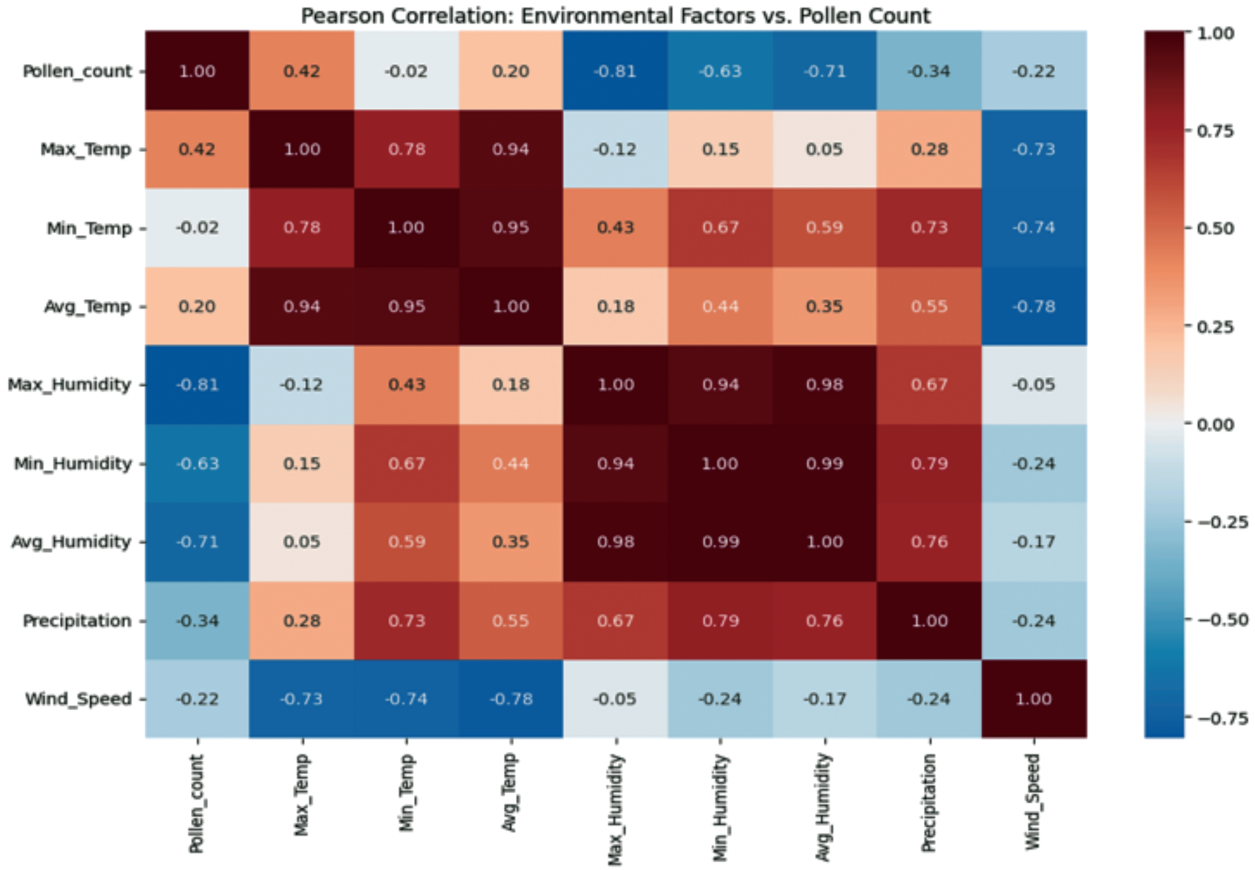


Fig. 3.4: Pearson Correlation – Environmental Factors vs. Pollen Count

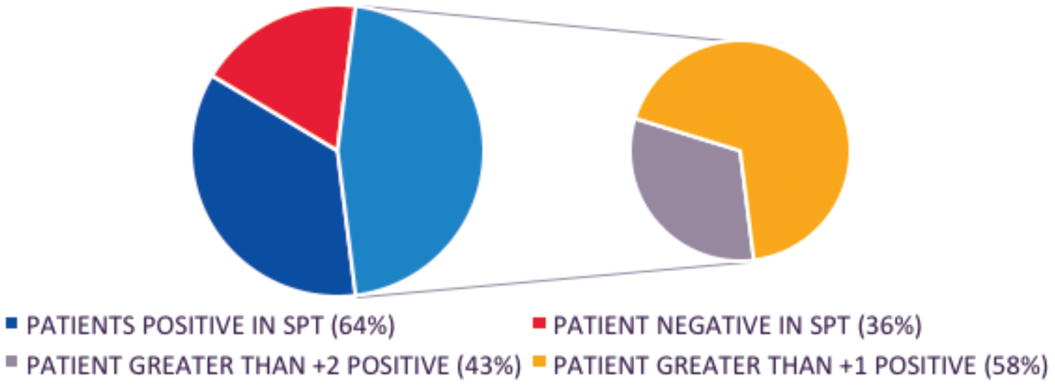


Fig. 3.5: Results of skin prick (SPT) with *Shorea robusta* antigenic extract at diagnostic clinic on 180 patients.

was found to be predominant, followed by +2. Only 20 patients with marked positive reactions in SPT agreed to donate blood, and the serum samples collected were analysed for specific IgE estimation by indirect ELISA.

Estimation of total and specific IgE

Twenty-five clinically symptomatic patients and three healthy persons as controls were included in the study for testing sensitivity to *Shorea robusta* pollen allergens. For each

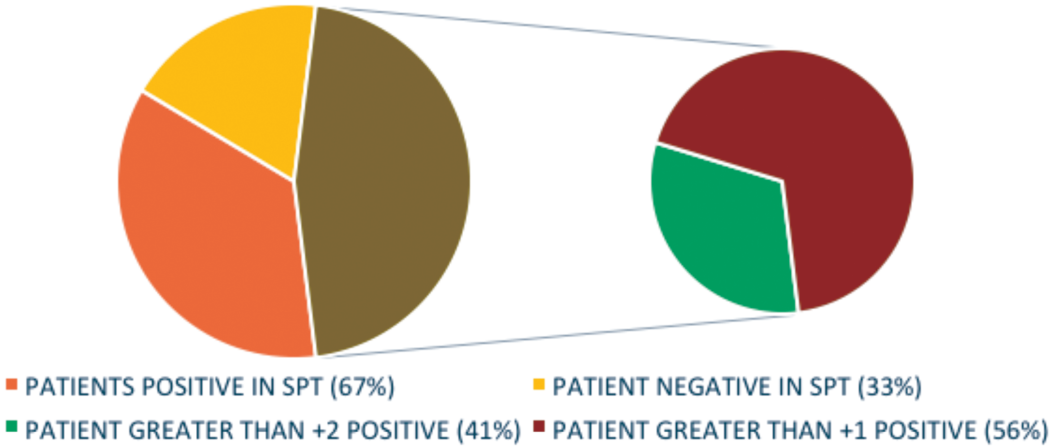


Fig. 3.6: Results of skin prick (SPT) with *Ricinus communis* antigenic extract at diagnostic clinic on 180 patients

Table 3.1: Clinical characteristics of the 25 *Shorea robusta* pollen sensitive patients

Sl. No.	Age/ Sex	Symptoms/Clinical history	Grades of SPT	Total IgE	Specific IgE-Titer by ELISA (P/N Value)	Established Co-Sensitization
P1	44/M	B, S	++++	344.34	5.45	AI, PS, CF, AA
P2	30/M	C, B, S	++	388.98	3.32	SC, SR
P3	45/M	B, NB, S, NB, SR	+++	345.66	3.23	CN, RN, SR, PP
P4	28/F	B, SR	+++	456.89	4.54	CD, AAl, SC
P5	32/F	C, B, SR	++	326.66	3.21	CD, SR, CN, TA
P6	23/M	C, S, SR	++++	443.87	4.73	AI, AN, CO
P7	36/F	NB, AC, SR	++	377.67	3.23	AA, SR, CD
P8	53/M	NB, C, B	+++	456.32	3.66	BF, AI, CS, CD
P9	43/F	B, AC, SR	+++	389.66	4.61	BF, AAI, RN, AN, SR
P10	25/F	C, B, AC, S, NB, SR	+++	422.12	3.88	AI, SR, AF, SR
P11	38/M	AC, NB, SR	++	258.89	3.11	SR, AI, AN, AP
P12	44/M	AC, NB	+++	301.89	3.96	SC, AN, RN, SR, CP
P13	36/M	B, S, NB	+++	499.12	4.78	AN, CN, SC, SR
P14	33/F	C, B, NB, SR	++	279.45	3.22	AAl, AA, SC
P15	52/M	B, AC, SR	++	425.67	4.19	PE, CS, SC
P16	54/M	C, AC, NB, SR	++++	498.34	5.62	CS, SR
P17	39/F	B, AC, SR	+++	489.22	4.52	CD, RN, AM

Contd.

Contd. Table 3.1

Sl. No.	Age/ Sex	Symptoms/Clinical history	Grades of SPT	Total IgE	Specific IgE-Titer by ELISA (P/N Value)	Established Co-Sensitization
P18	36/M	AC, C, B	+++	252.38	4.56	BF, CP, SR
P19	24/F	AC, NB	++	318.56	3.22	SR, BF
P20	28/M	B, C, AC, S	++++	546.34	5.34	AI, CD, SR
P21	33/M	B, SR	+++	434.21	3.54	CD, AAl, SC
P22	46/M	NB, AC	++	356.53	3.96	PE, CS, SC
P23	31/F	C, B, NB, SR	+++	269.32	3.54	BF, AI, CS
P24	22/F	B, AC, SR	+++	521.24	4.32	BF, AAI, RN, AN, SR
P25	19/M	S, SR	++	259.36	3.31	SR, BF
Healthy Control Patients						
C1					1.02	No
C2					0.86	No
C3					0.57	No
C4					1.06	No

Note: Symptoms like Cough (C), Breathlessness (B), Allergic Conjunctivitis (AC), Sneezing (S), Nasal Blockage (NB), and Skin Rash (SR).

The grading scale of skin prick test like negative if wheal diameter is <3mm, +1 if wheal diameter is 3-5mm, + 2 if wheal diameter is >6mm, +3 if wheal diameter is >6mm, with one or two small pseudo pods, and +4 is any reaction that is more pronounced than +3.

Aeroallergen abbreviations like *Acacia auriculiformis* (AA), *Chromolaena odorata* (CO), *Azadirachta indica* (AI), *Borassus flabellifer* (BF), *Carica papaya* (CP), *Typha angustifolia* (TA), *Syzigium cumini* (SC), *Cocos nucifera* (CN), *Peltophorum pterocarpum* (PP), *Shorea robusta* (SR), *Phoenix sylvestris* (PS), *Argemone mexicana* (AM), *Cassia sophera* (CS), *Solanum sisymbriifolium* (SS), *Ricinus communis* (RC), *Cynodon dactylon* (CD), *Tridax procumbens* (TP), *Delonix regia* (DR), *Alangium salvifolium* (AS), *Alternaria alternata* (AAI), *Aspergillus flavus* (AF), *Aspergillus niger* (AN), *Rhizopus nigricans* (RN).

patient, demographic details (age and sex), clinical symptoms, skin prick test (SPT) grades, Total IgE levels, Specific IgE (P/N values), and established co-sensitizations were recorded. The symptomatic patients (P1–P20) presented with various allergic manifestations, including cough (C), breathlessness (B), sneezing (S), nasal blockage (NB), allergic conjunctivitis (AC), and skin reactions (SR). SPT grades ranged from +2 to +4, indicating moderate to extreme reactivity.

In *Shorea robusta*, pollen-sensitized patients' total IgE levels showed (Table 3.1) wide variation (range approx. 252–546 IU/mL), reflecting varying degrees of systemic allergic response. Specific IgE values (P/N ratios) measured by ELISA ranged from approximately 3.11 to 5.45, suggesting measurable allergen-specific sensiti-

Table 3.2: Clinical characteristics of the 20 Ricinus communis pollen sensitive patients

Sl. No.	Age/ Sex	Symptoms/ Clinical history	Grades of SPT	Total IgE	Specific IgE-Titer by ELISA (P/N Value)	Established Co-Sensitization
P1	42/F	C, B, S	+++	314.03	3.49	SC, AI, PS, SS, TP
P2	30/M	B, NB, SR	++	280.67	3.22	CF, AA, RC
P3	25/M	C, B, AC, NB, SR	+++	491.57	4.55	CD, CN, PP, PS, TP
P4	39/M	C, SR, AC	+++	423.16	4.39	Al, SC, RN, AF, DR
P5	38/F	NB, SR, B	++++	523.56	5.21	AN, RN, CN, RC
P6	42/F	C, NB, SR	++++	454.67	4.78	PE, AC, TP
P7	36/M	C, B, AC, NB	++	387.23	3.22	AA, TP, CD, AI, RN
P8	40/M	NB, SR, C	++	412.11	4.32	BF, AI, CS, AN, AF, RC
P9	33/F	CB, AC, NB, SR	+++	329.49	3.55	RN, BF, AI, CS, RC
P10	28/F	C, B, AC, S, NB, SR	+++	394.76	3.95	AA, PE, RN, AF, TP
P11	39/M	B, S, NB, SR	+++	387.23	3.23	AA, AI, AN
P12	45/F	B, S, AC, SR	++	275.44	3.04	SC, AN, RN, TP
P13	36/F	B, NB, SR	+++	480.55	4.76	CP, SC, AN, TP
P14	38/F	AC, NB, SR	++	311.59	3.59	SC, Al, AAI, CO
P15	42/M	B, C, SR, NB	+++	491.57	4.89	AA, AAI, CC, SC
P16	52/F	B, AC, NB, SR	++++	526.45	5.69	AA, CD, AA, TP
P17	46/M	B, AC, NB, SR	+++	412.11	4.32	SC, CD, TP, RC
P18	30/M	B, C, SR	++	311.59	3.54	AI, BF, CP, RC
P19	21/M	C, S, NB, SR	++	309.22	3.42	AA, CP, CF, SC
P20	26/F	B, NB, AC, SR	+++	454.67	4.34	AN, TP, AS
Healthy Control Patients						
C1					0.78	No
C2					0.34	No
C3					1.02	No
C4					0.95	No

Note: Abbreviations same as Table 3.1

vity. In contrast, the healthy controls (C1-C4) showed very low Specific IgE values (0.57-1.06) and no co-sensitization, confirming their non-allergic status.

In *Ricinus communis* pollen-sensitized patients, total IgE levels showed (Table 3.2) a range approx 275-526 IU/mL, reflecting different levels of systemic allergic response. Specific IgE values (P/N ratios) measured by ELISA ranged from approximately 3.04-5.69, suggesting measurable allergen-specific sensitivity. In contrast, the healthy controls (C1-C4) showed very low Specific IgE values (0.78-1.02) and no cosensitization, confirming their non-allergic status.

DISCUSSION

This one-year aerobiological survey provides a comprehensive understanding of airborne pollen diversity, seasonal patterns, and allergenic potential in rural study areas of Purulia district. During the study period, a total of 75 different types of airborne pollen belonging to 32 plant families were recorded. The most dominant pollen grains incluse *Shorea robusta*, followed by Poaceae, *Acacia* sp., *Eucalyptus* sp., *Amaranthus spinosus, Tridax procumbens, Malvaceae, Alangium salviifolium, Lantana camara, Butea monosperma, Argemone mexicana, Ricinus communis, Alstonia scholaris, Cocos nucifera, Peltophorum pterocarpum, Bombax ceiba, Borassus flabellifer, Delonix regia, Alternanthera sessilis, Azadirachta indica*, and *Madhuca indica*. Clear seasonal trends were observed, with the highest pollen concentrations recorded during late winter to early summer. It was observed that pollen count has a strong inverse relationship with relative humidity (RH). As RH increases, pollen count decreases significantly. Most patients exhibited moderate to strong SPT responses, which were associated with elevated total IgE concentrations in the case of *Shorea robusta* (252-546 IU/mL) and increased specific IgE titers (P/N: 3.11-5.45). *Ricinus communis* pollen-sensitive patients showed a range of approx 275-526 IU/mL, and (P/N: 3.04-5.69). In contrast, healthy controls showed very low specific IgE levels (<1.1), confirming the specificity of the allergen-induced immune response. Overall, this work highlights the need for region-specific diagnostic assessment and immunotherapeutic approaches and develops a thorough aerobiological and clinical profile for Purulia. Incorporating antigens from to *Shorea robusta* and *Ricinus communis* pollen into routine allergy testing could greatly enhance patient care and diagnostic precision in this area.

ACKNOWLEDGEMENT

The authors are thankful to Dr. Arindam Datta for the clinical test (SPT) in Shakti Sangha Health Unit, Purulia. We also express our gratitude to Dr. Kalosona Paul for his valuable assistance in preparing the location map for this study.

REFERENCES

1. Gosling, S. N., Bryce, E. K., Dixon, P. G., Gabriel, K., Gosling, E.Y., Hanes, J. M. & Wanka, E.R. 2014. A glossary for biometeorology. International Journal of Biometeorology 58: 277-308.
2. Davies, J. M., Beggs, P. J., Medek, D.E., Newnham, R. M., Erbas, B., Thibaudon, M. & Huete, A. R. 2015. Transdisciplinary research in synthesis of grass pollen aerobiology and its importance for respiratory health in Australasia. Science of the Total Environment 534: 85-96.
3. Pawankar, R., Canonica, G.W. & Holgate, S.T. 2013. World Allergy Organization (WAO) White Book on Allergy: Update 2013. World Allergy Organization.
4. Bhattacharya, K., Sircar, G., Dasgupta, A. & Gupta Bhattacharya, S. 2018. Spectrum of allergens and allergen biology in India. International Archives of Allergy and Immunology 177: 219-237.

5. Obtulowicz, K., Kotlinowska, T., Stobiecki, M., Dechnik, K., Obtulowicz, A., Manecki, A., Marszalek, M. & Schejbal-Chwastek, M. 1996. Environmental air pollution and pollen allergy. Annals of Agricultural and Environmental Medicine 3: 131-138.
6. Hjelmroos, M. 1991. Evidence of long-distance transport of Betula pollen. Grana 30: 215-228.
7. Maya-Manzano, J. M., Sadys, M., Tormo-Molina, R., Fernández-Rodríguez, S., Oteros, J., Silva-Palacios, I. & Gonzalo-Garijo, A. 2017. Relationships between airborne pollen grains, wind direction and land cover using GIS and circular statistics. Science of the Total Environment 584-585: 603-613.
8. D'Amato, G. & Akdis, C. 2020. Global warming, climate change, air pollution and allergies. Authorea Preprints.
9. Eguiluz-Gracia, I., Mathioudakis, A. G., Bartel, S., Vijverberg, S. J., Fuertes, E., Comberiati, P., Cai, Y.S., Tomazic, P.V., Diamant, Z., Vestbo, J. & Galan, C. 2020. The need for clean air: the way air pollution and climate change affect allergic rhinitis and asthma. Allergy 75: 2170-2184.
10. Damialis, A., Charalampopoulos, A., Lazarina, M., Diamanti, E., Almpanidou, V., Maraidoni, A. M., Symeonidou, A., Staikidou, E., Syropoulou, E., Leontidou, K., Tsiripidis, I., Halley, J.M. & Vokou, D. 2020. Plant flowering mirrored in airborne pollen seasons: evidence from phenological observations in 14 woody taxa. Atmospheric Environment 240: 117708.
11. Katelaris, C. H. & Beggs, P. J. 2018. Climate change: allergens and allergic diseases. Internal Medicine Journal 48: 129-134.
12. Jenerowicz, D., Silny, W., Danczak-Pazdrowska, A., Polanska, A., Osmola-Mankowska, A. & Olek-Hrab, K. 2012. Environmental factors and allergic diseases. Annals of Agricultural and Environmental Medicine 19.
13. Recio, M., Cabezudo, B., Trigo, M. M. & Toro, F. J. 1998. Pollen calendar of Malaga (Southern Spain), 1991-1995. Aerobiologia. 14: 101-107.
14. Belmonte, J., Roure, J. M. & Franch, J. 1995. Aerobiologia de Baleares, Ciutat de Mallorca, Mao´y Ciutadella. REA 1: 65-73.
15. Erdtman, G. 1969. Handbook of Palynology: An Introduction to the Study of Pollen Grains and Spores. Munksgaard, Copenhagen.
16. Huang, T. C. 1972. Pollen Flora of Taiwan. Department of Botany, National Taiwan University, Taipei, 297 pp.
17. Nayar, T. S. 1990. Pollen Flora of Maharashtra State, India. Today and Tomorrow's Printers and Publishers, New Delhi, India, pp. 59-64.
18. Bhattacharya, K., Majumdar, M. R. & Gupta Bhattacharya, S. 2006. A Textbook of Palynology. New Central Book Agency, Kolkata, India, 199 pp.
19. Bera, S.K. 1990. Palynology of *Shorea robusta* (Dipterocarpaceae) in relation to pollen production and dispersal. Grana 29: 251-255.
20. Dreborg, S. & Frew, A. 1993. Position paper: Allergen standardization and skin tests. Allergy 48 (Suppl. 14): 49-82.
21. Stytis, D. P., Stobo, J. D., Fudenberg, H. & Wells, J. V. 1982. Basic and Clinical Immunology. 4th ed. Lange Medical Publications, Maruzen Asia (Pvt.) Ltd., Singapore, p. 409.
22. Mandal, J., Chakraborty, P., Roy, I., Chatterjee, S. & Gupta-Bhattacharya, S. 2008. Prevalence of allergenic pollen grains in the aerosol of the city of Calcutta, India—a two-year perspective study. Aerobiologia. 24: 151-164.

Ind. J. Aerobiol., Vol. 39, No. (1), pp. 45-52 [2026] ISSN No. 0971-1546

Research Article

MORPHOLOGICAL CHARACTERIZATION, FLORAL BIOLOGY AND POLLEN PRODUCTIVITY OF SOME SPECIES OF MALVACEAE

NIKITA ARVIND SONTAKKE, KAMLAKAR CHANDAR MORE AND PRASHANT ASHOKRAO GAWANDE*

DEPARTMENT OF BOTANY, SANT GADGE BABA AMRAVATI UNIVERSITY, AMRAVATI - 444602, MAHARASHTRA STATE, INDIA.

CORRESPONDING AUTHOR: prashantgawande@sgbau.ac.in

The family Malvaceae comprises approximately 245 genera and 4,465 species worldwide and is represented in India by 52 genera and 219 species. Comparative studies on floral biology and reproductive attributes are essential for understanding breeding systems, taxonomy, and ecological adaptation. The present investigation aimed to characterize the morphology, floral biology, pollen production, pollen viability, and pollen: ovule ratio of selected Malvaceae species.

Three species, *Hibiscus hirtus* L., *Hibiscus rosa-sinensis* L., and *Malvaviscus arboreus* Cav., were collected from the Western Ghats and Sant Gadge Baba Amravati University campus, Maharashtra, India. Morphological characters, flowering phenology, pollen production, pollen: ovule ratio, and pollen viability were studied using standard taxonomic methods, light microscopy, and 1% acetocarmine staining. The three species differed in flowering season, anthesis, floral morphology, and reproductive parameters. *Hibiscus rosa-sinensis* produced the highest pollen count (6530 ± 327 grains per flower) and pollen: ovule ratio (130.6 ± 81.75), followed by *H. hirtus* (5530 ± 227; 110.6 ± 56.75) and *Malvaviscus arboreus* (4132 ± 423; 103.3 ± 84.6). Pollen viability remained high in all species, ranging from 90.10% to 93.10%. Based on pollen: ovule ratios, all species were categorized as facultative autogamous.

Variations in floral morphology, flowering phenology, pollen production, and pollen: ovule ratio indicate species-specific reproductive adaptations associated with pollination strategies. High pollen viability across all species suggests successful reproductive potential, while facultative autogamy provides reproductive assurance under varying environmental conditions. The study enhances understanding of the reproductive biology of Malvaceae and provides valuable baseline information for taxonomy, conservation, breeding programmes, and future investigations integrating palynology, pollination ecology, and scanning electron microscopy.

Key Words: Morphological characterization, floral biology, phenology, pollen production, Malvaceae.

Received: 20.03.2026 Revised: 04.04.2026 Accepted:18.04.2026

INTRODUCTION

Malvaceae family distributed in the tropical and subtropical regions of the world and consist of approximately 245 genera and 4465 species[1]. In India, the family is represented by 52 genera and 219 species[1]. The reproductive and vegetative organs of this family exhibit several unifying features. Leaves and stems contain stellate hairs and mucilaginous sap. The epicalyx is

mostly present. The stamens, containing one-celled anthers and spiky pollen, are joined into a column around the style in the center of the flower, and the calyx of the flowers contains valvate lobes in the bud. The blooms have five or more carpels, a superior ovary, a branched style, and ovules with axile placentation. The fruits are capsules or schizocarps[2].

Reproductive biology of the flowering plant is vital in creating effective strategies for their sustainable utilization[3]. Palynological research can offer a more precise foundation for plant species identification. The study of pollen biology has direct impact on agriculture, horticulture, forestry, plant breeding, forensic sciences and biotechnology[4]. The pollen: ovule ratio is strongest indicator of breeding system of species[5]. Pollen: ovule ratio shows the effectiveness of pollination or the probability of a pollen grains that gets to the stigma[6,7].

The present study has been undertaken to investigate the morphology, floral biology and pollen production in some species of Malvaceae.

MATERIALS AND METHODS

Study area

Present study was carried out in Department of Botany, Sant Gadge Baba Amravati University, Amravati, Maharashtra, India (Table 4.1). Field identifications were verified using the available taxonomic literature[8, 9, 10,11].

Flowering phenology

The plant species of the Malvaceae family under study were visited daily for collection of blooming phenological data from study area. The species under study were observed from the onset of flowering to the opening of last flower. The timing of onset and termination of blooming were studied for each species[12].

Flower morphology

Size of different parts of plants such as vegetative and floral parts were measured by scale as well as binocular stereomicroscope ALMICRO DSZ-99. Images of different parts were captured by using digital camera 4k Ultra HD. Stigma type and leaf texture were described using terminology consistent with Radford *et al*.[13] and Bendre and Kumar[14]. The specimens were deposited to the herbaria of Department of Botany, Sant Gadge Baba Amravati University, Amravati.

Pollen production per flower

Undehisced anthers from bud were collected for the estimation of pollen production. In a

Table 4.1: Collection and identification of plants

Sl. No.	Name of Plant	Flowering season	Latitude	Altitude
1.	*Hibiscus hirtus* L.	August to January	20.71024°	78.166425°
2.	*Hibiscus rosa-sinensis* L.	Round the year	20.941938°	78.800169°
3.	*Malvaviscus arboreus* Cav. Var. *penduliflorus* (DC.)	Round the year	16.815675°	74.111012°

10 ml test tube, the undehisced anthers were crushed in 50% glycerin. After standardization of glass dropper, pollen per drop was counted[15,16].

Pollen ovule ratio

The pollen: ovule ratio of plants under study was obtained by dividing the number of pollen grains per flower by the number of ovules per flower[6].

Pollen grain viability

Pollen viability of studied species were assessed by using 1% acetocarmine stain. Un dehisced mature anthers were squashed in 1% acetocarmine and observed under 40x compound microscope. Pollen grains which are deeply stained were viable[16,17].

RESULT AND DISCUSSION

1. *Hibiscus hirtus* L.

Flowering phenology: In *Hibiscus hirtus* L. floral bud initiation starts within 7-8 days from vegetative shoots, whereas floral bud takes 25-28 days to flourish (Fig. 4.1). Flowers turn into mature fruits within 8-10 days (Fig. 4.1F). Opening of flowers takes place near about 12:00-01:00 h. and anther dehiscence was noted between 12:15-12:30 h. Flower life was more than 9-10 hours after opening and corolla fall off by the successive days (Fig. 4.1). It was observed that flowering limited only for few months in the year.

Flower morphology: *Hibiscus hirtus* L., Sp. Pl. 694, 1753; Mast. in Hook. f. Fl. Brit. India

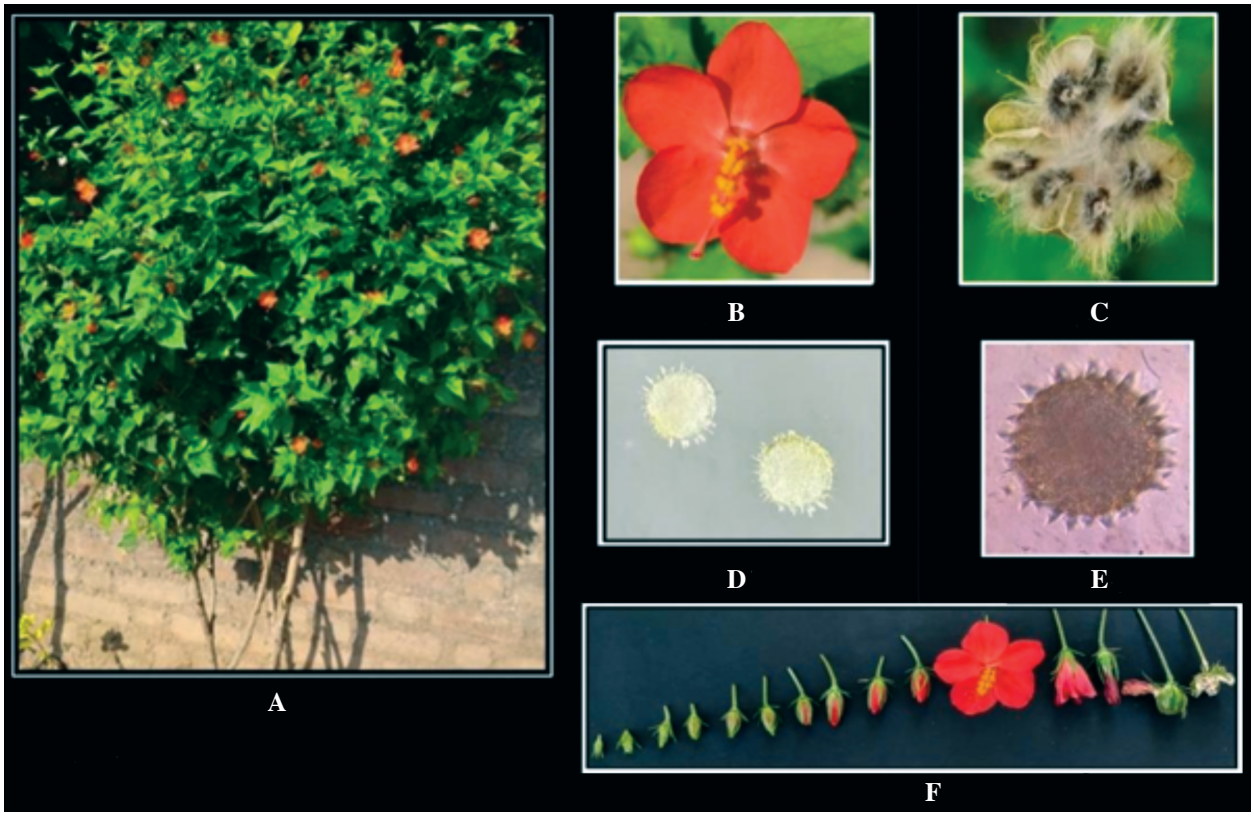


Fig. 4.1: Morphological and reproductive features of *Hibiscus hirtus* L. [A. Plant habit, B. Flower, C. Mature fruit, D. Pollen grain under 10 x, [B-E. Pollen grain under 40 x, F. Different stages of flowering].

1:335. 1874; Cooke, Fl. Pres. Bombay 1:113. 1958 (Repr.); Paul in Sharma *et al*. Fl. India 3:329. 1993; Venkanna & Das Das in Singh *et al*. Fl. Maharashtra St. Dicot. 1:312. 2000. Witt 17. Inflorescence solitary. Flower pedicellate, complete, bisexual, actinomorphic, pentamerous, hypogynous, orange. Flower pedicel 2.6 cm. Epicalyx 6-7 measuring 2.79-3.50 × 0.40-0.50 mm, linear, hairy 0.41 mm. Number of sepals 5, gamosepalous, valvate, persistent, 4.80-5.85 × 0.30-0.40 mm, green. Number of petals 5, polypetalous, twisted, 1.1-1.6 × 1.1-1.5 cm, orange. Number of stamens numerous, fertile, fused, monadelphous, filament 0.33 × 0.10 mm, monothecous, basifixed. Staminal column measuring 5.82 × 0.77 mm. Number of carpels 5, pentacarpellary, syncarpous, superior ovary of 2.04 × 1.80 mm, number of locules five, axile placentation, branched style measuring 9.03 × 0.37 mm with five capitate 0.22 × 0.35 mm white stigmas with tiny hairs of 0.10 mm. Produces capsular, longitudinally dehiscent fruits with a diameter of 5-7 mm, fruit pedicel is of 3 cm, the calyx persists and beyond the capsule; the seeds are cottony, reniform, 3.40-3.47 × 3.85-3.95 mm.

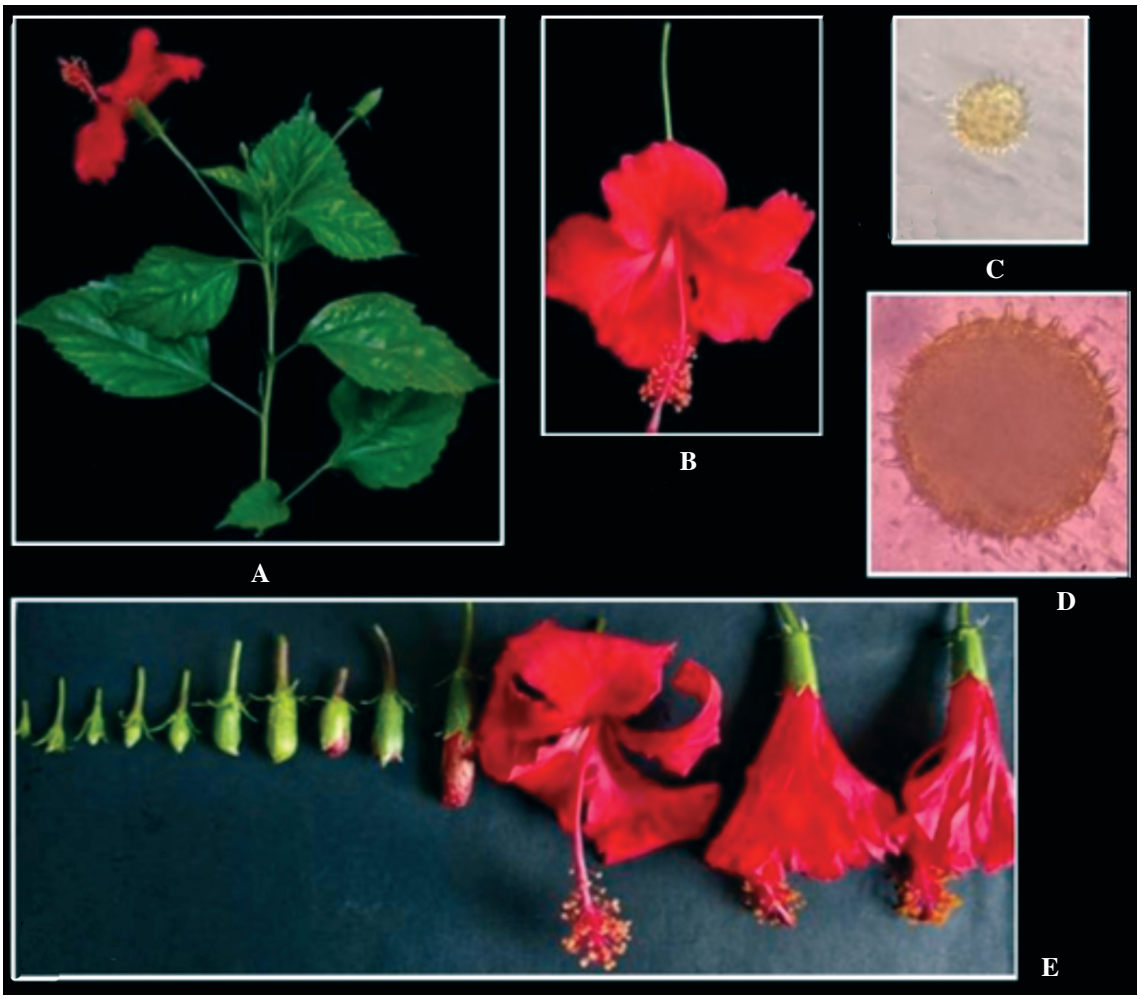


Fig. 4.2: **Morphological and reproductive feature of *Hibiscus rosa-sinensis* L.** [A. twig showing Plant habit, B. Flower, C. pollen grain under 10 x, D. pollen grain under 40 x, E. Different stages of flowering].

Pollen production per flower: The number of pollen grains produced per flower were found to be 5530 ± 227.

Pollen: ovule ratio: The pollen: ovule ratio was found to be 110.6 ± 56.75.

Pollen viability: The pollen viability percentage of *Hibiscus hirtus* L. was recorded as 92.05%.

2. *Hibiscus rosa-sinensis* L.

Flowering phenology: In *Hibiscus rosa-sinensis* L. floral buds initiation starts within 8-10 days from vegetative shoots, whereas floral bud takes 28-30 days to flourish (Fig. 4.2). Opening of flowers takes place near about 06:30-07:00 h. and anther dehiscence was noted between 07:00-08:00 h. Flower life was more than 9-10 hours after opening and corolla fall off by the successive days (Fig. 4.2). It was observed that flowering throughout the year. Present observations confirmed the results reported by Annahwi *et al*.[18].

Flower morphology: *Hibiscus rosa-sinensis* L., Sp. Pl. 694. 1753; Mast. in Hook. f. Fl. Brit. India 1:334. 1874; Cooke, Fl. Pres. Bombay 1:120. 1958 (Repr.); Paul in Sharma *et al*. Fl. India 3:391. 1993; Venkanna & Das Das in Singh *et al*. Fl. Maharashtra St. Dicot. 1:340. 2000.

Flowers solitary, upright, sub-pendulous, bracteate, bracteolate, complete, bisexual, actinomorphic, pentamerous, hypogynous, trumpet shaped, red. Pedicel glabrous, 1-6 cm long, articulated towards the tip. Epicalyx 6-8 segments, glabrous, linear- lanceolate, 6-15 × 1-2 mm. Number of sepals 5, gamosepalous, tubular-campanulate, valvate, 1.1-1.6 × 1.2-1.9 cm, green. Number of petals 5, polypetalous 5-8 x 4.5-5.5 cm, single, red, twisted, oblong-obvate. Number of stamens numerous, fertile, fused, monadelphous, filament 9.95 × 0.26 mm, monothecous, basifixed. Staminal column measuring 10.5 × 0.46 mm. Number of carpels 5, pentacarpellary, syncarpous, superior ovary of 5.29 × 2.40 mm, number of locules five, axile placentation, branched style measuring 10.8 × 0.39 cm with five capitate 1.98 × 1.96 mm red stigmas with tiny hairs. Capsule oblong -ovoid, glabrous. Seeds are reniform, blackish and have a significant amount of stellate hair.

Pollen production per flower: The number of pollen grains produced per flower were found to be 6530 ± 327.

Pollen: ovule ratio: The pollen: ovule ratio was found to be 130.6 ± 81.75.

Pollen viability: The pollen viability percentage of *Hibiscus rosa-sinensis* L. was recorded as 90.10%.

3. *Malvaviscus arboreus* Cav.

Flowering phenology: In *Malvaviscus arboreus* Cav. floral bud initiation starts within 9-12 days from vegetative shoots, whereas floral bud takes 28-32 days to flourish (Fig. 4.3). Opening of flowers takes place near about 06:00 to 06:30 h. and anther dehiscence was noted between 06:15 to 06:30 h. Flower life was more than 9 to 10 hours after opening and corolla fall off by the successive days (Fig. 4.3). It was observed that flowering throughout the year.

Flower morphology: *Malvaviscus arboreus* Cav., Scheryin Ann. Miss. Bot. Gard. 29. 223. 1942; Paul in Sharma *et al*. Fl. India 3:394. 1993; Venkanna & Das Das in Singh *et al*. Fl. Maharashtra St. Dicot. 1:342. 2000. *M. penduliflorus* Mocino & Sesse ex DC. Prodr. 1:445. 1824.

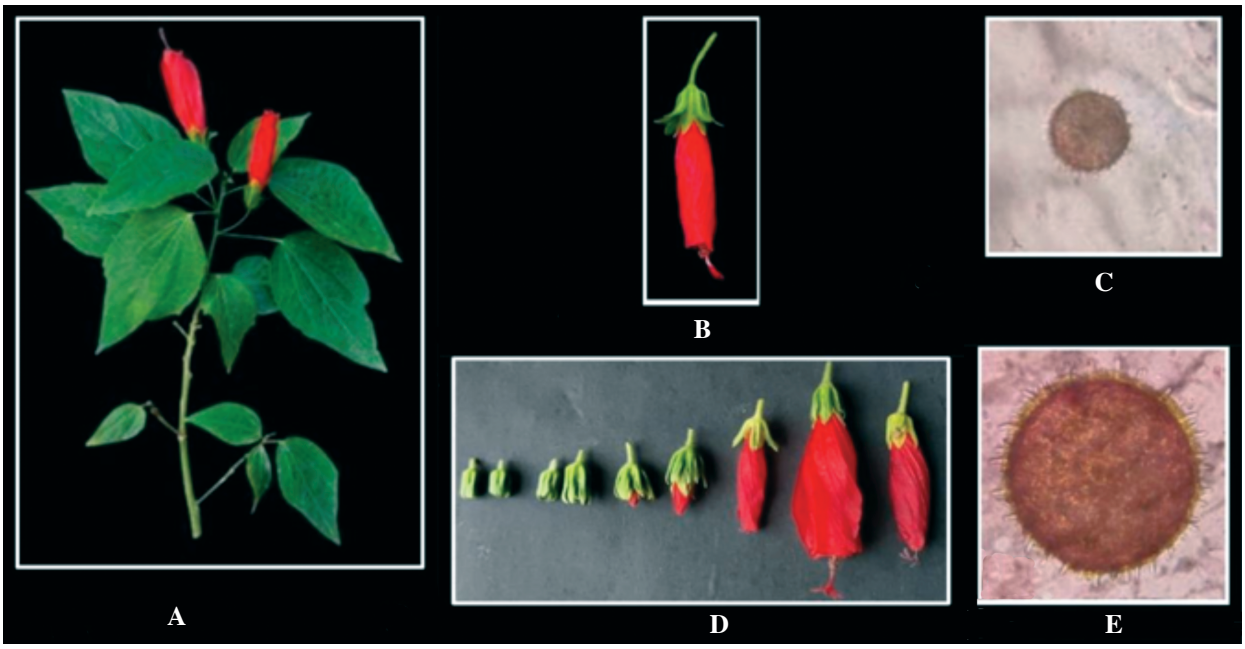


Fig. 4.3: **Morphological and reproductive feature of *Malvaviscus arboreus* Cav**. [A. twig showing Plant habit, B. Flower, C. pollen grain under 10 x, D. pollen grain under 40 x, E. Different stages of flowering].

Flower bracteate, bracteolate, pedicellate, complete, bisexual, actinomorphic, pentamerous, hypogynous, tubular, pendular, drooping, bright red with petals remains mostly closed. Flower pedicel 2.3 × 0.1 cm. Epicalyx 7-8 measuring 14.76-15.50 × 4.42-5. mm, linear. Number of sepals 5, gamosepalous, valvate, persistent, 13.95-15.95 × 3.44-5.44 mm, green. Number of petals 5, polypetalous, twisted, 3.3-5.5 × 1.5-2.0 cm, red, partly closed. Number of stamens numerous, fertile, fused, monadelphous, filament 1.64 × 0.28 mm, monothecous, basifixed. Staminal column measuring 11.35 × 1.36 mm. Number of carpels many, polycarpellary, syncarpous, superior ovary of 2.80 × 3.21 mm, number of locules five, axile placentation, branched style measuring 5 × 0.05 cm with ten capitate 0.35 × 0.51 mm velvety red stigmas. Oblate capsule with flat few seeds.

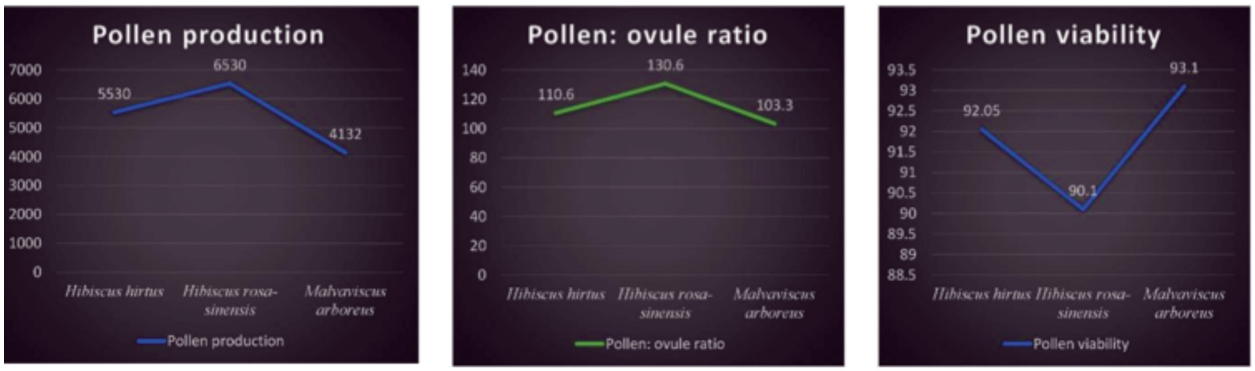
Pollen production per flower: The number of pollen grains produced per flower were found to be 4132 ± 423.

Pollen: *ovule ratio*: The pollen: ovule ratio was found to be 103.3 ± 84.6.

Pollen viability: The pollen viability percentage of *Malvaviscus arboreus* Cav. was recorded as 93.10%.

The results obtained are presented in Figs. 4.1-4.3 and Fig. 4.4(A, B, C). Flower phenology of *Hibiscus rosa-sinensis* L. observation is confirmed by the results reported by Annahwi *et al*.[18]. Flower phenology of Malvaviscus arboreus observations were matched with the results reported by Johri[19].

Pollen production is maximum in *Hibiscus rosa-sinensis* followed by *Hibiscus hirtus* and *Malvaviscus arboreus*. Result was altogether different for studied species as compared to Annahwi *et al*.[18]. Results of pollen viability of



A **B** **C**

Fig. 4.4: **Pollen study of three Malvaceae plant species** [A. Showing pollen production of *Hibiscus hirtus, Hibiscus rosa-sinensis* and *Malvaviscus arboreus*; B. Showing pollen: ovule ratio of *Hibiscus hirtus, Hibiscus rosa-sinensis* and *Malvaviscus arboreus*; C. Showing pollen viability of *Hibiscus hirtus, Hibiscus rosa-sinensis* and *Malvaviscus arboreus*].

studied plants were different with results obtained by Annahwi *et al*.[18].

The variation in the P/O ratios is due to a wide range of parameters such as pollen grain size, stigmatic papillae surface, time duration of stigma receptivity and pollination[7]. Pollen: ovule ratio was highest in *Hibiscus rosa-sinensis* followed by *Hibiscus hirtus* and *Malvaviscus* arboreus. In comparison to Cruden's classification of breeding system based on P/O ratio, all three plants under study may be regarded as having facultative autogamy breeding system[6].

CONCLUSION

The present study provides a morphological analysis, floral biology and pollen production of three species of two genera belonging to the family Malvaceae collected from the western ghat and Sant Gadge Baba Amravati University campus. Three Malvaceae species were studied and the results showed differences in pollen: ovule ratio, pollen viability, floral morphology and flower phenology. *Malvaviscus arboreus* and *Hibiscus hirtus* having low pollen output and pollen: ovule ratio. All species showed high pollen viability and a facultative autogamy breeding system suggesting their ecological significance. It is recommended that by combining macro and micro-morphology, pollen morphology using scanning electron microscopy and pollination mechanism we can refine the systematic classification of this family.

REFERENCES

1. The Plant List. 2013. The Plant List: A Working List of All Plant Species, Version 1.1. Royal Botanic Gardens, Kew & Missouri Botanical Garden.
2. Chase, M. W., Christenhusz, M. J., Fay, M. F., Byng, J. W., Judd, W. S., ... & Stevens, P. F. 2016. An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG IV. Botanical journal of the Linnean Society, 181(1), 1-20.
3. Kevan, P. G., Clark, E. A., & Thomas, V. G. 1990. Pollination: a crucial ecological and mutualistic link in agroforestry and sustainable agriculture.
4. Yousaf, Z. 2016. Palynology a marker for the identification of medicinally important arboreal species from province Punjab.
5. Plitmann, U., & Levin, D. A. 1990. Breeding systems in the Polemoniaceae. Plant Systematics and Evolution, 170(3), 205-214.

6. Cruden, R. W. 1977. Pollen-ovule ratios: a conservative indicator of breeding systems in flowering plants. Evolution, 32-46.
7. Cruden, R. W. 2000. Pollen grains: why so many? Plant Systematics and Evolution 222: 143-165.
8. Alemida, M. R. 1996. Flora of Maharashtra, Vol. 1. Orient Press, Mumbai. 294 pp.
9. Singh, N. P., & Karthikeyan, S. 2001. Flora of Maharashtra state (Vol. 1, p. 898). Calcutta: Botanical Survey of India.
10. Dhore, M. A. 1986. Flora of Amravati district with special reference to the distribution of tree species. Amravati University, Amravati, Maharashtra.
11. Yadav, S. R., & Sardesai, M. M. 2002. Flora of Kolhapur district. Shivaji University.
12. Dafni, A. 1992. Pollination ecology: a practical approach (pp. xv+-250).
13. Radford AE, Dickison WC, Massey JR & Bell CR. Vascular plant systematics. New York: Harper and Row; 1974. pp. 105-8. 61.
14. Bendre AM & Kumar A. A textbook of practical botany II. India: Rastogi; 2009. p. 452
15. Nair, P. K. K., & Rastogi, K. 1963. Pollen production in some allergenic plants. Current Science, 32(12), 566-567.
16. Tidke, J. A., & Dharamkar, R. O. 2003. Flowering phenology, pollen production and insect behaviour in some ornamentals.
17. Tidke, J. A., & Patil, G. V. 2000. Floral biology and pollination of *Crotalaria sericea* Retz.
18. Annahwi, D., Ratnawati, R., & Budiwati, B. 2017. Flower and Fruit Development Phenology and Generative Reproduction Success of *Hibiscus rosa-sinensis* spp. YRU Journal of Science and Technology, 2(2), 19-30.
19. Johri, A. 2021. Phenological Events of *Malvaviscus arboreus* Dill. Ex Cav. (Malvaceae) in Contemporary Global Issues and Challenges edited by Dr. Bhartendu Gautam and Dr. Vikas Kumar Sharma. Sunrise Publisher, Jaipur, 1st Edition 2021. Pp 27-33.

Ind. J. Aerobiol., Vol. 39, No. (1), pp. 53-63 [2026] ISSN No. 0971-1546

Research Article

AEROBIOLOGICAL INSIGHTS INTO AIRBORNE FUNGAL SPORES AND SOYBEAN DISEASE MANAGEMENT IN INDIA

DEEPALI SAWANT AND VAISHALI THAKUR*

POSTGRADUATE DEPARTMENT OF BOTANY, FERGUSSON COLLEGE (AUTONOMOUS), PUNE 411004, MAHARASHTRA, INDIA

CORRESPONDING AUTHOR: vaishali.thakur@fergusson.edu

Soybean is one of the most widely cultivated crops in India and plays a vital role in meeting the country's demand for edible oil and animal feed. However, its productivity is frequently threatened by fungal diseases, particularly those spread by airborne spores. Aerobiological research has become an essential tool for understanding the behaviour of airborne pathogens and supporting effective disease management. The present paper provides a comprehensive analysis of airborne fungal spores in Indian soybean fields, with particular emphasis on the geographical dynamics of pathogen dispersal, aerobiological sampling methods, and techniques for spore identification and quantification. It also presents the principal airborne fungal pathogens affecting soybean, including *Cercospora, Phakopsora,* and *Alternaria*. The evidence indicates a strong association between airborne spore concentrations and disease incidence, demonstrating that aerobiological monitoring can be used to predict disease outbreaks. The paper further highlights the value of integrating aerobiological data into disease management strategies and emphasises the need for continuous monitoring of airborne pathogens in Indian soybean-growing regions. The findings consistently demonstrate the influence of meteorological variables on fungal spore activity: ascospores were strongly associated with precipitation, basidiospores with minimum temperature, whereas conidiospores showed no clear meteorological preference.

Key Words: Soybean, Airborne fungal spores, Fungal diseases, Pathogen dissemination.

Received: 06.04.2026 Revised: 24.04.2026 Accepted:08.05.2026

INTRODUCTION

Soybeans are among the most widely cultivated seed crops in India and rank fourth globally. This crop is predominantly cultivated in Madhya Pradesh, Maharashtra, Rajasthan, and Andhra Pradesh, which together account for approximately 85% of India's total soybean production[1]. The primary aim of soybean cultivation in India is to satisfy the increasing demand for edible oils and animal feed. The soybean crop is affected by over 100 pathogens, including 66 fungi, 6 bacteria, 8 viruses, and 7 nematodes, resulting in significant yield losses globally, estimated at over 7 million tonnes due to diseases alone[2]. Such an environment leads to substantial output losses, with reductions of up to 90% at certain sites for specific diseases, such as soybean rust and downy mildew, which are particularly devastating in regions like India. India plays a crucial role in the global soybean market; however, its potential output is consistently threatened by fungal diseases, particularly those transmitted through airborne

spores. Diseases such as soybean rust, induced by *Phakopsora pachyrhizi*, combined with leaf spot and stem rot, have been recognized as significant contributors to output losses[3].

The analysis of airborne biological variables in soybean fields across India is crucial, given the growing importance of soybean as a profitable crop in regions such as Punjab, Haryana, and Uttar Pradesh[4]. This study aimed to detect the different types and amounts of airborne fungal spores in soybean fields, providing essential insights into their possible impact on crop health and informing future agricultural strategies. Aerobiological research in India began in the 1873[5], with notable research institutions sub-sequently developed in various places in our country[5]. The use of volumetric spore traps or impaction samplers enables the creation of detailed profiles of fungal spore populations across diverse environments and with seasonal variation[6]. By analyzing diverse types and concentrations of fungal spores in the atmosphere at different times and locations, experts can assess the potential risk of fungal diseases affecting crops, forest ecosystems, and urban areas, thereby conserving resources and reducing crop losses. This information is essential for predicting potential disease outbreaks and for developing targeted management strategies[7]. Experts can assess the potential risk of fungal infections in agricultural areas, forests, and urban environments by analyzing the diverse types and quantities of fungal spores present at different times and locations[8]. Algorithms and models are being developed to predict fungal spore concentrations by examining meteorological conditions, vegetation parameters, and historical data[9]. These models have considerable potential to enhance the prediction of and response to fungal-related challenges across agriculture and public health.

Role of Aerobiology in soybean disease management

Aerobiology plays a crucial role in disease control by developing forecasting models that can predict disease outbreaks using environmental and aerobiological data. These models employ data on spore concentration, wind speed, humidity, and temperature to predict the timing and location of future disease outbreaks. A forecasting model for soybean rust was created using aerobiological data collected in Central India[10]. The software precisely predicted rust outbreaks up to two weeks in advance, allowing farmers to apply fungicides before the disease could spread.

Aerobiology, which examines the dynamics and characteristics of airborne biological particles, such as fungal spores, has emerged as a significant tool for understanding crop disease epidemiology[11]. Given India's high humidity and prolonged monsoon season, which favor fungal growth and dispersal, understanding aerobiological patterns in soybean fields is essential for timely disease management[12]. Results from various studies emphasize the importance of integrating airborne data into disease management approaches. The study demonstrating that fungicide application guided by aerobiological monitoring significantly reduced the severity of rust epidemics in soybean fields[3]. The research demonstrated that fungicides were most effective when applied during periods of high spore concentrations, thereby preventing the disease from infecting healthy plants.

STUDY AREA AND SAMPLING DESIGN

Aerobiological research has been conducted across diverse soybean cultivation areas in India, each with distinct environmental factors that influence the dissemination of airborne diseases. These investigations offer significant insights into the geographical dynamics of pathogen dissemination and outbreaks.

Central India, encompassing the states of Madhya Pradesh and Maharashtra, is a major soybean-producing region. In Madhya Pradesh, the research focused on the districts of Ujjain and Indore. In Maharashtra, the selected districts were Latur, Pune, and Nashik. Both states are highly significant for soybean production and have reported frequent outbreaks of fungal diseases, particularly during the monsoon season when conditions are optimal for spore dispersal[13]. Aerobiological research in this region indicates that concentrations of airborne pathogens, including rust spores and bacterial aerosols, peak during the monsoon season, when environmental conditions are optimal for disease proliferation. A multi-year aerobiological survey performed in Madhya Pradesh, focusing on the seasonal dispersion of rust spores[14]. A preliminary survey conducted in the Latur district identified the airborne fungal flora associated with soybean fields, highlighting the need for continuous monitoring and management of airborne diseases to mitigate crop losses[15].

Aerobiological studies in northern India, particularly in soybean-producing areas such as Uttar Pradesh and Punjab, have focused on the influence of wind on the dissemination of pathogens. Researchers have shown that elevated wind velocities in the pre- and post-monsoon periods enhance the long-range dissemination of rust spores and powdery mildew conidia. A study conducted in Uttar Pradesh revealed that wind significantly influenced the dissemination of soybean rust, with spore concentrations peaking in fields located downwind of affected regions[16]. This research highlighted the necessity for regional aerobiological surveillance to anticipate the dissemination of airborne infections and prevent disease outbreaks.

Aerobiological research in southern India, particularly in Karnataka and Andhra Pradesh, where soybean is cultivated, has focused on the effects of rainfall and humidity on disease spread. These places experience elevated humidity during the monsoon season, creating conditions conducive to the spread of diseases such as bacterial blight and downy mildew. In 2016, an aerobiological investigation was conducted in fields in Karnataka to examine the influence of humidity on the dissemination of bacterial blight. Research indicates that atmospheric bacterial levels peak after intense rainfall, leading to widespread infections in soybean crops[17].

TYPES OF AIR SAMPLERS

The primary tool used for air sampling is the Tilak Air Sampler, an electrically operated device designed for continuous air sampling. This sampler can trap airborne spores for a specified period, typically 8 days, enabling both qualitative and quantitative analyses of aerospora. It operates at approximately 2 m above ground level to ensure effective sampling of the air surrounding soybean plants[18]. In addition to

Table 5.1: The data on the soybean diseases reported on various areas in India

Sl. No.	Specific objective	Pathogenic fungal spores	Air sampler	Sampling period and place	Sampling height	Conclusions	Findings
1.	To conduct fungal survey in the soybean (*Glycine max*) field to analyze the aeromicroflora population, including fungal spores, pollen, insect parts.	*Alternaria, Cladosporium, Cercospora, Curvularia,* and *Helminthosporium*.	Tilak air sampler	The Kharif season occurred from June 25 to September 30, 2019. Rajuri, Dist. Beed, Maharashtra, India.	1 meter	The researchers conducted a fungal survey in a soybean (*Glycine max* L.) field. A total of 61 fungal spore types were identified, with *Cladosporium* (14.28%) and *Alternaria* (11.37%) being the most dominant.	A wide variety of fungal spores were present in soybean fields during the Kharif season, 61 types identified. *Cladosporium* and *Alternaria* were the most dominant spores, indicating their prevalence in the region's air spora[20].
2.	To understand the incidence and prevalence of airborne pathogenic fungal spores affecting soybean crops, particularly during the Kharif season, and to establish a disease forecasting system.	*Alternaria, Corynespora, Cercospora, and Colletotrichum*	Tilak air sampler	The kharif season is from June to October 2021-2022 in Niphad Tehsil, Nashik, Maharashtra, India.	1 meter	Improved understanding of airborne fungal spores and their correlation with weather changes, field operations, plant growth, and disease incidence.	Airborne pathogenic fungal spores cause diseases in soybean crops, particularly during the Kharif season[21].
3.	The investigation aimed to analyze fluctuations in spore concentration across different growth stages of the soybean crop.	*Cercospora, Alternaria, Curvularia, and Helminthosporium*	Tilak Air sampler	From June 20 to October 15, 2016, at Udgir District, Latur, Maharashtra, India.	4 feet	*Cercospora* spores in soybean fields was significant (12138 spores/m^3) – a high potential for disease incidence. The various fungal diseases like leaf spot affect soybean crops,	The study found that the percentage contribution of pathogenic spores was highest in October and lowest in September, suggesting seasonal variation in disease risk[22].

Contd.

Contd. Table 5.1

Sl. No.	Specific objective	Pathogenic fungal spores	Air sampler	Sampling period and place	Sampling height	Conclusions	Findings
4.	To understand the relationship between meteorological parameters and the growth of *Glycine max* (L.) Merr. crops, particularly during the summer and kharif seasons.	*Alternaria, Cercospora, Phakopsora,* and *Oidium*	Tilak Air Sampler.	Summer (February 2021 to May 2021) and Kharif (June 2021 to September 2021) at Pune, Maharashtra, India.	1 meter	73 biocomponents were identified in the summer and 98 in the kharif, with Deuteromycotina as the dominant group. Climatic factors play a crucial role in disease outbreaks. Increased humidity can lead to higher concentrations of airborne pathogens that trigger such outbreaks.	Fungal spore concentration was significantly higher during the kharif season than the summer season, peak in August. Temperature, RH, rainfall, and wind velocity, significantly influence the development, release, and dispersal of spores[23].
5.	To study airborne fungal spores in village localities of the Pondicherry region, and to determine the influence of climatic factors on fungal spore distribution.	*Aspergillus, Penicillium.*	Burkard Personal Volumetric Sampler	2015–2016 (One year, 15 day interval) village localities, Pondicherry.	(Approx. 1–1.5 m)	*Aspergillus* and *Penicillium* were predominant due to Wide host range, Environmental adaptability, Opportunistic nature. Noon hours are most favorable for spore dispersal. Aeromycoflora variation observed among different villages.	The high diversity of airborne fungi in village localities, Pondicherry region, with huge *Aspergillus, Penicillium.* Maximum spore counts during winter and noon hours, strong influence of environmental factors on spore distribution[24].

the Tilak Air Sampler, other air-sampling devices may be used for comparative analysis, including the Burkard Seven-Day Spore Trap[19], which collects spores on adhesive tape and is widely used to monitor airborne pollen and fungal spores.

SAMPLING PROCEDURE

Aerobiological sampling was conducted using a Tilak air sampler, which is a widely recognized device for capturing airborne spores and pollen in agricultural fields[18]. In both Madhya Pradesh and Maharashtra, the sampling duration covered the entire soybean growing seasons, Kharif from June to September, and summer from January to April. Slides were replaced weekly to capture variations in spore concentrations during different stages of crop growth and disease progression[25]. After eight days, the sampler was turned off, and the drum containing the cellophane tape was carefully removed. Spores collected from these regions were transferred onto adhesive-coated slides and examined microscopically.

The Burkard volumetric portable air sampler, produced by Burkard Manufacturing company in Rickmansworth, Hertfordshire, UK, functions with a nominal air throughput of ten liters per minute. The glass transparencies were then marked accordingly. A thin layer of high-quality red-stained glycerine jelly was applied to effectively capture the pollen and fungal spores. The slide was then placed into the Burkard sampler and allowed to function for about 15 minutes each day. The exposed region of the microslide has been covered with a 24 × 24 mm cover glass and examined under a light microscope[26].

SPORE IDENTIFICATION AND QUANTIFICATION

After collection, slides from the sampler were examined microscopically. Spores were identified based on morphological characteristics, such as size, shape, and surface texture, using standard taxonomic keys for fungal spores[18]. Spore identification was based on morphological features (size, shape, and surface ornamentation) and molecular techniques (PCR amplification of the ITS region) to confirm spore types that were difficult to identify morphologically[27]. Compile findings in a comprehensive report detailing the spore types identified, their concentrations, and any observed relationships with disease incidence in soybean crops. The spore counts of major pathogens affecting soybean crops, including *Cercospora, Alternaria, Septoria,* and *Phakopsora*, were quantified. Spore counts were expressed as the number of spores per cubic meter of air (spores/m^3)[28].

Disease spread and prevention strategies, such as those used for frogeye leaf spot (*Cercospora sojina* Hara), are characterized by dark leaf spots that can severely affect photosynthesis, leading to reduced yields. *Alternaria* Leaf Spot (*Alternaria alternata* (Fr.) Keissl) is a disease that manifests as dark, circular spots on leaves and is commonly seen during the vegetative stage of the soybean plant. It thrives in wet conditions and can spread rapidly, causing significant crop damage if not managed effectively.

DISEASE INCIDENCE

Observations in the field indicated that the highest levels of spore concentration frequently occurred one to two weeks before the appea-

rance of disease symptoms. In late August, elevated spore counts of *Phakopsora pachyrhizi* in Madhya Pradesh subsequently correlated with the emergence of rust symptoms in early September. The relationship between spore concentrations and disease severity was notable in this region, with soybean rust severity showing a strong association with *Phakopsora* spore counts ($r = 0.84$, $p < 0.05$)[29].

Weather conditions influence the sporulation, dissemination, and deposition of spores, and their elements are interrelated. Warm and arid conditions promote the growth, sporulation, and spread of *Cladosporium, Epicoccum,* and *Alternaria* conidia. Warm, humid weather positively correlates with the incidence of many diseases. A few of these are Alternaria leaf spots, which are caused by Alternaria alternata, a necrotrophic fungus[21]. Alternaria is detected from pre-sowing to crop harvest, with the highest concentrations recorded during the Kharif season. The peak daily concentration of conidia from the above-mentioned genera often occurs at midday and during the afternoon, coinciding with the highest temperatures and lowest humidity levels[23].

In Maharashtra, symptoms of leaf spot, attributed to *Cercospora* spp., emerged shortly after spore concentrations peaked in late August. The severity of leaf spots exhibited a strong correlation with the concentration of *Cercospora* spores. Studies conducted in soybean growing areas of Madhya Pradesh and Maharashtra found a significant correlation between airborne spore counts and rust incidence. Monitoring of airborne biomass showed that rust spore counts increased during the rainy season, when high humidity and low temperatures favor disease development. A multi-year aerobiological study in Eastern India was carried out to identify the seasonal distribution of rust spores and their relationship with climatic variables, such as wind speed, direction, and temperature[30].

DISEASE OBSERVATION

Simultaneously with aerobiological sampling, field observations were performed to monitor the onset and severity of fungal diseases. Disease assessments were conducted biweekly by visually inspecting soybean plants for symptoms of leaf blight, leaf spots, and other fungal diseases. Disease severity was rated on a scale of 1 to 5, with 0 indicating no symptoms and 5 indicating severe infection affecting > 75% of the plant. These data were correlated with spore concentrations to assess the predictive potential of aerobiological monitoring[31].

STATISTICAL ANALYSIS

Statistical analyses were conducted to correlate spore concentrations with meteorological variables and disease incidence. Meteorological data including temperature, humidity, wind speed, and rainfall were collected from local weather stations near the study area. These factors influence spore dispersal and disease dynamics. Analysis of variance (ANOVA) was used to test the effect of seasonal variation on spore counts, and Pearson's correlation coefficient was used to evaluate relationships among environmental factors, spore counts, and disease severity[32]. Additionally, multiple regression models were developed to predict airborne fungal spore concentrations based on meteorological factors, including humidity, temperature,

wind speed, and rainfall. These models aim to provide a predictive framework for disease outbreaks based on spore counts and environmental conditions[33].

DISCUSSION

These results confirmed the significant role of airborne spores in the epidemiology of soybean diseases. Spore concentrations were the highest during periods of favorable environmental conditions, including high humidity and moderate temperatures, which are conducive to fungal growth and dispersal. These findings are consistent with previous studies that identified meteorological factors as key drivers of fungal spore release and movement in crop fields. The periodicity of the predominant spore types peaked during the kharif season, specifically in July. This corresponds to the soybean reproductive stage during the rainy season. The class Deuteromycetes contributed 31 spore types, with *Alternaria* and *Cercospora* being important for initiating leaf spot infections in soybeans. The study revealed that the percentage disease index of *Alternaria* leaf spot increased from the onset of the disease, with maximum severity recorded in crops sown on 18th June and minimum in those sown on 9th July 34.

The research carried out in Latur revealed a *Cercospora* spore concentration of 12,138 spores/m^3. The highest concentration of *Cercospora* was observed at 4970 spores/m^3 of air in September, whereas the lowest was 1442 spores/m^3 of air in August. Meteorological conditions significantly influence spore release and variations in pathogen spore concentrations across crop growth stages. On humid days with intermittent rainfall, disease incidence was higher across more plants, correlating with higher spore concentrations in the air. It indicates that damp weather, low temperatures, and high concentrations of airborne conidia were the most favorable conditions for disease incidence[22]. In both states, combining spore-monitoring data with meteorological information enabled us to predict the onset of major soybean leaf spots. These diseases cause significant yield losses if not controlled promptly[35]. The optimal conditions for the development of frogeye leaf spot include warm temperatures (25-30°C) and prolonged leaf wetness[36].

The study indicates a significant correlation between environmental factors and the severity of *Alternaria* leaf spot disease in soybeans. Higher temperatures positively correlated with disease severity, while increased relative humidity and rainfall negatively impacted it. Specifically, maximum temperatures were positively correlated, whereas minimum temperatures, relative humidity, and rainfall were negatively correlated with disease progression across different sowing dates. The analysis revealed that the disease severity increased with rising temperatures (15.1-34.4°C) and decreased rainfall, particularly during the critical period from September 24 to October 2834. This highlights the importance of weather parameters in managing disease outbreaks.

Across both regions, the spores of *Phakopsora pachyrhizi* (soybean rust pathogen) were the most abundant. In Madhya Pradesh, *Phakopsora pachyrhizi* spores were recorded at high concentrations in late August, coinciding with

the onset of rust. The study found that the soybean rust pathogen, *Phakopsora pachyrhizi*, did not survive during the summer months in Madhya Pradesh, suggesting a seasonal pattern of infection. Uredospores germinated optimally at temperatures of 18-20°C, with disease incidence favored by moderate temperatures and high humidity[29]. The predominance of *Phakopsora* spores is consistent with the region's soybean rust prevalence, further validating the importance of airborne spore monitoring for managing this disease.

CONCLUSION

Considering the socio-economic importance of soybeans in India, understanding aerobic diseases and their relationship with environmental variables is essential for disease control. Aerobiological monitoring provides an invaluable tool for managing fungal diseases in soybean crops in India. By tracking airborne spore concentrations and correlating them with meteorological data and disease incidence, farmers and agricultural scientists can better predict and mitigate the impact of fungal pathogens. The findings of this study suggest that aerobiology could be integrated into existing crop protection strategies, providing a more proactive approach to disease management, particularly by allowing for timely interventions based on spore concentration forecasts. Further research is needed to investigate the impact of climate change on the dynamics of airborne fungal spores and their potential effects on soybean disease management in India.

CONFLICT OF INTEREST

The authors declare no conflicts of interest.

ACKNOWLEDGMENTS

The authors would like to sincerely thank the Principal of Fergusson College (Autonomous), Pune, for encouraging and providing the necessary facilities. The author (VT) is also thankful to BARTI for granting the fellowship under BANRF-2021, Pune.

REFERENCES

1. Dupare, B., Billore, S., & Joshi, O. 2010. Farmers' Problems Associated with Cultivation of Soybean in Madhya Pradesh, India. Journal of Agricultural Science and Technology, 4(6): 71-78. https://www.researchgate.net/publication/315117147.
2. Sinclair, J. B. & Backman, P. A. 1989. Compendium of soybean diseases (J. B. S. and P. A. Backman (Ed.). 3rd edition. APS Press.
3. Negrisoli, M. M., Silva, F. N. da, Negrisoli, R. M., Lopes, L. da S., Souza Júnior, F. de S., Freitas, B. R. de, Velini, E. D., & Raetano, C. G. 2022. Impact of fungicide application timing based on soybean rust prediction model on application technology and disease control. Agronomy, 12(9:2119). https://doi.org/10.3390/agronomy12092119
4. Agarwal, D., Billore, S., Sharma, A., Dupare, B., & Srivastava, S. 2013. Soybean: introduction, improvement, and utilization in India—problems and prospects. Agric Res, 2: 293-300. https://doi.org/10.1007/s40003-013-0088-0.
5. Cunningham, D. D. 1873. Microscopic examinations of air. Government Printing.
6. Martinez-Bracero, M., Markey, E., Clancy, J. H., McGillicuddy, E. J., Sewell, G., & Connor, D. J. O. 2022. Airborne fungal spore review: new advances and automation. Atmosphere, 13(2): 308. https://doi.org/10.3390/atmos13020308
7. Narayanasamy, P. 2011. Microbial plant pathogens: detection and disease diagnosis. This work is part of the series Microbial Plant Pathogens-Detection and Disease Diagnosis (Vol. 1). Springer Netherlands. https://doi.org/10.1007/978-90-481-9735-4.
8. Hernandez, H., & Martinez, L. R. 2018. Relation-

ship of environmental disturbances and the infectious potential of fungi. Microbiology (Reading, England), 164(3): 233-241. https://doi.org/10.1099/mic.0.000620.

9. Vida, M., Foret, G., Siour, G., Couvidat, F., Favez, O., & Uzu, G. 2024. Modeling of atmospheric concentrations of fungal spores: a 2-year simulation over France using CHIMERE. Atmos Chem Phys, 24, 10601-10615. https://doi.org/acp-24-10601-2024, 2024.
10. Johri, K. J., Gupta, K. N., Singh, N., Shukla, D., Singh, A., & Ilyas, T. 2021. SOYBEAN: Collar rot, leaf spot, and rust. In: Today & Tomorrow's Printers and Publishers (pp. 437-450). http://www.indexfungorum.org.
11. Khandelwal, A. 2008. Aerobiology: aspects and prospects. The Palaeobotanist 57:251-255.
12. Singh, B., Delgado-Baquerizo, M., Egidi, E., Guirado, E., Leach, J., Liu, H. & Trivedi, P. 2023. Climate change impacts on plant pathogens, food security, and paths forward. Nature Reviews Microbiology, 10: 640-656. https://doi.org/10.1038/s41579-023-00900-7.
13. Prashnani, M., Dupare, B., Vadrevu, K., & Justice, C. 2024. Towards food security: Exploring the spatiotemporal dynamics of soybean in India. PLOS ONE, 19(5). https://doi.org/10.1371/journal.pone.0292005.
14. Singh, H., Singh, S., Singh, K., Singh, A. & Singh, A. 2023. Integrated management of leaf rust in wheat. Journal of Agriculture, Biology and Applied Statistics, 3(1), 21-27. https://doi.org/10.47509/JABAS.2024.v03i01.03.
15. Lohare, S., Kamble, R., Kareppa, V. S., & Nagpurne, B. M. 2009. Aerobiology of the soybean field at Udgir. Shodh, Samiksha Aur Mulyankan, II(6): 804-805.
16. Singh B. B. & Thapliyal P. N. 1977. Breeding for resistance to soybean rust in India. In: "Rust of Soybean"- the problems and research needs, (Editors: R.E. Ford & J. B. Sinclair) INTSOY series 12, Illinois, 626.
17. Ravikala, K. L. & Nagalakshamma, K. V. 2016. Survey on outdoor airborne fungal spores of Tumkur city, Karnataka state, India. Int J Pharm Bio Sci, 7(1): 575-577.
18. Tilak, S. T., & Kulkarni, R. L. 1970. A new air sampler. Experientia, 26(4): 443-444. https://doi.org/10.1007/BF01896940.
19. Cox, C. S., & Wathes, C. M. (Eds.). 1995. Bioaerosols Handbook (1st Edition). CRC Press. https://doi.org/10.1201/9781003070023.
20. Kshirsagar, J. J., Pachkore, G. L., & Dharasurkar, A. N. 2019. Fungal spores of soybean fields, Rajuri (N), Dist. Beed. Think India Journal, 22: 485-489.
21. Kapadi, M. R., & Pawar, N. B. 2022. Incidence of airborne spores in context to fungal diseases on *Glycine max* L. (soybean) from Niphad tehsil of Nashik district, Maharashtra. Environmental Science Archives, 1(1): 64-69. https://doi.org/10.5281/zenodo.7496787.
22. Lohare, S. D. 2019. *Cercospora* concentration of soybean field at Udgir. International Journal of Scientific Research and Reviews, 8(3): 310-314. www.ijsrr.org.
23. Sawant, D., & Thakur, V. 2023. Meteorological influence on aerobiological investigation over *Glycine max* (L.) Merr. crop field at Pune, India. Ind J Aerobiol, 36(2): 21-28.
24. Nayak, B., Prabhakar, V., & Nanda, A. 2017. Aeromycological studies by volumetric sampler on agar plates in a few village localities of Pondicherry region. Research Journal of Pharmacy and Technology, 10(11): 3701-3704. 10.5958/0974-360X.2017.00671.0.
25. Tilak, S. T. 2010. Aerobiology to astrobiology. Bharati Vidyapeeth Scientific Monograph No. 1.
26. Datta, K., Chatterjee, A., Nigam, Deepa, D., Singh, S. P., & Verma, P. 2012. Recent scenario of airborne pollen in Lucknow, India, with special reference to intra- and interannual, diurnal, and vertical variation. Research and Reports in Biodiversity Studies, 2:1-22. https://doi.org/10.2147/RRBS.S32113.
27. Tekpinar, A. D., & Kalmer, A. 2019. Utility of various molecular markers in fungal identification and phylogeny. Nova Hedwigia. 109. 187-224. 10.1127/nova_hedwigia/2019/0528.

28. Hosseini, B., Voegele, R.T., & Link, T. I. 2023. Diagnosis of soybean diseases caused by fungal and Oomycete pathogens: existing methods and new developments. Journal of Fungi, 9(5): 587. https://doi.org/10.3390/jof9050587

29. Shukla, B. N., Bhargava, P. K., Gupta, M., & Patel, R. P. 2005. Epidemiology and management of soybean rust (*Phakopsora pachyrhyrhizi*). The Indian Journal of Agricultural Sciences, 75(3): 150-153. https://epubs.icar.org.in/index.php/IJAgS/article/view/9334.

30. Chakraborty, P., Gupta-Bhattacharya, S., & Chanda, S. 2003. Aeromycoflora of an agricultural farm in West Bengal, India: A five-year study (1994-1999). Grana, 42(4): 248-254. https://doi.org/10.1080/00173130310016941.

31. Sharma, R. K., Patel, M. M., Patel, D. R., Chaudhari, D. R., & Kumar, V. 2021. Management of foliar fungal diseases of soybean through chemicals and its impact on yield. Indian Journal of Pure & Applied Biosciences, 9(4):192-198. doi: http://dx.doi.org/10.18782/2582-2845.8775.

32. Priyamvada, H., Singh, R. K., Akila, M., Ravikrishna, R., Verma, R. S., & Gunthe, S. S. 2017. Seasonal variation of the dominant allergenic fungal aerosols – One-year study from the southern Indian region. Scientific Reports, 7:11171. https://doi.org/10.1038/s41598-017-11727-7

33. Roy, S., Chakraborty, A., Moitra, S., & Bhattacharya, K. 2017. Monitoring of airborne fungal spore load in relation to meteorological factors, air pollutants, and allergic symptoms in Farakka, an unexplored biozone of eastern India. Environmental Monitoring and Assessment, 189(8): 370. 10.1007/s10661-017-6044-x.

34. Fagodiya, R. K., Trivedi, A., & Fagodia, B. L. 2022. Impact of weather parameters on *Alternaria* leaf spot of soybean incited by *Alternaria alternata*. Scientific Reports, 12(1): 6131. https://doi.org/10.1038/s41598-022-10108-z.

35. Borah, M., & Deb, B. 2022. Fungi causing leaf spot diseases of soybean: Epidemiology and integrated management strategies. International Journal of Economic Plants, 9: 88-94.

36. Camera, J. N., Ghissi, V. C., Reis, E. M., & Deuner, C. C. 2016.The combined effects of temperature and leaf wetness periods on soybean frogeye leaf spot intensity. Semina: Ciências Agrárias, 37(1): 77-84. https://doi.org/10.5433/1679-0359.2016v37n1p77.

Author's guidelines

INDIAN JOURNAL OF AEROBIOLOGY is an OFFICIAL PUBLICATION OF *Indian Aerobiological Society*. This journal considers original articles, short communications, letters to the editor, and review articles/books in the field of Aerobiology, Allergology, Palynology, Biochemistry, Geology, Climatology, Biopollution and allied subjects, for publication.

Contributors must send three copies of the text (ward file), tables (Word file) and figures (maximum 6 figs. in JEPG) etc. along with a floppy disc and they should retain one copy of the manuscript with them as the editor does not accept any responsibility for damage or loss of the manuscript submitted. Manuscript should be type written(double space) on one side of the paper only and a separate sheet should bear the title of the paper, author(s) name, institutional address where the work was done and corresponding author.

Manuscripts are evaluated critically by the member(s) of the editorial board personally or by outside experts chosen by the members. Although manuscripts received will be sent to referee for comments, the decision of the editor will be final. Acceptance of manuscripts for publication is based on: (a) originality of the contribution; (b) proper analysis of the scientific data; (c) clarity of presentation; and (d) ethically acceptable design of the study. Papers are accepted on the understanding that no substantial part of the work has been or will be published elsewhere and once they have been accepted, they become the copyright of the journal.

Authors should submit manuscripts to:

Dr. Swati Gupta Bhattacharya
Chief Editor
INDIAN JOURNAL OF AEROBIOLOGY
Former Senior Professor and Chairperson,
DIVISION OF PLANT BIOLOGY
Bose Institute (Main Campus)
93/1 Acharya P. C. Road
Kolkata-700009, West Bengal, India
Fax: 91-33-2350-6790
E.mail: ***swati@jcbose.ac.in***

The paper should generally be divided into the following heads and the order indicated.

Manuscript

(i) **Summary:** About 3% of the length of the paper but not exceeding 250 words.

(ii) **Introduction:** Should emphasize the reasons for undertaking the study and must be brief.

(iii) **Materials and Methods:** The methods used in the study should be described giving sufficient information to enable the work to be repeated. If an accepted technique has been used or with slight modification, only the reference should be cited mentioning the modification adopted.

(iv) **Results:** This should be concise and the results compiled in tables and figures should not be repeated in the text.

(v) **Discussion:** This should highlight the findings of the results in the light of the relevant literature and should not merely be repetition of results.

(vi) **Acknowledgment:** This should include financial support also.

(vii) **Reference:** References in the text should appear as **numbers** or they may follow author's names in the text if necessary. The reference should be typed on a separate page after the text in numerical order in which they appeared in the text and not in a alphabetical order. The full title of the paper should be given with first and last page numbers. The journal should be abbreviated according to the system adopted by "World list of periodicals". An abstract should be cited only when it is the only source of information.

Example: *Journal*: Sircar, G., Chakraborty, H.S., Saha, B. & Gupta Bhattacharya, S. 2012. Identification of aero-allergens from *Rhizopus oryzae*: an immunoproteomic approach. Journal of Proteomics 77: 455-468.

Books: Lewis, W.H., Vinay, P. & Zenger, V.E. 1983. Airborne and Allergenic Pollen of North America – 254pp. John Hopkins University Press, Baltimore, U.S.A.

Erickson, E. H. & Buchmann, S.L. 1983. Electronics and pollution – In Handbook of Experimental Pollination Biology (Eds. C. E. Johns & R. P. Little), pp 173 van Noestrand Reinhold, New York, U.S.A.

(viii) **Illustraions:** These should be labelled with the figure number and authors name with pencil on the back and the direction identified with arrow. Photograph should be glossy prints of good contrast, suitable for reproduction. The exact magnification of the microphotographs should be given. Captions and legends to figures should be self explanatory and should provide enough information without reference to the text. Their position in the text should also be indicated. All legends should be typed in double space on separate sheets in numerical order.

(ix) **Tables:** Each table should be typed on separate sheet in Arabic numerals and should be compact. Approximate position of each table in the text should be indicated.

Page Proofs: Page proofs will be submitted to the contributors for minor corrections and should be returned to the Editor within 48 hours. Major alterations from the text cannot be accepted.

Book Reviews: Books submitted for reviews in the journal must be sent in duplicate to the Editor. One copy will be retained in the Library of the Society while the other copy will be retained by the Reviewer for his personal use.

(x) **Reprints:** No reprints will be supplied free of cost.

Published by Dr. Swati Gupta Bhattacharya (for and on behalf of Indian Aerobiological Society)
Bose Institute, 93/1 Acharya P. C. Road, Kolkata-700 009

INDIAN AEROBIOLOGICAL SOCIETY (Registration No. S/32742)

Established in 1980 [Website: www.indianaerobiologicalsociety.org]

[Office Bearers and Council Members of the Society]

President

Dr. Surekha Kalkar
Nagpur, Maharashtra

Vice-President

Dr. Shailesh Kumar Jadhav
Raipur, Chhattisgarh

Secretary-Treasurer

Dr. Prashant Gawande
Amravati, Maharashtra

Joint Secretary

Dr. Subrata Raha
Purulia, West Bengal

Editor-in-Chief

Prof. Swati Gupta Bhattacharya
Indian Journal of Aerobiology
Former Senior Professor & Chairperson
Division of Plant Biology, Bose Institute
93/1 A.P.C. Road, Kolkata- 700 009
E.mail: swatigb29@gmail.com, Mobile: 09433270725

Executive Council Members

Dr. A. H. Rajasab
(Bangalore, Karnataka)

Dr. K.S. Ramchandra Rao
(Hyderabad, Telengana)

Dr. J. A. Tidke
(Amaravati, Maharashtra)

Dr. Manas Ranjan Majumdar
(Kolkata, West Bengal)

Dr. Suvarna Patil
(Nagpur, Maharshtra)

Dr. Kashinath Bhattacharya
(Santiniketan, West Bengal)

Dr. B. M. Lall
(Raipur, Chhattisgarh)

Dr. Suvarna Patil
(Nagpur, Maharshtra)

Dr. Shriram Kunjam
(Raipur, Chhattisgarh)

Dr. K. L.Tiwari (Patron)
(Raipur, Chhattisgarh)