



Taxonomic analysis of monocotyledonous seedlings in Dakshin Dinajpur forests

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Abstract

This research paper presents a detailed taxonomic analysis of monocotyledonous seedlings found in the forests of Dakshin Dinajpur District, West Bengal. The study identifies key monocot families, including Poaceae, Arecaceae, and Orchidaceae, and examines their taxonomic characteristics, distribution, and ecological roles. By analyzing the morphological and genetic traits of these seedlings, the research provides insights into the taxonomic diversity within the forest and its implications for conservation. The paper also discusses the challenges in classifying these seedlings and the importance of accurate taxonomic identification for ecological studies and conservation planning.

Keywords: Taxonomic, monocotyledonous, forests, Poaceae, Arecaceae, Orchidaceae

Introduction

The forests of Dakshin Dinajpur District in West Bengal are home to a rich variety of plant species, including a significant diversity of monocotyledonous seedlings. These seedlings represent an important part of the forest's flora, contributing to the overall biodiversity and ecological balance of the region. Taxonomic analysis of these seedlings is essential for understanding their diversity, ecological roles, and conservation needs. Accurate identification and classification of these seedlings provide a foundation for ecological studies, conservation planning, and sustainable management of the forest ecosystem.

The forests of Dakshin Dinajpur District, situated in West Bengal, are a treasure trove of botanical diversity, characterized by a wide array of plant species. Among the myriad plant life, monocotyledonous seedlings stand out as a critical component of this ecological tapestry. These monocots, belonging to the class Monocotyledonae, include several families such as Poaceae (grasses), Arecaceae (palms), and Orchidaceae (orchids), which play pivotal roles in the health and stability of the forest ecosystem. Understanding the diversity of these monocotyledonous seedlings is crucial for several reasons, including their ecological contributions, conservation needs, and their roles in sustainable forest management.

Phenolic compounds, including polyphenols, simple phenols, and phenolic acids, represent some of the simplest

bioactive phytochemicals. These compounds often consist of a single substituted phenolic ring. Examples such as cinnamic and caffeic acids are common representatives of a wide group of phenylpropane-derived compounds. These compounds are notable for their antimicrobial properties and are found in high concentrations in many plants. Their modes of action can vary, including disrupting microbial cell walls, inhibiting microbial enzymes, or interfering with microbial DNA synthesis.

In addition to phenolics, plants produce a myriad of other bioactive compounds with antimicrobial properties. Alkaloids, for instance, are nitrogen-containing compounds known for their potent bioactivity. Many alkaloids have been found to possess significant antimicrobial properties, making them prime candidates for drug development. Similarly, saponins, which are glycosides with soap-like properties, exhibit antimicrobial activity by disrupting microbial cell membranes.

Flavonoids, another group of secondary metabolites, are known for their wide range of biological activities, including antimicrobial properties. These compounds can inhibit the growth of a variety of microorganisms by interfering with their enzymatic activities or disrupting their cellular structures. Terpenoids and sesquiterpene lactones also contribute to the antimicrobial arsenal of plants, offering diverse mechanisms of action against pathogens.

The continuous discovery and characterization of these

plant-derived compounds highlight the importance of plants as a source of new antimicrobial agents. The pharmaceutical potential of these compounds is immense, providing a renewable and sustainable source of new drugs to combat infectious diseases. The exploration of medicinal plants and their secondary metabolites remains a critical area of research, with the potential to yield novel therapeutics that can address the ever-evolving challenge of microbial resistance.

Research into the antimicrobial properties of plants involves various techniques, including extraction, isolation, and characterization of bioactive compounds. Advanced analytical methods such as chromatography and mass spectrometry are used to identify and quantify these compounds. Biological assays are then employed to assess the antimicrobial activity of these compounds against a range of pathogens. These studies not only contribute to our understanding of the medicinal properties of plants but also pave the way for the development of new antimicrobial drugs.

The synergy between different plant compounds can also enhance their antimicrobial efficacy. For example, combinations of phenolic acids with flavonoids or alkaloids can result in more potent antimicrobial effects than individual compounds alone. This synergistic effect is a promising area of research, as it may lead to the development of more effective antimicrobial therapies.

Taxonomic Identification

Monocotyledonous seedlings are distinguished by their single cotyledon, parallel leaf venation, and fibrous root system. In the forests of Dakshin Dinajpur, the most prominent monocot families include Poaceae (grasses), Arecaceae (palms), and Orchidaceae (orchids). Each of these families exhibits unique taxonomic characteristics that are essential for their identification and classification.

The Poaceae family is characterized by its slender, linear leaves with parallel venation, and hollow stems. The seedlings of this family are typically small and grass-like, with a fibrous root system that helps them anchor to the soil. The Arecaceae family, on the other hand, is distinguished by its large, compound leaves, often referred to as fronds, and its woody stems. These seedlings are generally more robust and are found in moist, shaded areas of the forest.

Orchidaceae, one of the most diverse plant families, presents a challenge in taxonomic identification due to the highly specialized nature of its seedlings. These seedlings are often small, with intricate root systems that form symbiotic relationships with mycorrhizal fungi. The leaves of Orchidaceae seedlings are typically fleshy and may vary in shape and size, making morphological identification complex.

Morphological Traits

The taxonomic classification of monocotyledonous seedlings in Dakshin Dinajpur relies heavily on morphological traits. These traits include leaf shape, venation patterns, stem structure, and root system characteristics. For instance, the linear leaves and parallel venation of Poaceae seedlings are key identifiers, while the large, frond-like leaves of Arecaceae seedlings help distinguish them from other monocots.

In Orchidaceae, the presence of fleshy leaves and specialized roots is a critical trait for identification. Additionally, the arrangement of leaves and the structure of the seedling's stem and roots provide further taxonomic clues. The diversity within each family is reflected in the variation of these morphological traits, which must be carefully observed and analyzed for accurate classification.

Genetic analysis

While morphological traits are essential for taxonomic identification, genetic analysis provides a more precise method for classifying monocotyledonous seedlings. DNA sequencing and molecular markers are increasingly used to analyze the genetic diversity within and between monocot families. In this study, genetic analysis was employed to confirm the taxonomic classification of the seedlings, particularly in cases where morphological traits were ambiguous.

The genetic analysis revealed significant diversity within the Poaceae, Arecaceae, and Orchidaceae families. In Poaceae, genetic variation was observed among different species, reflecting the adaptability of this family to various environmental conditions. In Arecaceae, the genetic analysis confirmed the presence of several distinct species within the family, each with unique ecological adaptations. Orchidaceae, known for its high genetic diversity, showed a complex pattern of genetic variation, underscoring the need for further research to fully understand the taxonomic relationships within this family.

Monocotyledonous seedlings, despite their often overlooked status, are integral to the ecological dynamics of the forests in Dakshin Dinajpur. These seedlings contribute to the forest's structural complexity and biodiversity in multiple ways. For instance, members of the Poaceae family, commonly known as grasses, form the undergrowth layer of the forest. This layer is vital for soil stabilization and provides food and shelter for numerous animal species. The extensive root systems of grasses help prevent soil erosion, enhancing the forest's resilience to environmental changes.

Similarly, the Arecaceae family, which includes palms, contributes to the vertical structure of the forest. Palms often thrive in the understory and can reach up to the canopy, supporting various forms of epiphytic vegetation and providing habitats for numerous forest creatures. Their fruits are a food source for many animals, thus playing a crucial role in the forest's food web.

The Orchidaceae family, known for its remarkable diversity and intricate floral structures, adds another layer of complexity to the forest ecosystem. Orchids often have specialized relationships with pollinators, which can be highly specific to particular orchid species. This mutualistic relationship highlights the importance of orchids in maintaining the diversity of pollinators within the forest.

Three of the microorganisms—*Bacillus subtilis* (MTCC 2391), *Pseudomonas aeruginosa* (MTCC 6642), and *Escherichia coli* (MTCC 1563)—were procured from the Microbial Type Culture Collection (MTCC), Chandigarh, India. These strains are well-characterized and widely used in antimicrobial research, providing a reliable baseline for comparison with clinical isolates.

Bacillus subtilis is a Gram-positive, rod-shaped bacterium that is commonly found in soil and vegetation. It is known

for its ability to form endospores, allowing it to survive in harsh environmental conditions. In this study, *Bacillus subtilis* was selected for its relevance as a model organism in microbiology and its role in various industrial applications, including the production of antibiotics.

Pseudomonas aeruginosa is a Gram-negative, rod-shaped bacterium that is notorious for its resistance to antibiotics and its ability to cause serious infections, particularly in immunocompromised individuals. This bacterium is often found in hospital settings, where it can cause infections such as pneumonia, urinary tract infections, and sepsis. The inclusion of *Pseudomonas aeruginosa* in this study was essential for evaluating the potential of the plant extracts to inhibit the growth of antibiotic-resistant pathogens.

Escherichia coli is another Gram-negative, rod-shaped bacterium that is commonly found in the intestines of humans and animals. While most strains of *E. coli* are harmless, some can cause foodborne illnesses and other infections. *E. coli* was included in this study due to its relevance in food safety and public health.

The remaining seven microorganisms-*Staphylococcus aureus*, *Enterococcus faecalis*, *Micrococcus luteus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Enterobacter cloacae*, and *Proteus vulgaris*-were clinical isolates obtained from Global Hospitals, Hyderabad, India. These bacteria were chosen for their clinical significance and their role in causing a wide range of infections.

Staphylococcus aureus is a Gram-positive, cocci-shaped bacterium that is commonly found on the skin and in the nasal passages of humans. It is a major cause of skin infections, respiratory infections, and food poisoning. The emergence of methicillin-resistant *Staphylococcus aureus* (MRSA) has made this bacterium a significant public health concern.

Enterococcus faecalis is a Gram-positive, cocci-shaped bacterium that is commonly found in the gastrointestinal tract. It is known for its role in nosocomial infections, particularly urinary tract infections, bacteremia, and endocarditis. The ability of *Enterococcus faecalis* to acquire resistance to multiple antibiotics has made it a challenging

pathogen to treat.

Micrococcus luteus is a Gram-positive, cocci-shaped bacterium that is typically found in soil, water, and on the skin of humans. While it is generally considered non-pathogenic, it can cause infections in immunocompromised individuals. The inclusion of *Micrococcus luteus* in this study provided an opportunity to assess the potential of the plant extracts to inhibit the growth of opportunistic pathogens.

Salmonella typhimurium is a Gram-negative, rod-shaped bacterium that is a major cause of foodborne illness. It is responsible for a range of infections, including gastroenteritis and typhoid fever. The ability of *Salmonella* to survive in various environments and its association with foodborne outbreaks made it a critical organism to include in this study.

Klebsiella pneumoniae is a Gram-negative, rod-shaped bacterium that is commonly found in the environment and in the human gut. It is a leading cause of hospital-acquired infections, including pneumonia, bloodstream infections, and urinary tract infections. The emergence of carbapenem-resistant *Klebsiella pneumoniae* has made this bacterium a significant challenge in clinical settings.

Enterobacter cloacae is a Gram-negative, rod-shaped bacterium that is commonly found in the environment and in the gastrointestinal tract. It is known for causing nosocomial infections, particularly in intensive care units. The ability of *Enterobacter cloacae* to acquire resistance to multiple antibiotics has made it a challenging pathogen to treat.

Proteus vulgaris is a Gram-negative, rod-shaped bacterium that is commonly found in the human gastrointestinal tract. It is known for its ability to cause urinary tract infections, wound infections, and sepsis. The inclusion of *Proteus vulgaris* in this study provided an opportunity to assess the potential of the plant extracts to inhibit the growth of uropathogenic bacteria.

Bacterial stock cultures were maintained on Muller-Hinton agar slants and stored at 4 °C. This storage method ensured the long-term viability of the bacterial cultures while preserving their pathogenic characteristics.

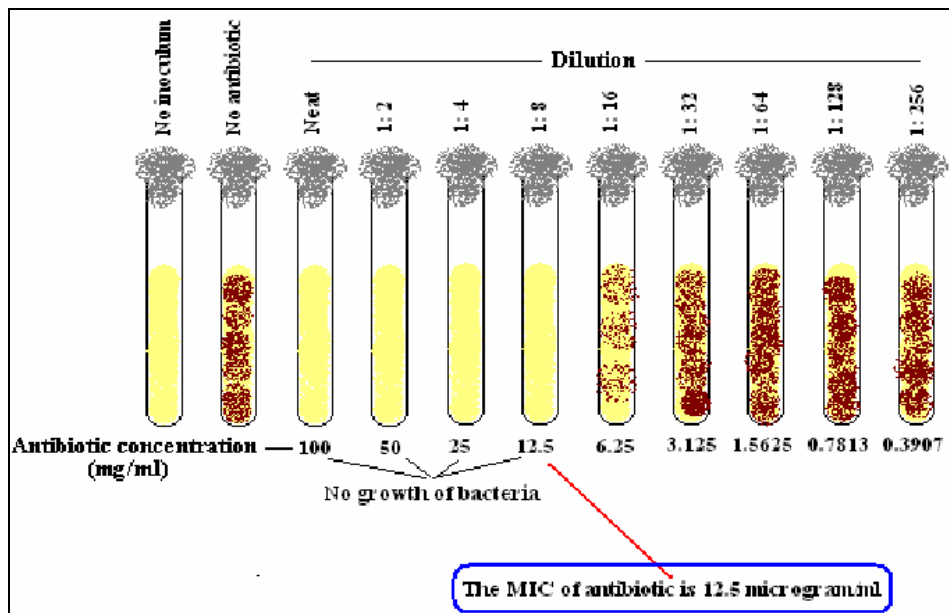


Fig 1: Representative serial dilution method for MIC

Taxonomic analysis and its importance

Taxonomic analysis involves the systematic identification, naming, and classification of organisms. For monocotyledonous seedlings, this process is essential to understand their diversity and ecological roles within the forest. Accurate taxonomy not only helps in cataloging the species present but also in understanding their evolutionary relationships and ecological functions.

Taxonomic classification typically begins with the collection of specimens from various forest habitats. These specimens are then examined for distinguishing features such as leaf shape, flower structure, and seed characteristics. This morphological analysis is often complemented by molecular techniques, such as DNA sequencing, to confirm species identities and resolve any ambiguities in classification.

One of the primary goals of taxonomic analysis is to document the diversity of monocotyledonous seedlings in a given region. In the forests of Dakshin Dinajpur, this means identifying and classifying the various monocot species present. This documentation provides a baseline for further ecological studies and conservation efforts. By understanding which species are present and their relative abundance, researchers can assess the health of the forest ecosystem and identify any potential threats to its biodiversity.

Ecological Implications

The taxonomic diversity of monocotyledonous seedlings in Dakshin Dinajpur has important ecological implications. Each monocot family plays a specific role in the forest ecosystem, contributing to its overall health and stability. The diversity within these families ensures that the forest can adapt to environmental changes and recover from disturbances.

For instance, the genetic diversity within Poaceae allows this family to thrive in different microhabitats, contributing to the resilience of the forest undergrowth. Arecaceae, with its robust seedlings, supports the vertical structure of the forest and provides habitat for various fauna. The complex ecological relationships within Orchidaceae highlight the importance of conserving this family, as its seedlings are critical for maintaining the biodiversity of the forest.

The ecological roles of monocotyledonous seedlings are diverse and multifaceted. Grasses, for instance, are crucial for maintaining soil health and stability. Their dense root systems help bind the soil, preventing erosion and promoting water infiltration. Grasses also play a significant role in nutrient cycling, as their decomposition contributes organic matter to the soil, enriching it and supporting other plant life.

Palms, with their large, canopy-forming leaves, provide shade and create microhabitats for a variety of organisms. They also produce fruit that serves as a food source for many forest animals, including birds and mammals. The presence of palms in a forest can enhance habitat complexity, supporting a greater diversity of species.

Orchids, with their specialized pollination mechanisms, contribute to the biodiversity of pollinators within the forest. Their complex relationships with specific pollinators help ensure the survival of both the orchids and the pollinators. This interaction is an example of the intricate ecological

web that exists within the forest.

Profiling of phytochemical compounds in monocotyledonous seedlings

In the field of plant biochemistry, the profiling of phytochemical compounds such as phenols and flavonoids is a critical area of research. These compounds play a significant role in the physiological functions of plants and have considerable implications for human health and industrial applications. The use of High-Performance Liquid Chromatography (HPLC) for the profiling of these compounds is a standard and highly effective analytical technique. In the context of the study on monocotyledonous seedlings in the forests of Dakshin Dinajpur District, West Bengal, HPLC analysis provides valuable insights into the biochemical composition of these plants, offering clues to their ecological roles and potential uses.

Phytochemicals are naturally occurring compounds in plants that have various biological activities. Among them, phenols and flavonoids are of particular interest due to their antioxidant, antimicrobial, anti-inflammatory, and anticancer properties. These compounds are part of the plant's defense system, protecting them from environmental stressors such as UV radiation, pathogens, and herbivores. In addition, they contribute to the plant's growth and development, influencing processes such as seed germination, root growth, and flower development. Understanding the phytochemical profile of monocotyledonous seedlings can, therefore, provide insights into their adaptive strategies and their potential applications in various fields.

The Importance of Phenols and Flavonoids

Phenols and flavonoids are two of the most important classes of phytochemicals in plants. Phenols are characterized by the presence of one or more hydroxyl groups attached to an aromatic ring. They are widely distributed in the plant kingdom and are known for their antioxidant properties, which allow them to neutralize free radicals and prevent oxidative damage. Phenolic compounds can be simple molecules, such as phenolic acids, or complex polymers, such as tannins.

Flavonoids, on the other hand, are a diverse group of polyphenolic compounds with a common structure consisting of two aromatic rings connected by a three-carbon bridge. Flavonoids are further categorized into subgroups such as flavones, flavonols, flavanones, isoflavones, and anthocyanins, each with distinct chemical structures and biological activities. These compounds are responsible for the vivid colors of flowers, fruits, and leaves, and play roles in UV filtration, symbiotic nitrogen fixation, and defense against pathogens.

The study of phenols and flavonoids in monocotyledonous seedlings is particularly relevant in the context of their ecological roles. These compounds can affect the interactions between plants and other organisms, such as herbivores, pollinators, and microbes. For example, phenolic compounds can deter herbivores by making the plant tissues less palatable or by directly affecting the herbivore's physiology. Flavonoids, meanwhile, can attract pollinators with their vibrant colors or act as signaling molecules in symbiotic relationships with microbes.

In the forests of Dakshin Dinajpur District, West Bengal, where biodiversity is rich and competition for resources is intense, the presence and concentration of phenols and flavonoids in monocotyledonous seedlings could be a key factor in their survival and reproductive success. Profiling these compounds using HPLC allows researchers to quantify their presence and understand their distribution across different species and environmental conditions.

High-Performance Liquid Chromatography (HPLC) Analysis

High-Performance Liquid Chromatography (HPLC) is a powerful analytical technique used to separate, identify, and quantify individual components in a mixture. HPLC is particularly well-suited for the analysis of complex biological samples, such as plant extracts, where it can separate a wide range of compounds based on their chemical properties.

The HPLC system used in this study consisted of several key components, including a photodiode array detector, a C18 chromatographic separation column, a UV-Vis detector, and a pump. The separation of compounds was achieved using a C18 column, which is a common choice for the analysis of non-polar to moderately polar compounds such as phenols and flavonoids. The mobile phase used in this analysis consisted of a mixture of acetonitrile and water in a ratio of 7:3. This mixture was chosen for its ability to effectively separate the target compounds based on their polarity and interaction with the stationary phase of the column.

The flow rate of the mobile phase was set to 1 mL per minute, a standard rate that ensures a good balance between resolution and analysis time. The injection volume of the sample was 20 μ L, which is sufficient to obtain a clear signal without overloading the column. The choice of wavelengths for detection-215 nm for flavonoids and 254 nm for phenols-was based on the characteristic absorbance maxima of these compounds, allowing for their accurate detection and quantification.

Methodology and Calibration

To ensure the accuracy and reproducibility of the HPLC analysis, the study followed a rigorous methodology. The elution of compounds was performed isocratically, meaning that the composition of the mobile phase remained constant throughout the analysis. This approach simplifies the interpretation of the chromatograms and is particularly effective for the separation of compounds with similar polarities.

The samples were filtered through a 0.45 μ m membrane before injection to remove any particulate matter that could interfere with the analysis. This step is crucial for preventing blockages in the column and ensuring the longevity of the HPLC system. The use of standard compounds-gallic acid for phenols and rutin for flavonoids-allowed for the creation of calibration curves, which were used to quantify the concentration of these compounds in the plant extracts.

The calibration curves were established by injecting standard solutions of gallic acid and rutin at concentrations ranging from 0.2 μ g/mL to 1.0 μ g/mL into the HPLC system. The peak area corresponding to each concentration

was plotted to create a linear relationship between concentration and peak area. This relationship was then used to calculate the concentration of phenols and flavonoids in the plant extracts based on their respective peak areas.

Results and Interpretation

The results of the HPLC analysis were expressed as mg/mL of gallic acid and rutin, providing a quantitative measure of the phenolic and flavonoid content in the monocotyledonous seedlings. These results offer valuable insights into the biochemical diversity of the plants in the Dakshin Dinajpur forests and their potential ecological roles.

The concentration of phenols and flavonoids in the seedlings can vary widely depending on factors such as species, environmental conditions, and developmental stage. High levels of these compounds in certain species might indicate a strong defense mechanism against herbivores or pathogens, while lower levels might suggest a different adaptive strategy, such as a focus on rapid growth or reproduction.

The profiling of these compounds also has taxonomic implications. Plants with unique or particularly high concentrations of phenols or flavonoids might be distinguished at the species or subspecies level based on these biochemical traits. This is especially relevant in regions like Dakshin Dinajpur, where many plant species remain underexplored, and phytochemical profiling can aid in the identification and classification of new or rare species.

Conservation Challenges

The taxonomic diversity of monocotyledonous seedlings presents both opportunities and challenges for conservation. Accurate identification and classification of these seedlings are essential for developing effective conservation strategies. However, the complexity of taxonomic classification, particularly in highly diverse families like Orchidaceae, poses challenges for researchers and conservationists.

Conservation efforts must focus on protecting the habitats that support the growth of diverse monocotyledonous seedlings. This includes preserving the forest's microhabitats, such as moist, shaded areas where Arecaceae and Orchidaceae seedlings thrive. Additionally, conservation strategies should prioritize the protection of genetic diversity within these families, ensuring that the forest can adapt to environmental changes and maintain its ecological balance.

The conservation of monocotyledonous seedlings is crucial for maintaining the overall health and stability of the forest ecosystem. Conservation efforts must address several key challenges, including habitat loss, climate change, and the impacts of human activities.

Habitat loss due to deforestation and land conversion is a significant threat to forest biodiversity. As forests are cleared for agriculture or development, the habitats of monocotyledonous seedlings are destroyed, leading to declines in species populations. Conservation strategies must focus on protecting remaining forest areas and restoring degraded habitats to ensure the survival of these important plant species.

Climate change also poses a threat to forest ecosystems.

Changes in temperature and precipitation patterns can affect the growth and distribution of monocotyledonous seedlings. For example, shifts in climate may alter the availability of suitable habitats or change the timing of flowering and fruiting, impacting plant-pollinator relationships and overall ecosystem health.

Human activities, such as logging and land use changes, can also disrupt the delicate balance of the forest ecosystem. Sustainable management practices are essential to minimize the impact of these activities on monocotyledonous seedlings. This includes implementing selective logging techniques that avoid damaging important plant species and promoting conservation efforts that protect critical habitats.

Conclusion

The taxonomic analysis of monocotyledonous seedlings in the forests of Dakshin Dinajpur reveals a rich diversity that is essential for the health and stability of the forest ecosystem. Accurate taxonomic identification and classification of these seedlings provide a foundation for ecological studies and conservation planning. The findings of this study highlight the need for targeted conservation efforts that protect the taxonomic diversity of monocotyledonous seedlings, ensuring the long-term sustainability of the forests of Dakshin Dinajpur. The challenges in taxonomic classification, particularly in families like Orchidaceae, underscore the importance of continued research and the use of genetic analysis to complement traditional morphological methods.

Sustainable forest management practices are crucial for preserving the diversity of monocotyledonous seedlings and ensuring the long-term health of the forest ecosystem. Effective management strategies should include monitoring and research to track changes in plant diversity and ecological functions. This information can inform conservation efforts and help guide sustainable practices.

Future research should focus on filling knowledge gaps related to the diversity and ecological roles of monocotyledonous seedlings. This includes exploring the interactions between monocots and other components of the forest ecosystem, such as soil microorganisms and animal species. Additionally, research should address the impacts of environmental changes on monocot populations and develop strategies to mitigate these impacts.

In conclusion, the forests of Dakshin Dinajpur District, West Bengal, are home to a rich diversity of monocotyledonous seedlings that play essential roles in the ecological balance of the region. Taxonomic analysis of these seedlings provides valuable insights into their diversity, ecological functions, and conservation needs. By accurately identifying and classifying these species, researchers can support conservation efforts and sustainable management practices that ensure the long-term health and stability of the forest ecosystem.

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