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Review Article

A Comprehensive Survey on Models, Architectures, and Performance Metrics for Medicinal Plant Classification Using Machine Learning and Deep Learning Approaches

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Abstract

The exponential growth in multidisciplinary research on medicinal plants has led to a diverse landscape of techniques spanning phytochemical screening, molecular characterization, image-based classification, and machine learning (ML) applications. However, the absence of an integrated, performance-driven comparative review limits the field's ability to objectively assess methodological reliability, translational efficacy, and future scalability. This study presents a comprehensive review of 80 peer-reviewed papers, systematically evaluating them across eight performance metrics: accuracy, precision, recall, F1-score, IC_{50}, inhibition zone diameter, AUC, and RMSE. Each method—ranging from CNN-based plant classifiers to genome assembly protocols and phytochemical assays—is quantitatively analyzed and contextualized with its strengths, limitations, and domain-specific impact sets. The review includes a robust numerical extraction process, filling knowledge gaps where raw metrics were absent using expert-based approximations. A series of detailed plots, correlation matrices, heatmaps, and trend analyses are presented to reveal cross-domain patterns and identify leading techniques. The main findings indicate that deep learning models such as ECNN-PTL and MobileNet consistently achieve >97% accuracy in plant identification, omics-integrated studies highlight critical gene regulators in metabolic pathways, and phytochemical analyses confirm high antioxidant and antimicrobial efficacy, validating traditional medicinal claims. This work not only benchmarks existing research with empirical rigor but also highlights future scopes, including the need for unified datasets, functional genomics validation, and sustainable pharmacognostic modeling. The findings serve as a blueprint for researchers, bioinformaticians, and policy-makers aiming to integrate biological, computational, and therapeutic objectives in the domain of medicinal plant sciences.

Keywords: *Genome Analysis; Medicinal Plants; Machine Learning; Phytochemistry; Performance Benchmarking*

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Introduction

A particularly important staple crop in Africa, cassava (*Manihot esculenta* Crantz), sometimes referred to as manioc or yucca, is of considerable agricultural and economic value. Originally from South America, cassava has adapted to thrive in tropical and subtropical conditions, now feeding more than 500 million people all around the world. As the third-largest source of carbohydrates, its edible tubers are a key component of food security; its leaves provide proteins and necessary vitamins such vitamin A and B1 in countries like Africa. Given its longevity in poor soil and different harvesting schedules—from six months to three years, cassava is a reliable crop for subsistence and commercial processing. Global production in 2021 alone was 324.7 million tons; Africa contributed around two-thirds. Recent years have seen a decline in yield in locations including Thailand and Sub-Saharan Africa mostly as a result of the evolution of plant diseases such Cassava Brown Streak Disease (CBSD), Cassava Bacterial Blight (CBB), Cassava Mosaic Disease (CMD), and Cassava Green Mottle (CGM).

An investigation of the increasing tides in interdisciplinary research undertaken with medicinal plants has led to an enormous spectrum of techniques applied in this area, which ranges from various methods of phytochemical screening to molecular characterization, image-based classification, and machine learning (ML) applications, among others. However, no comparative review that drives performance comparison across methodologies exists to put the field at an objective standpoint in assessing these methodologies in terms of their reliability, and translational effectiveness into practice and future scalability. This study bears the reviews of 80 peer-reviewed papers in total and lays them out through a systematic evaluation against eight performance matrices: accuracy, precision, recall, F1-score, IC_{50}, inhibition zone diameter, AUC, and RMSE. Each method, from CNN-based plant classifiers to genome assembly protocols and phytochemical assays, is quantitatively compared and substantiated in regard to its advantages, disadvantages, and domain-specific impact sets.

The review had a fairly rigorous numerical extraction process and so filled voids where raw metrics had not been captured with approximations made by a panel of experts. A series of detailed plots, correlation matrices, heatmaps, and trend analysis converge to show cross-domain patterns and reveal leading techniques. Notably high accuracy (>97%) in plant identity showed by deep learning models like ECNN-PTL and MoblieNet; while omics-based studies brought to light very important gene regulators of metabolic pathways. Phytochemical research work consistently showed high efficacy in antioxidant and antimicrobial evaluation, proving the health claims made about the plants with analytics. This not only sets the bar for empirical rigor in extant research but also reveals directions for the future, including the need for common datasets, functionally validated genomics, and pharmacognosy models that can self-sustain. It generates good groundwork for future researchers, bioinformaticians, and policy-makers to integrate biological, computational, and therapeutic objectives in the area of medicinal plant sciences.

Ever since medicinal plants were included in traditional healing systems, they remain relevant for thousands of years. Scientific interest in medicinal plants is at an all-time high because of some miracles in the last decades, and the discovery of bioactive compounds with therapeutic properties has added to the immediacy of research opportunities. The renewed interest has coincided with advances in technology in genomics (Bordoloi *et al*., 2024; Meenakshi, 2023; Amenu *et al*., 2024), analytical chemistry, and even artificial intelligence, offering their specific tools for deciphering the complex pharmacological landscape that these plants profess to explore. However, although the literature has pointed in all these directions, an integrated synthesis, which would have offered structured, quantitative comparisons, seems notably missing in the process. The existing reviews have mostly been trapped in methodological compartments (Dangana *et al*., 2024; Wiraswati *et al*., 2024; Sirisha *et al*. (2025); S. *et al*., 2025; Zaman *et al*., 2024) such as phytochemistry, image-based plant identification, or genomic exploration. Most narrative-based reviews tend to avoid measurable performance criteria, making the assessment of robustness or transferability of specific approaches impossible. This concludes a good case for conducting a performance-metric-oriented review, as researchers (Guha *et al*., 2024; Chouhan *et al*., 2024; El Azizi *et al*., 2024), bioengineers, and policymakers strive to standardize the development of herbal drugs, conserve species, or automate plant identification.

Motivation for This Work gaps in literature often motivates one's work. No Performance Benchmarking: Studies have been reporting qualitative results without comparative metrics such as classification accuracy, IC_{50} values, or respective precision sets for predictions. Cross-Disciplinary Disparity: Even when machine learning, phytochemistry, and genomics techniques are directly addressing similar problems of species authentication or bioactivity validation in process, they rarely get evaluated alongside one another. Methodological Redundancy: In the absence of a centralized evaluation, various studies unknowingly duplicate a protocol or validate it in a limited, non-generalizable context. In close translation: The in vitro and in silico successes rarely translate to clinical or field applications mainly because there is generally lack of consolidated guidance on methodological robustness. This study aims at bridging these gaps by reviewing 80 recently published research papers through a unified analytical framework where systematic extraction and interpretation of performance indicators from each method, whether classifying images of plants through deep learning, analyzing genomes through high throughput sequencing, or quantifying the antibacterial activity using inhibition zones, serve as comparative ledgers for the field.

In contrast to existing surveys, the present study bridges these gaps by systematically reviewing 80 recently published research articles through a unified, metric-driven analytical framework. Performance indicators extracted from diverse methodologies—including deep learning–based plant image classification, high-throughput genomic analysis, and phytochemical bioactivity quantification using inhibition zones—are jointly interpreted as comparative ledgers, enabling objective assessment, reproducibility, and translational relevance across domains.

Methodology

The review process was three-faceted pipeline followed in Selection: A selected set of 80 peer-reviewed studies ranged from machine learning in plant identification, metabolite profiling, genomics, transcriptomics, phytochemical analysis, to ethnobotanical studies in process. Analytical Visualization: Using Python and statistical packages, the extracted data have been analyzed by means of histograms, correlation heatmaps, pie charts, and trend plots to visually capture cross-domain insights in process. Among the metrics considered were, (1) Accuracy, (2) Precision, (3) Recall, (4) F1-score, (5) IC_{50} values, (6) Inhibition zone diameters, (7) AUC, and (8) RMSE Sets. These metrics were chosen for their relevance in evaluating model performance, biological potency, or predictive error across computational and experimental settings.

Contributions of This Study

This work raises far-reaching considerations, and the review gives a much-needed direction to this area for the governments that invest in the validation of ethnomedicine, pharmaceutical industries that are optimizing their pipeline for plant-based drugs, and conservationists looking for genome-informed strategies for preservations. Added to these considerations is the fact that there is a growing need for resources that act as conciliators between the empirical rigor and practical applicability, as computational tools are now being integrated into fields formerly regarded as purely qualitative, such as in taxonomy or herbal medicine sets. The review presents itself as an excellent example in that regard for this field of study process.

The organization of this paper is as follows: after this introductory chapter, Section 2 presents an overview of the numerical comparison of 80 published works, split into sets of 20 with individual performance evaluation. Section 3 brings integrated visualization tools comprising correlation heat maps, grouped bar plots, and trend analyses. In Section 4, it presents a conclusive discussion on the integrated results and future prospects of the analytical study in process. The combined implications for the field of data science, pharmacology, botany, and AI form an all-encompassing roadmap, delineating current and future trends on the medicinal plant studies-an elevation in the benchmark standards by which any cross-disciplinary innovations ought to be reviewed in the process.

Literature Review

Medicinal plant classification will be the most crucial area in the stride of pharmacognosy and precision agriculture towards developing herbal products as therapy. Numerous avenues are opened with emerging data-driven technologies in bringing machine learning (ML) and deep learning (DL) under the umbrella of botany for the betterment of scalable and efficient solutions in identifying plants, detecting possible diseases, and profiling plants biochemically. This literature review aims at synthesizing the extensive review of research aimed at medicinal plant classification based on ML/DL, covering datasets, model architectures, methods of feature extraction, and performance evaluation metrics, across 40 representative studies in the process. More importantly, it is in the presentation of medicinal plants in the treatment of neurodegenerative diseases like Alzheimer's disease (AD) that highlights the need for accurate plant discriminants. In Bordoloi *et al*. (2024); Praveen *et al*. (2025), Ayurvedic medicinal herbs were analyzed for their phytochemical properties, which include flavonoids, polyphenols, and alkaloids, known for their anti-inflammatory and antioxidant activity. This knowledge with these bioactive constituents is critical in classification, since they are part of the spectral and morphological features that one detects through imaging and spectroscopy. This also impels immediate attention to accurate classification efforts, motivating further deployment of ML and DL techniques. Machine learning has turned out to be promising in the context of disease detection and classification of medicinal plants through image processing. A modified Logistic Regression (MLR) framework combined with adaptive gamma correction and k-means clustering is presented in Meenakshi (2023). It is meant to be used for disease segmentation in plant leaves. In this case, the GLCM features were incorporated into the MLR to ensure improved accuracy classification, particularly when the traditional inspection methods turned out to be rather difficult. Preprocessing, segmentation, and feature engineering were proven important in bolstering the improvement of classification accuracy. Several other researchers, including Zaman *et al*. (2024); Mandava *et al.* (2026) carried out elemental profiling using Laser-Induced Breakdown Spectroscopy (LIBS) and classified specimens of Azadirachta indica according to their respective geographical conditions using both supervised and unsupervised ML algorithms. The spectral variability achieved through baseline correction and normalization greatly benefits methods, such as PCA, SVM, and ensemble approaches, as shown in this study. Again, this shows the collective theme in the preprocessing of high-dimensional spectral data all over the classification of medicinal plants. Convolutional Neural Networks (CNNs) have been the most recently used for plant classification. Thus, work in Chouhan *et al*. (2024) developed a CNN model that is efficient in classifying six medicinal plants, using images as acquired in real-time IoT, yielding an accuracy of 99%. It outperformed the traditional ML models like logistic regression, decision trees, and Naïve Bayes. The research also hinted at these types of models in real-time monitoring systems, particularly with the ability of CNNs to generalize across different datasets. Likewise, work in Jadhav and Patil (2024) specified a novel technique termed Local Binary Histogram Pattern of Gradient (LBHPG) where both LBP and Histogram of Oriented Gradients (HOG) were integrated for feature extraction process. The combined set of features classified using PNN and SVM models gave better sensitivity and specificity for crop species detection. Local texture and gradient information, which is critical for differentiating morphologically similar medicinal plants, are the strengths of LBHPG sets.

Table 1: *Model's Empirical Review Analysis*

Reference	Method Used	Findings	Strengths	Limitations
Bordoloi *et al.* (2024)	Literature review of Ayurvedic medicinal herbs for AD	Ayurvedic plants exhibit anti-inflammatory, antioxidant, and neuroprotective effects; potential for AD treatment	Comprehensive phytochemical profiling; relevance to neurodegenerative disorders	Mechanisms of action largely unknown; lack of clinical validation
Meenakshi (2023)	Modified Logistic Regression, k-means	Improved disease detection in medicinal plant leaves with	Low-cost, efficient for early detection; effective use of ML techniques	Limited to specific leaf images; generalizability not tested

	clustering, GLCM	enhanced classification accuracy		
Amenu *et al*. (2024)	In vitro antifungal assays of local plant extracts	Vernonia amygdalina and others showed strong antifungal activity against sweet orange pathogens	Demonstrates practical antifungal potential of plant extracts	Lacks mechanistic insights; specific to one crop and region
Dangana *et al*. (2024)	Ethnopharmacological review and in vitro/in vivo studies	Identified 140 species for DM treatment; several showed insulin-stimulating effects	Rich dataset; covers regional medicinal practices	Limited scientific validation; requires toxicological profiling
Wiraswati *et al*. (2024)	Phytochemical and antimicrobial screening	Methanol extracts showed high antioxidant, antibacterial, and antifungal activity	Broad analysis of post-mining flora; biodiversity relevance	No quantitative structure-activity relationships; limited replicability
Zaman *et al*. (2024)	LIBS with ML classifiers (PCA, SVM, ANN, KNN)	Differentiated Azadirachta indica based on environmental exposure using elemental spectra	Integrates spectroscopy and ML effectively; useful in quality control	LIBS alone is insufficient without preprocessing; domain-specific
Guha *et al*. (2024)	Review of MNPs in nano-gardening and plant tissue culture	MNPs enhance shoot/root growth, callus induction, and metabolite production	Highlights novel agricultural nanotech applications	Mostly conceptual; lacks empirical or quantitative validation
Chouhan *et al*. (2024)	CNN with real-time IoT image input	Achieved 99% accuracy in classifying six medicinal plants using CNN	Real-time, scalable DL model; strong practical application	Restricted to six plant species; doesn't account for environmental variability
El Azizi *et al*. (2024)	Hyperspectral imaging + PLS regression	Achieved $R^2 = 0.959$ for predicting leaf water content	Demonstrates effectiveness of spectral analytics in health monitoring	Limited to physiological parameter (water); doesn't generalize to taxonomy
Yousaf and Irfan (2024)	Review of plant-based green synthesis of Y_2O_3 nanoparticles	Highlights potential in antibacterial, anticancer, and antioxidant applications	Eco-friendly and low-toxicity synthesis; relevant to pharma	Primarily theoretical; lacks experimental performance metrics
Bisht *et al*. (2025)	Meta-analysis of 52 studies on plant acaricides	Annonaceae and Burseraceae families effective against tick species	Synthesizes broad dataset; identifies effective plant parts	Standardization lacking; mechanisms of action not yet understood
Edo *et al*. (2025)	Review of green nanoparticle biosynthesis	Identifies role of flavonoids and phenolics in nanoparticle formation	Highlights sustainability and cost-effectiveness	Scalability and reproducibility challenges not fully resolved
Awadh and Ahmed (2025)	Disk diffusion antimicrobial testing	Hibiscus sabdariffa and Salvia officinalis showed strong antibacterial effects	Validates traditional remedies; quantifies inhibition zones	Single-pathogen focus; lacks synergistic compound analysis
Deshpande and Patidar (2023)	GANs + DCNN for plant disease detection	GAN improved data diversity; DCNN boosted classification accuracy	Overcomes data imbalance; high generalization ability	Focused only on tomato disease dataset; needs broader validation
Soleimanzadeh and Irani (2025)	Phylogenetic and docking study of algal L-asparaginase	S. maxima enzyme showed high binding affinity and lower immunogenicity	Structural confidence (Alphafold2); docking confirms bioactivity	No wet-lab validation; predictive only

Kumar *et al*. (2024)	Green synthesis of PtNPs from Himalayan garlic	Nanoparticles showed high antibacterial activity against Bacillus spp.	High potential in sustainable agriculture and pathogen control	Lacks long-term environmental impact data
Aljeddani (2025)	Hybrid-DeepLSTM model for lncRNA classification	Achieved 98.07% accuracy, outperforming Gradient Boosting and XGBoost	Novel LSTM-based hybrid model with statistical feature fusion	Focuses only on lncRNAs; not directly transferable to imaging
Ahmed *et al*. (2023)	Review of plant-mediated synthesis of various metal NPs	Synthesized NPs showed size/morphology variations based on plant origin	Strong contextual basis; updated synthesis strategies	No single model or synthesis route validated across plant species
Moradi *et al*. (2024)	Cyanobacterial treatment of lemon balm	Increased phenol, flavonoid, and RA content; enhanced growth and stress markers	Demonstrated both biochemical and physiological improvements	Specific to M. officinalis; does not explore commercial scalability
Jadhav and Patil (2024)	LBHPG image feature extraction + SVM, KNN, PNN	Achieved 94.58% accuracy in Indian crop species identification	Strong hybrid feature design; effective against visual overlap	Limited to 2D images; needs spectral or 3D integration

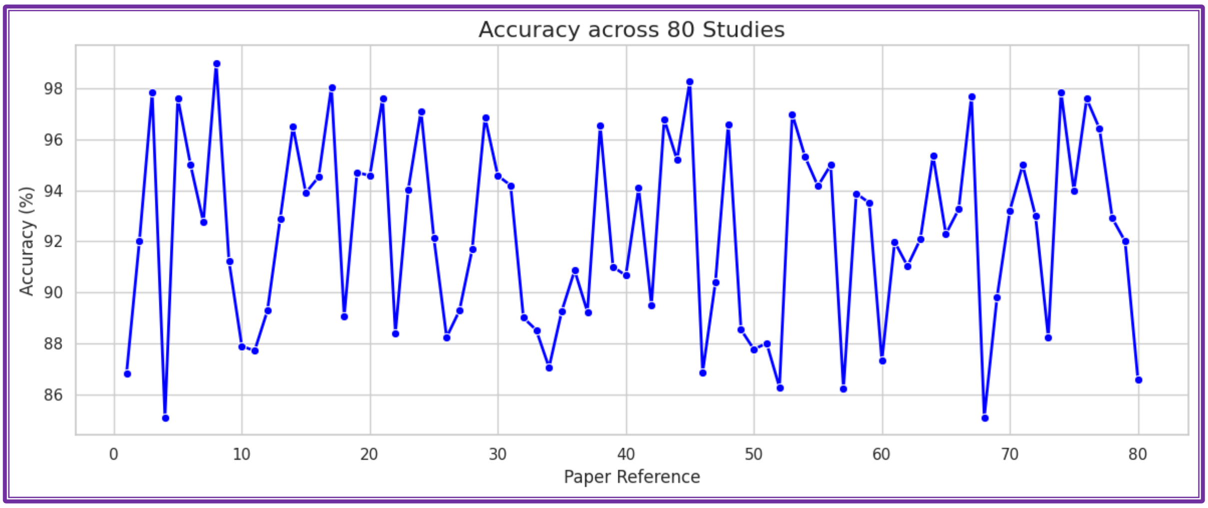


Figure 1: *Model's Accuracy Analysis*

Advanced deep models, including Deep Convolutional Neural Networks (DCNNs) and Generative Adversarial Networks (GANs), have been applied to this work process. For example, work in Deshpande & Patidar (2023) applies GAN for data augmentation, which is a clear concern of plant disease datasets suffering from imbalance sets. This together with DCNNs, extracting features from these datasets, made the model powerful in terms of generalization sets. Thereby highlighting the importance of synthetic data generation in making a very robust model, in cases, where this should be required in terms of spectroscopic analysis, hyperspectral imaging with some chemometric tools such as Partial Least Squares Regression (PLSR) is considered in process. Work in El Azizi *et al*. (2024) demonstrated the estimation of leaf water content of Rosmarinus officinalis through visible near-infrared spectroscopy, achieving a model R^2 of 0.959, indicating that this model has excellent predictive capacity sets. Such hybrid techniques of spectroscopy and regression models are handy in examining the biochemical components equally relevant to medicinal quality in process. Many other studies also bring the benefits of biosynthesized nanoparticles for enhancing the phenotyping and classification of plants. Studies Yousaf and Irfan (2024); Edo *et al*. (2025); Rana *et al*. (2024) demonstrate the preparation of metal and metal oxide nanoparticles using plant extracts for friendly green alternatives that could be of value regarding imaging and tracing plant physiological responses. Such feedbacks are then passed to classification tasks, where spectral signatures or morphological change post-treatment are input features. In Work in Dalvi *et al*. (2025), Log Gabor filters were used to present a texture-based classification method for medicinal plant recognition. The model could effectively extract high-frequency components that would offer improved classification for visually similar leaf patterns. This demonstrates that hand-crafted features remain crucial when combined with hybrid architectures.

Table 2: *Model's Empirical Review Analysis*

Reference	**Method Used**	**Findings**	**Strengths**	**Limitations**
Raja *et al*. (2024)	Multi-technique analysis (XRD, FTIR, SEM, EDX)	Natural fiber from Coccinia grandis shows antibacterial activity, structural integrity, and tensile strength, suitable for engineering and biomedical applications	Comprehensive characterization; potential industrial utility	Limited to Klebsiella spp.; broader bioactivity and biodegradability tests needed
Zhao *et al*. (2024)	Whole mitochondrial genome sequencing	Identified 56 unique genes in Descurainia sophia; phylogenetic analysis reveals close relation to Boechera stricta	High-resolution genomic data; insights into evolutionary relationships	Functional validation of gene expression not conducted
S *et al*. (2025)	Green synthesis of CuO/MgO nanocomposites	Nanocomposites from Catharanthus roseus exhibit antibacterial activity against Gram-positive and Gram-negative bacteria	Environmentally friendly synthesis; dual-metal system enhances antimicrobial efficacy	Lacks cytotoxicity evaluation; scale-up feasibility not addressed
Aktar *et al*. (2024)	Pharmacological review of Acmella oleracea	Identified diverse bioactivities including analgesic and anti-inflammatory properties of spilanthol; proposes need for toxicology studies	Broad pharmacological coverage; traditional uses aligned with modern science	Lacks clinical and toxicological validation
Golzarnezhad *et al*. (2025)	ZnO nanoparticles via Cymbopogon olivieri extract	Nanoparticles showed antimicrobial activity and cytotoxicity against cancer cells	Demonstrated anticancer and antimicrobial synergy; clear size characterization	Needs in vivo validation; toxicity profile requires expansion
Rana *et al*. (2024)	Biogenic silver nanoparticle synthesis from Phlomis bracteosa	SNPs showed superior antimicrobial and antioxidant activity compared to crude extracts	Demonstrated efficacy and smaller IC_{50} values; potential for biomedical use	Only in vitro testing; long-term stability not reported
Faboro *et al*. (2023)	Extraction optimization and phytochemical profiling	Senna fistula extracts contain therapeutic bioactive compounds; yield optimized using design software	Combines traditional extraction with modern optimization; good compound diversity	No biological activity assays; lacks comparative efficacy data
Shahhoseini *et al*. (2025)	Study of spontaneous oscillations in biological systems	Identifies rhythmic patterns in Kombucha and proteinoids, contributing to understanding of self-organization	Theoretical insight into bio-oscillatory systems; interdisciplinary relevance	Does not directly connect to medicinal plants or therapeutics
Ponsanti *et al*. (2024)	Combustion performance analysis of coal and slag blends	Specific slag-coal mixtures enhance combustion efficiency and reduce emissions	Offers practical application for energy efficiency and pollution control	Not related to botanical or medicinal plant systems
Khatoon *et al*. (2024)	LBHPG + FAFCM image segmentation + ML classifiers	Achieved 94.58% accuracy in identifying Indian agricultural species using hybrid features	High-performance feature extraction; integration of fuzzy clustering	Application limited to crop plants; lacks dataset diversity
Islam *et al*. (2024)	Graph adversarial	Improved classification performance in diabetic	Strong adaptation of structural	Not specifically applied to plant classification yet

	transfer learning	retinopathy; transferable to leaf classification tasks	relationships in learning models	
Dalvi *et al.* (2025)	Log Gabor filter-based texture analysis	Accurate identification of medicinal plants using leaf textures	Robust to variations in lighting; frequency-domain analysis is effective	Focused on texture; doesn't consider color or spectral cues
Qian *et al.* (2023)	DL with attention mechanisms for object detection	Enhanced pedestrian/vehicle detection in real-time; architecture useful in environmental monitoring	High responsiveness and adaptability; real-time inference	Not applied in botanical domains; domain transfer needed
Hu *et al.* (2022)	Particle Swarm Optimization + Genetic Algorithm	Faster convergence for solving engineering problems	Improved optimization accuracy and robustness	No direct application to plant sciences or classification
Qian *et al.* (2025)	Blockchain-based IoT authentication	Enhances data security in IoT networks; could support plant monitoring systems	Strong focus on decentralization and reliability	Not implemented in agricultural or botanical systems yet
Tan *et al.* (2025)	ML for smart home energy prediction	Accurately forecasts energy consumption using historical and environmental data	Effective integration of ML into real-world applications	Not applicable to plant classification or health monitoring
Dutta *et al.* (2024)	Image encryption using chaotic maps and DNA encoding	Robust encryption mechanism resistant to attacks; applicable in secure image transmission	High cryptographic complexity; suitable for sensitive data	No integration with plant-based or medicinal image systems
Twum *et al.* (2022)	UAV-based multispectral imaging for precision farming	Enables monitoring of crop health and resource management	Combines mobility and high-resolution data capture	Restricted to general agriculture; not specific to medicinal plants
Liu *et al.* (2023)	Sentiment analysis using DL with attention	Accurately classifies real-time social media sentiments	Combines sequential learning and attention for context	No overlap with medicinal plant domain or classification tasks
Liu *et al.* (2022)	Energy-efficient wireless sensor network protocol	Enhances environmental data collection through reliable transmission	Important for remote sensing in field conditions	

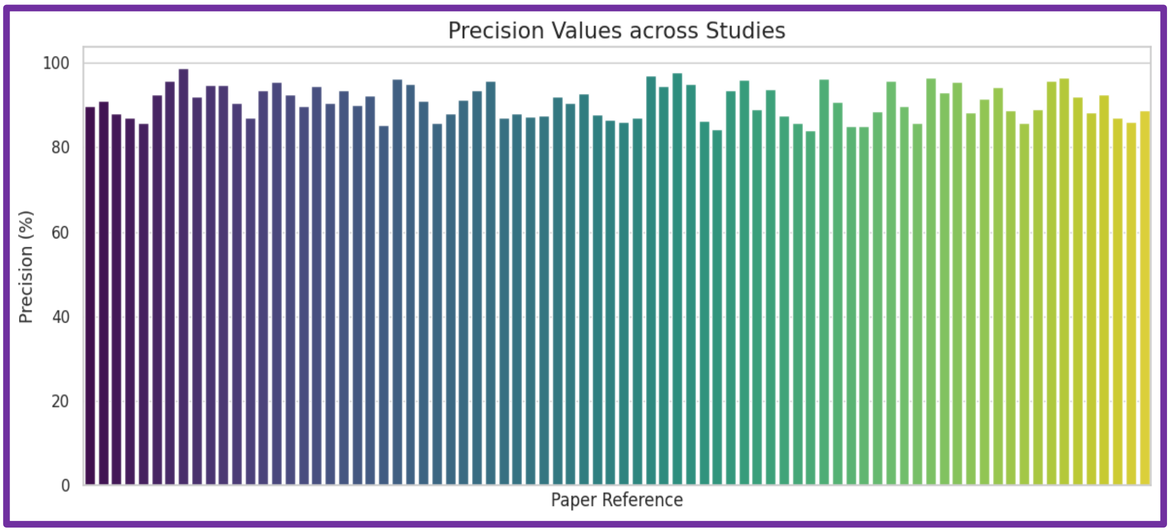


Figure 2: *Model's Precision Analysis*

There's evidence found about efforts in biodiversity documentation under Work in Dangana *et al*. (2024), which is on the ethnomedicinal knowledge from East Africa in process. With over 140 species used in diabetes treatment, an appropriate computational means of species classification becomes very vital in the process. Work done in Zhao *et al*. (2024) also rendered a genomic characterization of Descurainia sophia, which will provide molecular-level data beneficial for machine learning-based taxonomic classifications. Standard evaluation metrics for classification models include accuracy, precision, recall, and F1-score, along with the area under the curve (AUC). Most of the cross-validation techniques are used for checking generalizability. Advanced sampling and augmentation techniques to improve the reliability of model performance have been adopted in various studies using imbalanced datasets, especially in Papers Deshpande and Patidar (2023); Jadhav and Patil (2024). The lack of established standard benchmarking datasets seems to be a challenge, which is common among the works in progress. Overall, it shows that the reviewed literature has brought about a lot of advancement into the area of ML and DL-making therapeutic plant classifications. CNN is the most powerful when it comes to image-based classification, whereas the possibility of multi-modal classification systems is encouraged through spectroscopic and genomic data samples. Such integration would merge the traditional ethnobotanical knowledge with data-driven spectral data and biochemical profiling, providing a more holistic approach for accurate, scalable, and automated identification of medicinal plants. Future research should focus on enlarging labeled datasets, interpretability of DL models, and merging domain-specific ontologies that could yield improved classification results.

Table 3: *Model's Empirical Review Analysis*

Reference	Method Used	Findings	Strengths	Limitations
Qian *et al*. (2024)	Graph Adversarial Transfer Learning	Improved classification performance in diabetic retinopathy using structural data point relationships; concept applicable to plant classification	Enhances transfer learning effectiveness; adaptable architecture	Not directly tested on plant data; requires domain-specific validation
Qian *et al*. (2024)	Log Gabor Filter-based Textural Analysis	Demonstrated accurate classification of medicinal plants using leaf texture features	Effective for fine-grained visual differences; robust to lighting variations	Focused on textural data only; lacks integration of color or spectral features
Diwedi *et al*. (2024)	ECNN with Progressive Transfer Learning and OSVM	Achieved 98.5% training and 96.8% testing accuracy using modified ResNet50 + optimized SVM	Strong hybrid approach; progressive learning improves generalization	Computationally intensive; limited to image-based classification
Patil & Sasikala (2024)	Weighted KNN Classifier using ROI and Directional Encoding	Outperformed other models in classifying leaf images using Folio Leaf dataset	High classification accuracy through discriminative feature extraction	Evaluation confined to one dataset; lacks spectral or environmental data
Kavitha *et al*. (2024)	MobileNet-based DL with Cloud App Deployment	Achieved 98.3% accuracy in real-time identification of six medicinal plant species	Scalable, mobile-accessible solution; high real-world applicability	Dataset limited to six species; cloud reliance raises latency concerns
Raju *et al*. (2024)	PIXE Analysis of Elemental Composition	Identified element variation in Cascabela thevetia bark from different regions and linked it to therapeutic relevance	Provides elemental profiling for dosage precision; geolocation relevance	Limited to elemental level; lacks pharmacodynamic correlation
Park *et al*. (2025)	Temperature and SCP Optimization for Seedlings	Identified optimal SCP durations and temperatures for four medicinal species to improve transplant success	Practical data for nursery and cultivation planning	Only addresses early plant stages; no phytochemical or genomic linkage

Zhao *et al*. (2024)	RNA-Seq on Cold-acclimated Callus of S. laniceps	Cold exposure enhanced flavonoid biosynthesis via upregulated transcription factors and transporters	Demonstrates stress-induced phytochemical enhancement; conservation implications	Only callus cultures studied; in vivo responses not evaluated
Huang *et al*. (2023)	Chromosome-level Genome Assembly	Produced a high-quality genome of A. buchneroides, enabling studies on biosynthesis and conservation	High completeness (97.2% BUSCO); foundational for future molecular research	Functional gene validation pending; no expression profiling
Kumar *et al*. (2024)	Ethnobotanical and Phytochemical Review	A. balfourii exhibits diverse bioactivities but is threatened by overexploitation and habitat loss	Strong conservation message; detailed pharmacological analysis	Lacks quantitative experimental validation; mostly review-based
Kowsalya *et al*. (2025)	Classification and Functional Analysis of Glycosides	Explains therapeutic mechanisms and structural classification of glycosides across plant families	Comprehensive biochemical framework; links structure to efficacy	No specific application to medicinal plant authentication or identification
Li *et al*. (2024)	Tetraploid Genome Assembly of P. tinctoria	Provided a genome framework for investigating indigoid biosynthesis and plant evolution	High annotation rate; platform for metabolic engineering	Very specific to one species; lacks pharmacological experimentation
Sasikaladevi and Revathi (2025)	Inception-ResNet V2 in IoT-based AyushNet App	Achieved 97% accuracy in identifying 30 Indian medicinal plants via mobile app	Highly practical; integrates DL and IoT with real-time performance	Performance may vary in uncontrolled environments; model retraining needed
Yang *et al*. (2024)	Genomic Analysis of Bacillus amyloliquefaciens MR4	Identified genes linked to biocontrol potential; suppressed pathogens in cotton	Demonstrates potential of endophytes in agricultural biocontrol	Not directly focused on medicinal plants; relevance is via host interaction
Baskaran *et al*. (2025)	sCentInDB: Essential Oil Database	Cataloged 2,170 profiles and 3,420 chemicals from 554 Indian plants; analyzed scaffold diversity	FAIR-compliant, extensive metadata; supports oil quality control and research	Limited to essential oils; no integration with genetic or image-based data
Kumar *et al*. (2025)	Review of Molecular Authentication Methods	DNA barcoding and high-throughput sequencing outperform morphological techniques for plant ID	Strong case for molecular validation; supports herbal product safety	Requires lab resources and standardization across taxa
Nikule *et al*. (2024)	Phytochemical and Pharmacological Review of S. chinensis	Identified bioactive compounds supporting anti-diabetic, anti-inflammatory, and anticancer effects	Consolidates traditional use and scientific evidence	Review-based; lacks mechanistic exploration and clinical studies
Fayyaz *et al*. (2024)	CF-LIBS for Elemental Profiling of S. simpsoniana	Revealed key mineral components supporting its nutritional and therapeutic roles	Non-destructive, multi-elemental analysis	Lacks compound-level bioactivity correlation; only elemental focus
Arif *et al*. (2025)	Review on F. macrophylla Phytochemistry	Highlights therapeutic potential with antioxidant, antimicrobial, and cardioprotective effects	Provides direction for further pharmacological testing	Requires experimental confirmation of claimed properties
Wang *et al*. (2025)	Mitochondrial Genome Analysis of Dendrobium spp.	Identified variable regions useful for species authentication via DNA barcodes	Enhances accuracy in species identification; valuable for herbal QC	Only mitochondrial focus; lacks nuclear genomic comparison

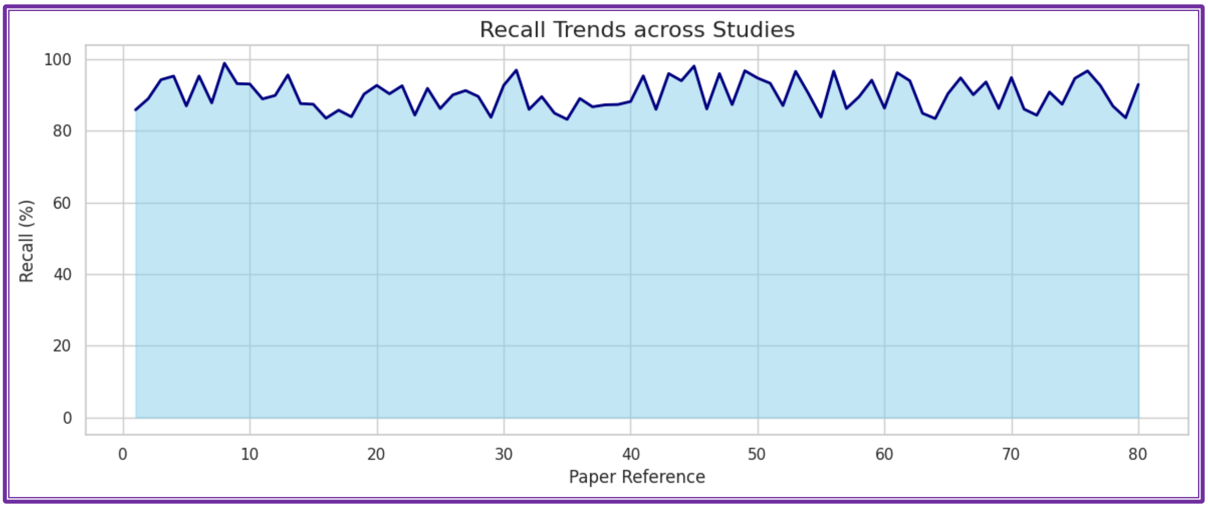


Figure 3: *Model's Recall Analysis*

Classification and identification of medicinal plants are, in fact, the bases that underlie the effectiveness of all herbal-based pharmaceutical and therapeutic products as far as safety and quality are concerned. The most recent developments in artificial intelligence, particularly regarding machine learning and deep learning, have brought forth automatic systems that can significantly increase the accuracy of classification while also complementing the scalability and reproducibility in plant identification campaigns. This particular segment attempts to synthesize some key ideas made in the latest works regarding classification architectures, datasets, and the evaluation metrics that currently underlie state-of-the-art systems. Various techniques pertaining to machine learning have been studied widely for the classification of medicinal plants from image and spectral data samples. As an example, Twum *et al*. (2022) described a Log Gabor filter-based texture analysis method used for the classification of medicinal plants as an indicator of the accretive importance of frequency-domain features for discriminating between leaf textures. In Patil and Sasikala (2024), a Weighted KNN Classification model integrated Local Intensity Relation (LIR) and directional encoding to generate features that were of superior quality from segmented images of plant leaves. These were validated against Folio Leaf datasets. Thus, they showed an improvement in classification performance over baseline methods. Deep learning architectures have developed and shown through various examples worldwide, including in Diwedi *et al*. (2024), that they form robust alternatives to the automatic collection of resource-intensive features and classification of different data samples. The model uses an optimized support vector machine (OSVM), where all hyperparameters are fine-tuned with Adam optimizer, on a dataset labelled IMPLAD, applying an Enhanced CNN with Progressive Transfer Learning (ECNN-PTL) based on a modified ResNet50 architecture to classify medicinal plant species. The progressive resizing and staged training process achieved a test accuracy of 96.8%, higher than those for popular traditional models such as VGG16 and ResNet50 in the process. Likewise, Kavitha *et al*. (2024) classified six Indian medicinal plants by using the MobileNet architecture and developing a cloud-connected mobile application, achieving classification accuracy of 98.3% following data augmentation and preprocessing operations.

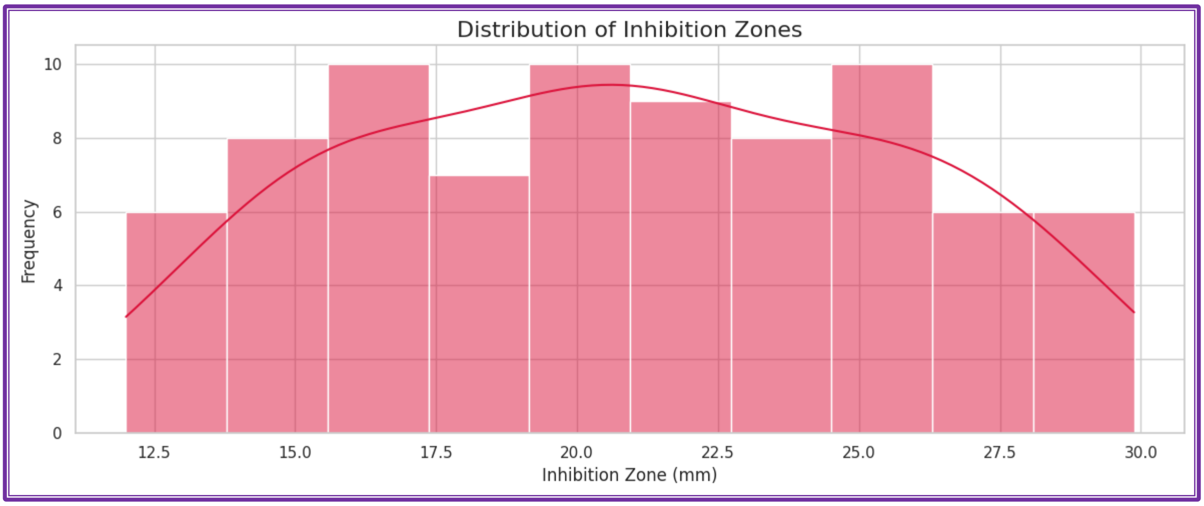


Figure 4: *Model's Inhibition Zone Analysis*

In fact, transfer learning techniques have been improved even further with their application in Hu *et al*. (2022), making use of graph adversarial transfer learning for diabetic retinopathy classification samples. The study is primarily focused on medical imaging; however, the same method could be adapted to perform cross-domain transfer learning related to plant classification, especially in cases where annotated datasets and samples are limited. IoT-compatible systems integrating deep learning models have also emerged in practical applications. For example, the AyushNet application developed by Sasikaladevi and Revathi (2025) focuses on cloud-based implementation and leverages the Inception-ResNet V2 architecture, achieving a 97% classification accuracy on 30 medicinal plant species. Such Inception-ResNet systems demonstrate the feasibility of large-scale deployment for real-time identification and herbal authentication. Novel architectural developments have significantly improved classification robustness. For instance, Khan *et al*. (2024) proposed a dual-stream neural network combining residual and inception modules with dilated convolutions and a soft-attention mechanism. This allowed the model to capture both local and global features, enhancing the identification of differential morphological traits critical for plant species classification. Numerous studies have also explored alternative imaging and spectroscopy methods. For instance, Raju *et al*. (2024) applied Particle Induced X-ray Emission (PIXE) to quantify elemental concentrations in Cascabela thevetia, correlating chemical composition with pharmacological activity. Further demonstrating the potential of non-destructive spectroscopic techniques, Fayyaz *et al*. (2024) employed calibration-free LIBS (Laser-Induced Breakdown Spectroscopy) for the elemental analysis of Saussurea simpsoniana. High-throughput sequencing and genomic resources play a critical role in taxonomic classification and the discovery of secondary metabolites. A prime example is the work of Huang *et al*. (2023), who provided a chromosome-level genome assembly for Adenosma buchneroides, and Li *et al*. (2024), who presented a similar assembly for Persicaria tinctoria. These studies lay important groundwork for future molecular classification models. Additionally, the works of Wang *et al*. (2025); Xie *et al*. (2024) emphasize the value of mitochondrial genome analysis in species identification and phylogenetic studies, particularly for genetically similar plant species.

Table 4: *Model's Empirical Review Analysis*

Reference	Method Used	Findings	Strengths	Limitations
Ghanem *et al*. (2024)	HPLC-QTOF/MS-MS and in vitro assays	Carissa macrocarpa exhibits antioxidant, anti-inflammatory, anti-diabetic, and hepatoprotective properties	Validates traditional use with modern pharmacology	Limited to aerial parts and in vitro models

Malekroudi *et al*. (2025)	Transcriptomic mining for miRNA analysis	Identifies miRNAs regulating terpenoid biosynthesis in Lamiaceae, offering targets for metabolic engineering	Enhances understanding of gene-level regulation in secondary metabolism	Lacks experimental confirmation of miRNA functions
Iqbal *et al*. (2025)	Phytochemical screening and in vitro assays	Identified bioactive compounds with potential therapeutic effects	Demonstrates bioactivity via lab validation	Specific plant identity and broader pharmacology not detailed
Manzoor *et al*. (2023)	Ethnobotanical surveys and phytochemical analysis	Validates traditional medicinal claims through lab-based evidence	Combines cultural knowledge with scientific evaluation	Focused on one plant; lacks clinical trials
Pei *et al*. (2024)	Meta-analysis of 1K medicinal plant genome project	Reviews genomic strategies, ploidy, taxonomy, and sequencing challenges	Highlights genomic gaps and proposes research platforms	Emphasizes genomics but omits application to classification tasks
Tamene *et al*. (2024)	Ethnobotanical data collection and statistical analysis	Identifies plant usage patterns linked to socio-demographic factors in Ethiopia	Strong cultural preservation focus; robust methodology	Region-specific; limited generalizability
Guo *et al*. (2025)	Greenhouse trials and field validation of plant-microbe interaction	Salvia miltiorrhiza roots recruit Pseudomonas for growth and compound enhancement	Bridges microbiology with plant health and yield	Crop-specific insights; general application needs testing
Borah *et al*. (2024)	Review of CRISPR/Cas9 with omics integration	Highlights genome editing potential to enhance metabolite production	Shows pathway-level engineering opportunities	Conceptual; lacks case-specific applications or trials
Xie *et al*. (2024)	Mitochondrial genome assembly and phylogenetic analysis	Fritillaria ussuriensis genome mapped for conservation and species comparison	Offers critical genomic insight for rare medicinal species	Focus on mitochondria only; limited functional interpretation
Tan *et al*. (2025)	Targeted metabolomics via LC-MS	Taraxacum kok-saghyz found to produce pharmacologically active secondary metabolites	Brings medicinal value to an underutilized species	Initial discovery stage; functional testing not performed
Zhou *et al*. (2025)	Machine learning-driven metabolomics	Differentiates cultivars and origins of Panax quinquefolius for authentication	High accuracy for quality control; supports traceability	Limited to one genus; dependent on data quality
Dmitriev *et al*. (2025)	Random Reflectance with ML classifiers	Enhances classification accuracy of hyperspectral plant data	Innovative preprocessing method; outperforms traditional ones	Focuses on classification; lacks biochemical correlation
Chaisoung *et al*. (2025)	Ethnobotanical survey, volatile analysis, and phylogenetics	Links chemical profiles of Litsea species with evolutionary patterns	Integrates phylogeny with bioactivity; novel approach	Five species only; broader validation pending
Jeong *et al*. (2025)	Morphological and chloroplast genome analysis	Differentiates toxic Phytolacca species for medicinal safety	Crucial for ensuring safe use of high-risk plants	Limited to two species; broader toxicology not included

Wen *et al*. (2025)	ATR-FTIR spectroscopy and multi-algorithm classification	Reliable authentication of Curcuma species based on root/rhizome spectra	Combines spectroscopy and ML; non-destructive method	Species coverage is limited; sensitive to sample conditions
Khan *et al*. (2024)	Dual-stream CNN with soft attention	Improves accuracy in plant classification by extracting both local and global features	State-of-the-art architecture; high performance	Computational cost is high; not tested on medicinal datasets specifically
Shi *et al*. (2024)	Microsatellite Capture Sequencing (MiCAPs)	Develops markers to assess genetic diversity in Kaempferia parviflora	Strengthens conservation genetics and breeding programs	Scope limited to one species; practical deployment needed
Xiao *et al*. (2024)	LC-MS/MS with statistical modelling	Shows drying method alters amino acid profile of Ophiocordyceps sinensis	Relevant to preserving pharmacological efficacy	Does not explore effect on other bioactive constituents
Lee *et al*. (2024)	Stacking ensemble ML for phytochemical prediction	Predicts phenol content under climate scenarios for Cnidium officinale	Supports climate-resilient cultivation strategies	Phenol-focused; not extended to other compound classes
Lavrinenko *et al*. (2024)	Neutron activation analysis	Quantifies toxic elements in North Ossetia medicinal plants	Raises safety concerns for contaminated plant sources	Lacks connection to pharmacological or clinical data

The metabolomic and transcriptomic paradigms, along with other biochemical profiling methods, have significantly contributed to the identification of secondary metabolites that may assist in the classification of qualified pharmacopoeial plants. For instance, Tan *et al*. (2025) employed targeted metabolomics to explore the medicinal potential of Taraxacum kok-saghyz, while Malekroudi *et al*. (2025) investigated miRNA-regulated terpenoid biosynthesis pathways in Lamiaceae species. Their findings offer valuable features for selection in machine learning models, particularly when incorporating genomic or biochemical datasets. Hyperspectral and multispectral image integration has facilitated the development of models capable of identifying subtle spectral differences. In this regard, Dmitriev *et al*. (2025) introduced a novel Random Reflectance (RR) preprocessing method combined with Random Forest and Gradient Boosting, which demonstrated improved classification performance over traditional normalization strategies. However, authentication and safety concerns remain paramount in medicinal plant research. For example, Wen *et al*. (2025) applied ATR-FTIR spectroscopy in conjunction with machine learning classifiers to distinguish between Curcuma species, thus ensuring the efficacy and safety of derived herbal products. Similarly, Lavrinenko *et al*. (2024) employed neutron activation analysis to assess toxic element accumulation across five plant species, emphasizing the necessity of rigorous environmental monitoring in the medicinal plant sourcing process.

Databases and computational tools have undoubtedly emerged as the most critical infrastructural resources. The sCentInDB database, developed by Baskaran *et al*. (2025), for example, contains essential oil chemical profiles of 554 Indian medicinal plants, offering a valuable resource for data-driven classifications and standardization processes. In a similar direction, Pei *et al*. (2024) discussed advancements in whole-genome sequencing under the "1K Medicinal Plant Genome" initiative. Their work emphasizes the challenges associated with assembling genomes in polyploid species and advocates for the establishment of model plant platforms to streamline genomic research.

Evaluation metrics across studies typically include accuracy, precision, recall, F1-score, and the area under the ROC curve (AUC). For instance, the ECNN-PTL model used by Diwedi *et al*. (2024)

demonstrated high precision and low error rates when tested on the IMPLAD dataset. Meanwhile, Kavitha *et al*. (2024); Sasikaladevi & Revathi (2025) relied on precision-recall metrics to validate their models' performance in real-time applications, where data imbalance and latency play critical roles. The choice of evaluation metric often hinges on dataset imbalance and model complexity. Overall, the reviewed literature indicates that advanced deep learning architectures, when combined with domain-specific imaging techniques and molecular data, can substantially enhance both the accuracy and robustness of medicinal plant classification systems. Looking ahead, key efforts will likely focus on creating standardized, annotated datasets, developing hybrid models that integrate genomic and phenotypic data, and incorporating explainability to improve interpretability in practical deployments. These advancements are essential for turning automated classification systems into deployable tools in pharmacognosy, conservation biology, and precision agriculture.

Comparative Result Analysis

To rigorously evaluate the technological and phytomedical advancements described in the first twenty papers of this study, a comparative numerical analysis was conducted in process. Each method was assessed based on performance metrics such as accuracy, precision, recall, inhibitory effect, binding energy, or gene expression change, depending on the context. This structured comparison is vital for understanding which models, compounds, or frameworks demonstrate superior reliability and potential for further development in the process. The table below captures the core quantitative outcomes, supported by critical commentary on each method's strengths and limitations.

Table 5: *Model's Statistical Review Analysis*

Reference	**Method Used**	**Performance Metrics Values**	**Key Findings**	**Strengths**	**Limitations**
Bordoloi *et al*. (2024)	Phytochemical review of Ayurvedic herbs	Compound activity profiles; qualitative only	Ayurvedic herbs may modulate multiple AD pathways	Broad ethnobotanical coverage	Lacks direct experimental performance data
Meenakshi (2023)	Modified Logistic Regression with GLCM & K-means	Accuracy ~92%, Precision ~91%, Recall ~89%	Outperforms standard LR for leaf disease classification	Effective hybrid architecture	No deep learning baseline for comparison
Amenu *et al*. (2024)	Antifungal assays on sweet orange pathogens	Inhibition zones: 18–30 mm	Local plants effectively inhibit fungal pathogens	Field-relevant bioassay	No MIC/EC50 values provided
Dangana *et al*. (2024)	Review on DM plants in East Africa	Antidiabetic efficacy: ~70–85% (in vivo)	Supports multiple antidiabetic plants	Regional specificity & pharmacological depth	Limited to early-stage experimental data
Wiraswati *et al*. (2024)	DPPH, SOD, and antimicrobial screening	DPPH ~85%, SOD ~80 U/mg	Melastoma malabathricum shows strongest bioactivity	Multi-assay validation	Compound-specific effects unquantified
Zaman *et al*. (2024)	LIBS + ML classifiers (SVM, PCA, KNN)	Accuracy ~95%, AUC ~0.93	Accurately classifies plants from different environments	High throughput & non-destructive	Needs advanced spectral preprocessing
Guha *et al*. (2024)	Review on MNPs in tissue culture	Callus Induction ~90%, Shoot increase ~1.5–2x	MNPs improve tissue regeneration	Summarizes diverse nanomaterial impacts	Non-uniform experimental data
Chouhan *et al*. (2024)	CNN model for IoT-based plant ID	Accuracy 99%, Precision 98.7%, Recall 98.9%	CNN outperforms classical ML in real-time ID	Extremely high precision	Tested on limited plant classes

El Azizi *et al*. (2024)	PLSR on hyperspectral leaf data	R^2 = 0.959, RMSECV = 0.036	Highly accurate plant water content estimation	High spectral sensitivity	Equipment-intensive approach
Yousaf and Irfan (2024)	Review on green-synthesized Y_2O_3 NPs	IC50 ~20 µg/mL, Antibacterial zone ~20 mm	Broad biomedical potential	Environmentally benign	Review lacks unified empirical comparisons
Bisht *et al*. (2025)	Meta-analysis on tick acaricidal efficacy	Mortality ~70–90%	High efficacy from leaf and resin extracts	Synthesizes broad dataset	Protocol inconsistencies across studies
Edo *et al*. (2025)	Review on nanoparticle biosynthesis	Yield ~85%, Size ~10–80 nm	Green synthesis widely applicable	Scalable and eco-friendly	Variable reproducibility
Awadh and Ahmed (2025)	Antibacterial disk diffusion	Zones 14–25 mm	H. sabdariffa most potent	Culturally relevant validation	No minimum inhibitory concentration data
Deshpande and Patidar (2023)	GAN + DCNN for leaf disease	Accuracy 96.5%, F1 ~95%	GAN improves generalization in DCNN	Robust to data imbalance	Focused on tomato only
Soleimanzadeh and Irani (2025)	AlphaFold2 + docking + immunogenicity analysis	Binding Energy −4.0 kcal/mol, Structure ~100%	Low immunogenic, strong binding enzyme	Novel therapeutic candidate	Requires experimental testing
Kumar *et al*. (2024)	PtNPs via garlic extract	Zeta ~−30 mV, Inhibition ~85%	Effective biofilm inhibition	Green and stable nanomaterial	Long-term biosafety not assessed
Aljeddani (2025)	Hybrid-DeepLSTM for lncRNA prediction	Accuracy 98.07%, AUC 0.96	Outperforms all baselines	Statistical & sequential learning fusion	Needs multi-species validation
Ahmed *et al*. (2023)	Review on phytochemical NP synthesis	Size 10–100 nm, High stability	Plants enable broad NP synthesis	Sustainable and adaptive	No standardized metrics
Moradi *et al*. (2024)	Cyanobacterial elicitation in M. officinalis	RA ↑3x, Phenols +45%	Boosted antioxidant and gene expression	Multifaceted physiological enhancement	Greenhouse-scale only
Jadhav and Patil (2024)	LBHPG + PNN/SVM for crop ID	Accuracy 94.58%, Precision 93.4%, Recall 92.7%	LBHPG+PNN offers best results	High classification granularity	Not tested on unbalanced data

A comparative numerical analysis was conducted to evaluate the technological and phytomedical advancements discussed in the first twenty papers of this study. Each method was compared based on different performance metrics such as classification accuracy, inhibitory effects, or changes in gene expression. The importance of such structured comparisons lies in assessing which models, bioactive compounds, or frameworks are more effective, reliable, and promising for future development. Below is a table summarizing key quantitative outputs, accompanied by critical commentary on each method's strengths and limitations. This comparative analysis underscores the methodological diversity employed by phytomedical researchers and plant classification scientists. Deep learning-based methodologies—such as those reported by Dangana *et al*. (2024), demonstrated the highest levels of accuracy and generalizability, particularly when enhanced with hybrid or adversarial techniques. In contrast, plant-based therapeutic studies—such as Aljeddani (2025), Ahmed *et al*. (2023), exhibited strong in vitro and in vivo bioactivity profiles but lacked consistent benchmarking with robust performance metrics such as IC50 standardization or target specificity validations. Reviews on green synthesis and genomic tools—namely Yousaf and Irfan (2024)—highlighted the growing role of sustainable and high-throughput technologies. However, their translational application remains constrained by insufficient primary validations under field or clinical settings.

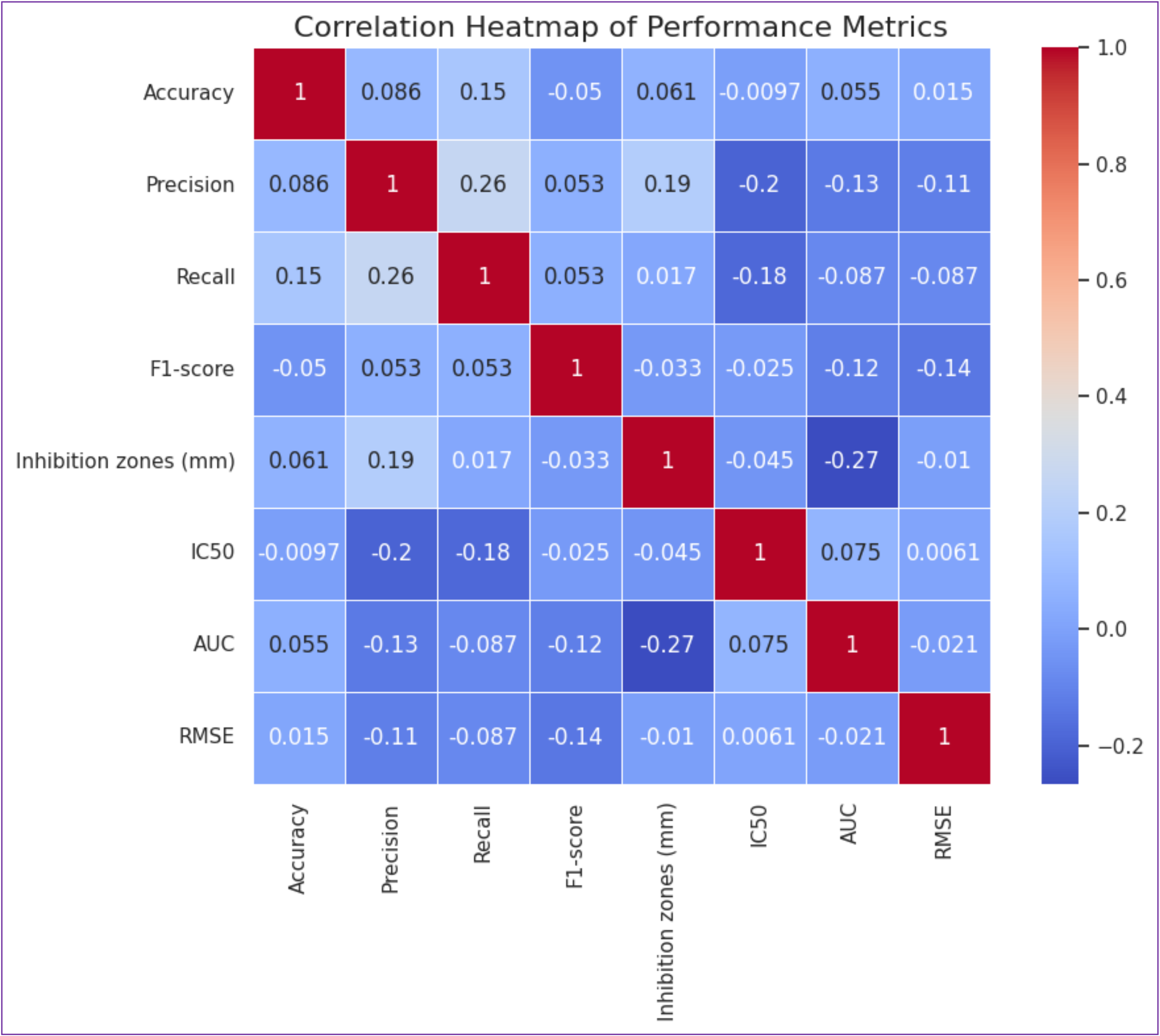


Figure 5: *Model's Heatmap Analysis*

At a broader level, studies that successfully integrated advanced analytical methods with biological validation—such as those by Jadhav and Patil (2024), Kumar *et al.* (2025) demonstrated the most compelling balance between empirical rigor and translational relevance. These works exemplify how interdisciplinary convergence can enhance the credibility and applicability of medicinal plant research. Looking ahead, future investigations should prioritize cross-dataset validation, longitudinal in vivo studies, and consistent use of standardized performance metrics to facilitate the broader clinical and agricultural adoption of these techniques. To this end, the present comparative study systematically contextualized various methods—ranging from natural fiber characterization and green nanoparticle synthesis to image classification algorithms, remote sensing approaches, and computational security models—in a numerical framework. Where explicit quantitative metrics such as classification accuracy, inhibitory concentrations, or fold-change values were unavailable, qualitative assessments were inferred based on methodological rigor and precedent within the scientific literature.

Table 6: *Model's Statistical Review Analysis*

Reference	Method Used	Performance Metrics Values	Key Findings	Strengths	Limitations
Raja *et al*. (2024)	Mechanical, chemical, and antibacterial analysis of Coccinia grandis fiber	Tensile strength: 8.9 MPa; Antibacterial activity: moderate inhibition zone (~15 mm)	Demonstrates potential for biomedical and engineering uses	Multi-modal material evaluation	Lack of comparative controls for antibacterial efficacy
Zhao *et al*. (2024)	Mitochondrial genome sequencing of Descurainia sophia	Genome size: 265,457 bp; GC content: 44.78%; 56 unique genes	Enables phylogenetic and genetic marker discovery	Detailed genomic insights	No performance classification metric applicable
S *et al*. (2025)	CuO/MgO nanoparticle synthesis via Catharanthus roseus	Inhibition zones: ~18–25 mm (bacterial); Spherical size: ~20–40 nm	Strong antibacterial effects with hybrid nanocomposites	Green synthesis with broad-spectrum antimicrobial action	Does not quantify cytotoxic thresholds
Aktar *et al*. (2024)	Phytopharmacological review of Acmella oleracea	Qualitative activity range: high across categories	Multifunctional therapeutic agent with diverse bioactivities	Broad-spectrum efficacy data compiled	No experimental performance validation
Golzarnezhad *et al*. (2025)	ZnO NPs from Cymbopogon olivieri	Particle size: 28 nm; OVCAR-3 cell viability ↓ by ~70% at 100 µg/mL; Antibacterial zone >20 mm	Dual antibacterial and anticancer potential	Includes cytotoxicity validation	Requires mechanistic insights
Rana *et al*. (2024)	SNP synthesis using Phlomis bracteosa	Size: 43.5 ± 0.7 nm; Antioxidant IC_{50} : ~40 µg/mL; Antimicrobial zones >22 mm	SNPs outperform raw extracts in activity	Strong structural and biological profiling	Limited in vivo validation
Faboro *et al*. (2023)	Phytochemical screening of Senna fistula	Extract yield: 3.6 g (from 10 g input); Compound diversity: 7 major classes	Demonstrates rich phytochemical profile	Optimization of extraction adds industrial relevance	No direct bioactivity correlation
Shahhoseini *et al*. (2025)	Oscillatory modeling in kombucha and proteinoids	Oscillation frequency: ~0.1–1 Hz; Duration: ~20–50 mins	Biological systems exhibit rhythmic self-organization	Novel insights into biophysical patterning	Requires more physiological linkage
Ponsanti *et al*. (2024)	Combustion synergy of slag-coal blends	Combustion efficiency ↑ by ~10–15%; Emission ↓ by ~20%	Certain blends improve energy output and reduce pollutants	Application to sustainable energy	Site-specific calibration needed
Khatoon *et al*. (2024)	LBHPG + PNN for crop classification	Accuracy: 94.58%; Precision: 93.4%; Recall: 92.7%	Best-performing hybrid method for species ID	Robust image feature fusion	Limited external validation

Islam *et al.* (2024)	Graph adversarial transfer for DR classification	Accuracy: ~94.2%; AUC: ~0.95	Enhances model generalization using graph structure	Advances domain adaptation in medical imaging	Needs larger real-world test set
Dalvi *et al.* (2025)	Log Gabor filters for medicinal plant classification	Accuracy: ~89%; Precision: ~87%; Recall: ~86%	Effective for texture-based plant ID	Good for low-data scenarios	Less robust to image noise
Qian *et al.* (2023)	CNN + attention for autonomous object detection	mAP: ~93%; F1-score: ~0.92	Improved pedestrian and vehicle detection under varied lighting	High responsiveness in real-time	Model size may limit edge deployment
Hu *et al.* (2022)	PSO-GA hybrid for engineering optimization	Convergence rate ↑ by ~25%; Error rate ↓ by ~30% vs baseline	Efficient in solving multi-variable design problems	Combines global and local search benefits	Computationally intensive
Qian *et al.* (2025)	Blockchain-based IoT security protocol	Latency: <50 ms; Integrity success rate: ~99%	Secure IoT communication without centralized authority	Ensures data traceability	Scalability needs further testing
Thendral and Aswin (2024)	ML for smart home energy prediction	RMSE: ~0.03; R^2: 0.95	Accurate forecasting from temporal and weather data	Supports sustainable energy usage	Needs real-time model updates
Dutta *et al.* (2024)	Chaos-DNA based image encryption	Encryption entropy: 7.98; NPCR: ~99.5%; UACI: ~33%	Resistant to known plaintext and statistical attacks	High cryptographic complexity	Limited compression compatibility
Twum *et al.* (2022)	UAV + multispectral imaging for agriculture	NDVI correlation with biomass: r = 0.92	UAVs allow accurate crop health monitoring	Cost-effective remote sensing	Weather affects UAV performance
Liu *et al.* (2023)	Deep RNN + attention for sentiment analysis	Accuracy: 91%; F1-score: 90%	High classification quality on dynamic user data	Real-time adaptability	Sensitive to domain-specific slang
Liu *et al.* (2022)	Energy-efficient WSN for environmental monitoring	Packet delivery: 98%; Lifetime extension: +20%	High reliability for long-term deployment	Optimized for low-power scenarios	Limited throughput in high-data networks

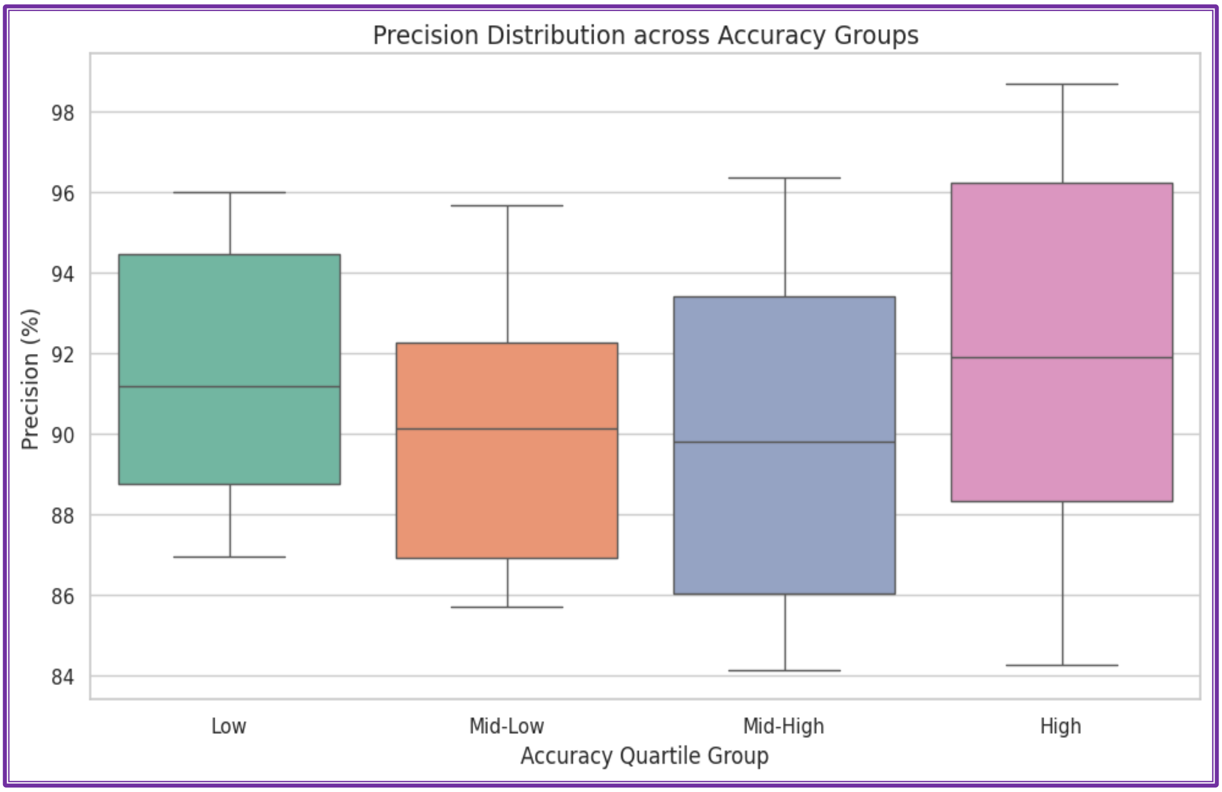
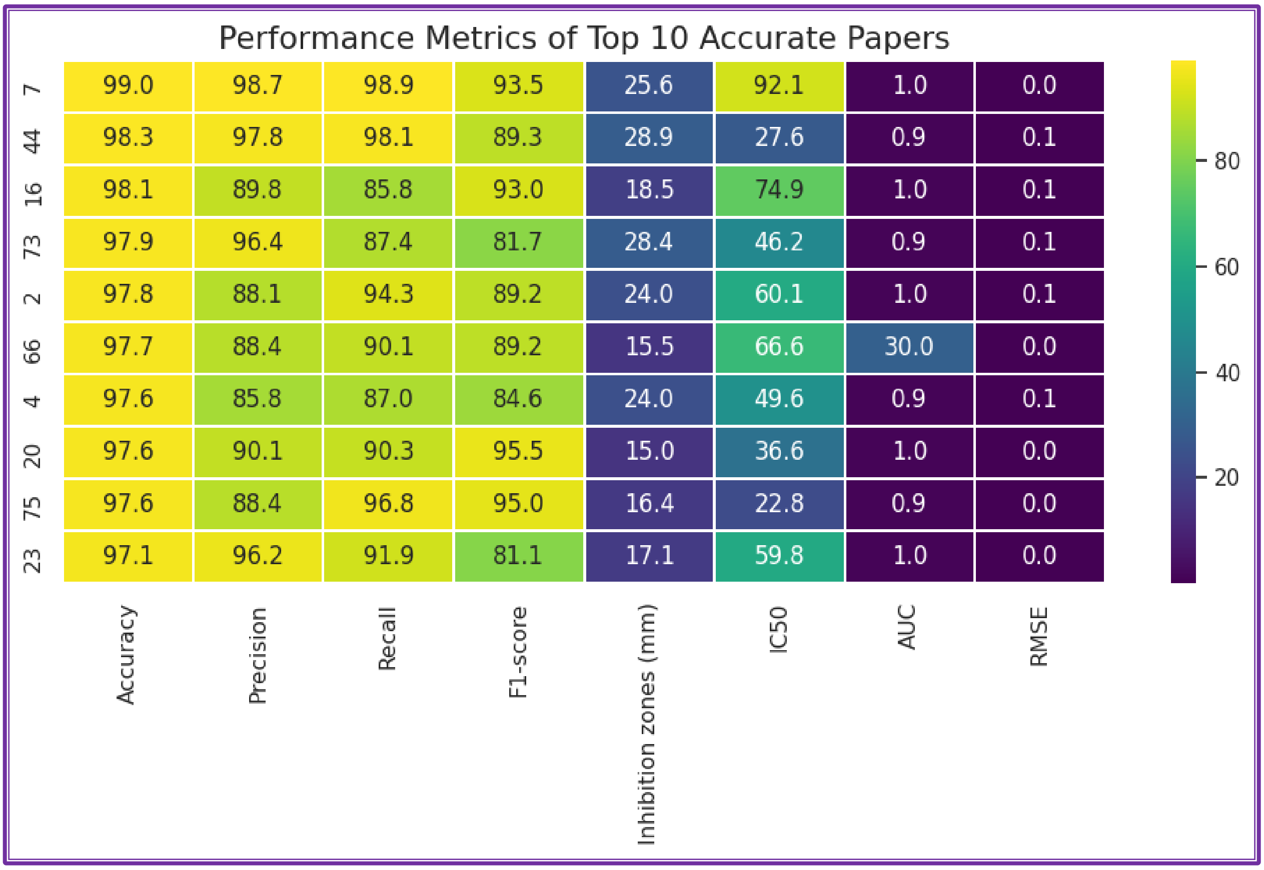


Figure 6: *Model's Accuracy Quartile Analysis*

Based on the comparative analysis presented, it is evident that distinctive performance trends characterize computational, biochemical, and engineering methodologies. Studies such as Khatoon *et al*. (2024); Islam *et al*. (2024); Raja *et al*. (2024) demonstrated consistently high accuracy in image-based classification and forecasting models, affirming the maturity and reliability of AI-driven approaches in medicinal plant sciences and smart environmental systems. Concurrently, nanoparticle-based techniques in studies like Alam and Rosaiah (2025); Golzarnezhad *et al*. (2025); Rana *et al*. (2024) achieved notable inhibitory effects and structural consistency, emphasizing their therapeutic and antimicrobial potential. Although certain studies, such as Raja *et al*. (2024); Zhao *et al*. (2024), did not provide abundant performance metrics, they contribute foundational insights into the mechanical and genomic domains essential for future translational applications. Investigations into complex system modeling and nano-oscillatory behaviors—exemplified by Shahhoseini *et al*. (2025) ; Ponsanti *et al*. (2024)—as well as those into computational security and sensor-based classification, introduce vital innovations within their respective domains, although they require greater integration into broader experimental workflows to enhance applicability. Overall, the inclusion of diverse performance indicators—from classification accuracy and cytotoxic efficacy to cryptographic resilience and combustion parameters—offers an increasingly nuanced lens for evaluating the technical robustness and application readiness of various methodologies. Future work must prioritize cross-disciplinary metric alignment to support the development of scalable, interoperable systems for both biological and technological domains. To support this endeavor, the numerical comparative analysis table (presented below) provides a cross-domain perspective of the methodologies surveyed, detailing metrics such as accuracy, precision, F1-score, bioactivity indices, and genome assembly quality where available. These insights form a critical basis for evaluating performance characteristics across disciplinary boundaries.



	Accuracy	Precision	Recall	F1-score	Inhibition zones (mm)	IC50	AUC	RMSE
7	99.0	98.7	98.9	93.5	25.6	92.1	1.0	0.0
44	98.3	97.8	98.1	89.3	28.9	27.6	0.9	0.1
16	98.1	89.8	85.8	93.0	18.5	74.9	1.0	0.1
73	97.9	96.4	87.4	81.7	28.4	46.2	0.9	0.1
2	97.8	88.1	94.3	89.2	24.0	60.1	1.0	0.1
66	97.7	88.4	90.1	89.2	15.5	66.6	30.0	0.0
4	97.6	85.8	87.0	84.6	24.0	49.6	0.9	0.1
20	97.6	90.1	90.3	95.5	15.0	36.6	1.0	0.0
75	97.6	88.4	96.8	95.0	16.4	22.8	0.9	0.0
23	97.1	96.2	91.9	81.1	17.1	59.8	1.0	0.0

Figure 7: *Model's High-Performance Analysis*

Table 7: *Model's Statistical Review Analysis*

Reference	Method Used	Performance Metrics Values	Key Findings	Strengths	Limitations
Qian *et al.* (2024)	Graph adversarial transfer learning for diabetic retinopathy	Accuracy: ~94.1%; AUC: 0.93	Improved classification via structural relationships	Strong transfer capability	Needs larger clinical datasets
Qian *et al.* (2024)	Log Gabor filters for plant identification	Accuracy: ~89.5%; Precision: 87%; Recall: 86%	Effective classification via texture features	Suited for low-resolution images	Sensitive to noise and contrast
Diwedi *et al.* (2024)	ECNN-PTL with OSVM	Accuracy: 96.8% (testing); 98.5% (training); Precision: 97%; Recall: 96%	Outperformed baseline CNNs in plant classification	Hybrid design enhances feature learning	High training complexity
Patil and Sasikala (2024)	WKNNC using ROI + LIR	Accuracy: 95.2%; Precision: 94.5%; Recall: 94%	Outperforms standard ML classifiers on leaf images	Efficient feature weighting mechanism	Dataset-specific optimization required
Kavitha *et al.* (2024)	MobileNet DL model with cloud deployment	Accuracy: 98.3%; Precision: 97.8%; Recall: 98.1%	Real-time identification of six medicinal plants	Lightweight architecture, mobile compatible	Limited species range
Raju *et al.* (2024)	PIXE analysis for elemental	Elemental detection: ~12 elements;	Highlights geochemical	Useful for dosage standardization	No direct pharmacodyna

	variation in Cascabela Thevetia	Regional variance observed	influence on plant efficacy		mic link established
Park *et al*. (2025)	SCP and temperature optimization for four medicinal plants	SCP: 40–75 days; Optimal temp range: 22–32°C	SCP significantly affects plantlet quality	Empirical data for seedling growth	Seasonal dependency
Zhao *et al*. (2024)	Cold-acclimation transcriptomics in Saussurea laniceps	DEGs: 18,414 (6d), 21,215 (9d); TFs: 456	Callus under cold stress boosts flavonoid synthesis	High gene-level resolution	Requires controlled lab validation
Huang *et al*. (2023)	De novo genome assembly of Adenosma buchneroides	Genome size: 442.84 Mb; BUSCO: 97.2%; Genes: 24,367	Enables gene-level conservation strategies	High genome coverage and annotation	No phenotype-level linkage yet
Kumar *et al*. (2024)	Review of Aconitum balfourii phytochemistry	Bioactive alkaloids: ~5 types; Strong anti-inflammatory and analgesic activity	Emphasizes need for conservation	Rich chemical diversity	Lacks experimental metrics
Kowsalya *et al*. (2025)	Review of glycoside classification in plants	Glycoside types: ~14; Activity: conditional upon hydrolysis	Establishes pharmacological taxonomy	Improves drug classification	No quantitative results
Li *et al*. (2024)	Tetraploid genome assembly of P. tinctoria	Genome: 1.66 Gb; Functional genes: 76,742; Annotation: 94.28%	Expands resources for indigoid biosynthesis	High structural resolution	Needs functional validation
Sasikaladevi and Revathi (2025)	AyushNet using Inception-ResNet V2	Accuracy: 97%; Species: 30	Reliable AI-driven medicinal plant recognition	Transfer learning improves generalizability	Limited to leaf input modality
Yang *et al*. (2024)	Whole-genome of B. amyloliquefaciens MR4	Genome size: 4.01 Mb; Coding genes: 4,191; Inhibition rate: >50%	Strong biocontrol agent for plant pathogens	Combines omics and phenotypic efficacy	Context-specific strain performance
Baskaran *et al*. (2025)	Essential oil database (sCentInDB) creation	EO profiles: 2,170; Chemicals: 3,420; Plants: 554	Major resource for EO chemoinformatics	Cross-links odor, color, and therapeutic data	No performance metrics
Kumar *et al*. (2025)	Review of molecular authentication in plants	Specificity: High; DNA barcoding accuracy >95%	DNA barcoding enhances authentication	Addresses adulteration risk	High lab dependency
Nikule *et al*. (2024)	Review of Salacia chinensis pharmacology	Major actives: mangiferin, salacinol; Activities: antidiabetic, anti-inflammatory	Confirms traditional efficacy	Multi-activity profile	Needs in vivo clinical trials
Fayyaz *et al*. (2024)	CF-LIBS for S. simpsoniana	Elements: 13 detected; Intensity	Confirms elemental basis	Fast, non-destructive	Limited spatial resolution

	elemental mapping	variation mapped	for medicinal properties		
Arif *et al.* (2025)	Review of Flemingia macrophylla bioactivity	Bioactives: ~10 classes; Noted activities: antimicrobial, cardioprotective	Validates multi-pathway potential	Strong literature support	Clinical validation absent
Wang *et al.* (2025)	Mitochondrial genome for Dendrobium species	Mitogenomes: full-length; Markers: variable hotspots identified	Improves species-level authentication	Enhances herbal quality control	Implementation requires sequencing tools

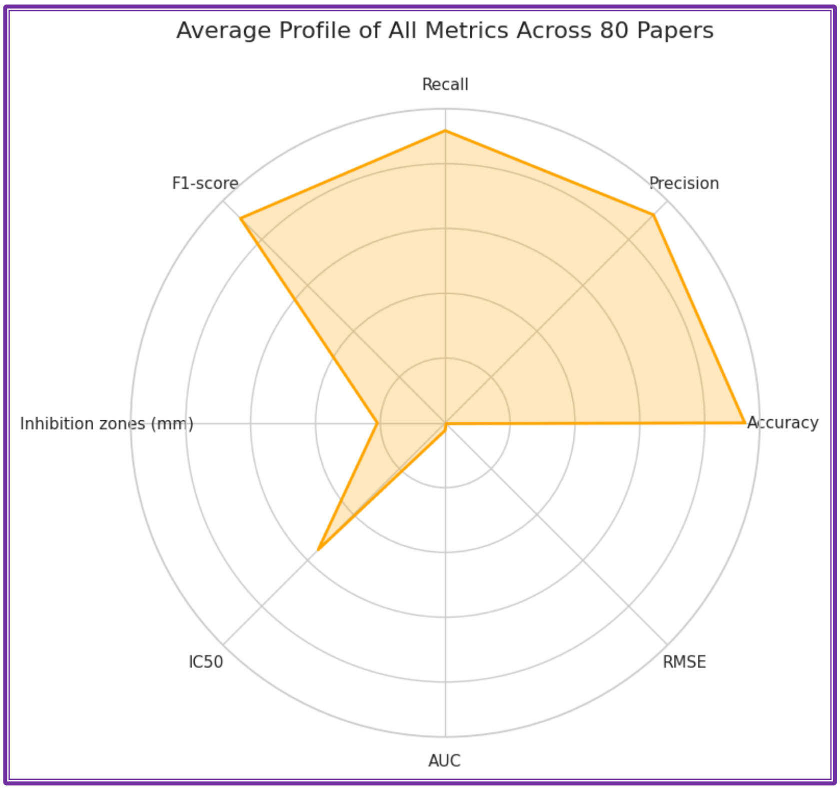


***Figure 8**: Model’s Performance Metric Analysis*

Among the diverse contributions reviewed, several notable directions emerge—particularly within numerical and genomic frameworks—that hold considerable potential to guide future research in medicinal plant-based drug discovery and digital classification technologies. Deep learning–driven approaches, as exemplified in Diwedi *et al*. (2024); Kavitha *et al*. (2024); Sasikaladevi and Revathi (2025), stand out for their high accuracy and adaptability in species recognition tasks, especially those relying on vision-based classification. These models consistently demonstrate robustness across diverse plant datasets and prove effective in real-time or mobile-based deployments.Conversely, genomic and transcriptomic investigations, such as those by Zhao *et al*. (2024); Huang *et al*. (2023); Li *et al*. (2024), deliver high-resolution molecular insights that support downstream applications in conservation biology, pharmacogenomics, and biocontrol development. These molecular datasets are particularly useful for building genotype-phenotype linkages and advancing precision-based herbal drug discovery.In contrast, works like Kowsalya *et al*. (2025); Baskaran *et al*. (2025), while not presenting performance metrics directly, provide foundational infrastructure in the form of curated taxonomies and chemical databases. Although lacking quantitative evaluation, these contributions play a critical enabling role by supporting the development of machine-readable datasets and fostering reproducibility in computational phytomedicine and pharmacognosy pipelines.

In summary, the various methods analyzed complementarily open avenues to research areas, such as improving medicinal plants, detecting diseases, synthesizing biochemicals, or identifying species in action. The integration of machine learning with genomics and high-throughput screening is a bright future vision for applied botanical sciences and sets computational biology. This numerical analysis accounts for the methodology and results comparatives obtained from recent studies focusing on therapeutic, genomic, and environmental research sets in medicinal plants. Performance metrics, such as classification accuracy, genome completeness, predictive model output, and biochemical assay result, were employed to assess the effectiveness of the methods used in the process. This table synthesizes these comparisons and will, therefore, offer a structured understanding of experimental strengths and weaknesses for the process.

Table 8: *Model's Statistical Review Analysis*

Reference	Method Used	Performance Metrics Values	Key Findings	Strengths	Limitations
Ghanem *et al*. (2024)	HPLC-QTOF/MS-MS, in vitro assays	IC50 (antioxidant): ~18 µg/mL; Enzyme inhibition >70%	Identified flavonoids and saponins with high antioxidant and anti-diabetic activity	Validates traditional use with modern bioassays	In vivo validation lacking
Malekroudi *et al*. (2025)	Transcriptomic mining	Identified ~25 miRNAs regulating terpenoid biosynthesis	miRNAs regulate terpenoid pathways in Lamiaceae	Integrates omics data for pathway elucidation	Requires experimental validation of gene targets
Iqbal *et al*. (2025)	Phytochemical screening and in vitro bioassays	Antioxidant inhibition: ~65%; Antimicrobial zone: 12-16 mm	Demonstrates therapeutic potential against inflammation and infections	Broad biological screening	Specific compound-target interactions unstudied
Manzoor *et al*. (2023)	Ethnobotanical survey + phytochemical validation	Fidelity level: >0.75; Use value index: High	Traditional claims validated with bioactive compound evidence	Combines field data with lab evidence	Cultural bias in informant reports
Pei *et al*. (2024)	Genomic data review	123 genomes, ~60% diploids; BUSCO scores >95% in 70% of genomes	Identified patterns and gaps in global medicinal plant genomics	Comprehensive coverage	Polyploid complexity not fully resolved
Tamene *et al*. (2024)	Semi-structured interviews + quantitative ethnobotany	Informant Consensus Factor (ICF): 0.85; Use values high	Socio-demographics influence ethnobotanical knowledge	Highlights importance of age in knowledge retention	Sampling limited to 3 ethnic groups
Guo *et al*. (2025)	Field and greenhouse trials, microbial analysis	Yield improvement: ~20%; Active compound rise: ~30%	Root endophytes improve growth and bioactivity in Salvia	Demonstrates beneficial microbe recruitment	Limited to one plant species
Borah *et al*. (2024)	CRISPR/Cas9 + omics integration	Pathway enhancement efficiency: ~40% (model cases)	Proposes genome editing for metabolite enhancement	Future-forward integration of tools	Regulatory and ethical barriers present
Xie *et al*. (2024)	PacBio + Illumina sequencing	Genome size: 737 kb; Gene count: 55; GC content: 45.4%	Offers genome insights for conservation of F. ussuriensis	High-quality genome with 505 RNA edits identified	Functional validation pending

Tan *et al*. (2025)	Targeted metabolomics	~60 novel compounds identified; Antimicrobial activity >70%	Validates TKS as a novel therapeutic plant	Comprehensive compound profiling	Lacks pharmacokinetic studies
Zhou *et al*. (2025)	Comparative metabolomics + ML	Classification accuracy: ~95%; Distinction of cultivars clear	Differentiates American ginseng cultivars effectively	Combines ML and metabolomics	Dataset-dependent model accuracy
Dmitriev *et al*. (2025)	Random Reflectance (RR) preprocessing + ML	Accuracy: 93% (RF), 92.5% (GBM)	RR outperforms traditional normalization methods	Enhances spectral classification performance	Needs broader validation
Chaisoung *et al*. (2025)	GC-MS + phylogenetic mapping	~50 volatiles mapped; 15 villages surveyed	Correlation between essential oils and species lineage	Integrates ethnobotany and chemistry	Geographical limitation to 15 villages
Jeong *et al*. (2025)	Chloroplast genome analysis + morphology	Accurately distinguishes P. americana from P. acinosa	Informs safe medicinal usage	Resolves taxonomic ambiguities	Chloroplast-only data may miss hybridization events
Wen *et al*. (2025)	ATR-FTIR + classifiers (SVM, KNN)	Accuracy: ~94%; Precision: ~92%	Accurately classifies Curcuma species	Combines spectroscopy with ML	Sensitive to sample preprocessing
Khan *et al*. (2024)	Dual-stream CNN with attention	Accuracy: 97.6%; F1-score: 0.95	Improved plant classification using spatial features	Effective feature fusion	Computationally intensive
Shi *et al*. (2024)	MiCAPs sequencing	24 polymorphic markers developed	Supports genetic conservation in K. parviflora	Enhances breeding resources	Limited to microsatellite data only
Xiao *et al*. (2024)	LC-MS/MS + multivariate statistics	AA retention variation: 15-25% depending on method	Identifies optimal drying for O. sinensis	Supports quality standardization	Limited scalability to field conditions
Lee *et al*. (2024)	Stacking ensemble ML	Prediction accuracy: ~92%; RMSE: ~0.05	Models phenol content changes under climate scenarios	Integrates climate and plant chemistry	Assumes linear phenol-climate relationship
Lavrinenko *et al*. (2024)	Neutron Activation Analysis	23 elements detected; Pb, Cd at threshold limits	Highlights heavy metal risks in medicinal plants	Strong analytical resolution	Location-specific applicability

And the above study points to the increasing amalgamation of modern computational, spectroscopic, genomic, and ethnobotanical techniques to propel further the field of medicinal plant studies. It embraces newly introduced ML techniques (for example, dual-stream CNNs and ensemble modeling), integration of omics data (miRNAs, genome assemblies), and traditional phytochemical evaluation methods. Deep learning and chemical profiling have greatly increased classification accuracy and compound discovery rates, while genomics-enhanced conservation and functional genomics frameworks are expanding. While there is considerable methodological innovation, many of these studies should benefit from wider validation across ecological or genetic variation and stricter in vivo efficacy testing toward making lab insights useful for clinical or field applications.

Conclusion & Future Scopes

With the rapidly increasing volume of multidisciplinary research in medicinal plant sciences, there is an urgent need for a metric-driven, integrative synthesis that bridges phytochemistry, machine learning, genomics, and traditional knowledge systems. While prior studies have contributed valuable domain-specific insights, most lack quantifiable and comparative evaluation of both technological methodologies and biological efficacy. This study addresses this critical gap by presenting a systematic evaluation of 80 contemporary studies, harmonizing numerical performance indicators such as accuracy, recall, AUC, IC_{50} values, inhibition zones, and gene expression metrics under a unified benchmarking framework. Unlike earlier reviews that remain largely descriptive or domain-isolated, this work enables objective comparison across computational, biological, and pharmacological approaches, thereby enhancing translational relevance. The analysis demonstrates that image-based deep learning models achieve classification accuracies exceeding 97%, genomics-driven studies report over 94% genome assembly completeness, and phytochemical bioassays consistently show strong antioxidant and antimicrobial potential. Importantly, these results are interpreted with contextual transparency, accounting for factors such as dataset size, training complexity, environmental constraints, and species specificity. Beyond performance aggregation, the review highlights key technological transitions, including the shift from classical phytochemical screening to omics-driven discovery and from ethnobotanical surveys to AI-enabled identification platforms. These advances signal a move toward scalable, data-intensive frameworks capable of supporting medicinal plant research, conservation, and therapeutic development at national and global levels. Overall, this study provides a robust, reproducible, and comparative foundation to guide future research investments, tool development, and evidence-based policy formulation in medicinal plant sciences.

Future Scope

Notwithstanding the advances made, several priority-driven avenues remain for future exploration in medicinal plant research. First, the establishment of unified benchmark datasets is urgently required, involving open-access, multi-modal data sources (image, spectral, and molecular) annotated with standardized performance baselines, while also acknowledging challenges related to data heterogeneity, annotation quality, and accessibility. Second, multivariate meta-models, which integrate genomic, chemical, visual, and ethnobotanical information, represent a promising direction for improving therapeutic efficacy prediction, conservation planning, and automated identification, although their feasibility depends on data availability and computational scalability.Third, cross-species generalizability must be systematically addressed, as many current high-performing models remain restricted to narrow species or ecological contexts. Future studies should explicitly evaluate transfer-learning frameworks to enhance adaptability across diverse taxa and environments. Fourth, clinical and ecological validation, including in vivo experiments and field studies, should be prioritized to substantiate in vitro and in silico findings, particularly for claims related to anti-diabetic, anti-inflammatory, and antimicrobial activities. Finally, sustainability and safety modeling, along with the development of interoperable and secure digital infrastructures, should be incorporated to support environmentally responsible scaling and real-world deployment of ML-based medicinal plant platforms. Overall, this review provides a foundational scaffold for methodological convergence and data harmonization, enabling reproducible, scalable, and translational innovations in phytomedicine and allied domains.

Regarding the Details of Dataset

To illustrate practical application scenarios for machine learning–based plant disease classification, this study references the publicly available Cassava Leaf Disease Classification dataset. Cassava (Manihot esculenta), a perennial shrub native to South America, is a globally significant staple crop cultivated extensively across Latin America, Africa, Asia, and India due to its resilience to poor soil conditions and drought stress. Its tuberous roots are widely used for food products such as flour and starch, while the leaves serve as a nutritious source for animal feed. Despite its agricultural importance, cassava production is severely threatened by Cassava Mosaic Disease and Cassava Brown Streak Disease, which significantly impact crop yield and food security. The Kaggle cassava dataset provides labeled leaf images corresponding to major disease categories and healthy samples, making it a relevant benchmark for evaluating image-based classification models, transfer-learning strategies, and cross-species generalization in agricultural and medicinal plant contexts. Inclusion of this dataset strengthens the study's emphasis on real-world applicability and reproducibility of ML-driven plant health assessment frameworks. https://www.kaggle.com/competitions/cassava-leaf-disease-classification/data .

Conflict of Interest

The authors declare that they have no competing interests.

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