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EXPLAINABLE ARTIFICIAL INTELLIGENCE FOR EARLY DETECTION, FORECASTING, AND INTEGRATED MANAGEMENT OF EMERGING PLANT DISEASES

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Abstract

Plant diseases caused by bacterial, viral and oomycete pathogens threaten global agricultural security. These diseases cause yield losses of 20 to 40 percent in major staple crops. This problem makes food insecurity worse in regions that have limited resources. Conventional ways to manage these diseases include checking fields by hand and using lab tests. These methods are time consuming and expensive. They also do not work well because they only find the diseases after symptoms are clearly visible. Some deep learning models like Convolutional Neural Networks, Vision Transformers and Graph Neural Networks have shown high accuracy when tested on standard data.. These models do not explain how they make decisions. This makes it hard for farmers to trust the results. Explainable Artificial Intelligence or XAI helps with this problem. XAI gives people information about how a model works. This review looks at how XAIs used in plant pathology, remote sensing and managing crops. It groups ways of explaining models based on whether they are built into the model or added after whether they explain one part or the whole model and whether they work for specific models or all models. The review looks at methods like SHAP, LIME, Grad-CAM, Grad-CAM++, Integrated Gradients and Focus Score. It checks how well different computer vision models work and how they balance accuracy with explainability. It shows that new models like ConvNeXt- focus on real disease areas. Older models like VGG16 often pay attention to things that're not important. The review also looks at using drones with cameras to find diseases before symptoms appear. It talks about predicting disease spread over time using models. It also looks at combining types of data to find genes that fight diseases and to discover new microbes. Finally, the review shows how to add XAI to computers and to systems that help make decisions, about crops. This makes it possible to spray chemicals where needed and to use these tools in the field easily.

INTRODUCTION

Plant diseases caused by fungi, bacteria, viruses and water molds are a danger to global farming. These diseases cause financial losses and reduce crop yields by 20% to 40% every year. These plant diseases hurt the lives of people in areas. They make agricultural markets unstable. They also make it harder to have food in places that don't have much to begin with (Gai & Wang 2024). For a time, people have tried to manage crop diseases by looking at plants in the fields. They also used labs to test for diseases. These tests include things like PCR and ELISA. Even though lab tests are very accurate checking plants in the field takes a lot of work. It is expensive. It can be biased. It also can't work for big areas. Often people only find the diseases after the plants show signs (Fones et al. 2020).

The use of intelligence, high-quality computer vision and different types of remote sensing has changed how plant diseases are studied. Deep learning models like CNNs, ViTs and GNNs have become really good at finding and classifying plant leaf diseases. They have accuracy over 98% when tested on data sets (Rhouma, 2025). Even though these models are very good at identifying problems they work in a way that's hard to understand. The way they make decisions is hidden in layers of math. This makes it hard to know why they make choices (Ezrari et al. 2024).

This lack of thinking behind the decisions makes it hard to use these models in real farming. Farmers and people who work with crops don't want to spend a lot of money on actions like using chemicals or destroying crops based on results they can't understand. Models that are not clear can also learn the things. They might focus on things, like the color of the soil or the light of the real problem. So even if the model works in the lab, it might not work well in real fields (Mahadevakumar & Sridhar 2021).

Explainable AI helps with this problem. It gives people a way to understand how the models make their decisions. In plant diseases this means showing people where the problems. It also means explaining the parts of the data that matter most. This helps turn models that're hard to understand into tools that people can trust (Lucas, 2011).

This review talks about how explainable AIs used in plant diseases remote sensing and managing crops. It looks at how to make models easier to understand. It checks the pros and cons of models. It also looks at using types of sensors to find diseases before they show up. It talks about predicting when diseases might happen and finding ways to study plants. It also explains how to add AI to tools that farmers use every day (Hariharan et al. 2022).

2. Paradigms of Explainable AI in Botanical Pathology

Establishing machine learning frameworks for precision agriculture means sorting XAI methods based on three main areas. These areas are intrinsic versus -hoc interpretability, local versus global explanations and model-specific, versus model-agnostic techniques (Pai et al., 2025).

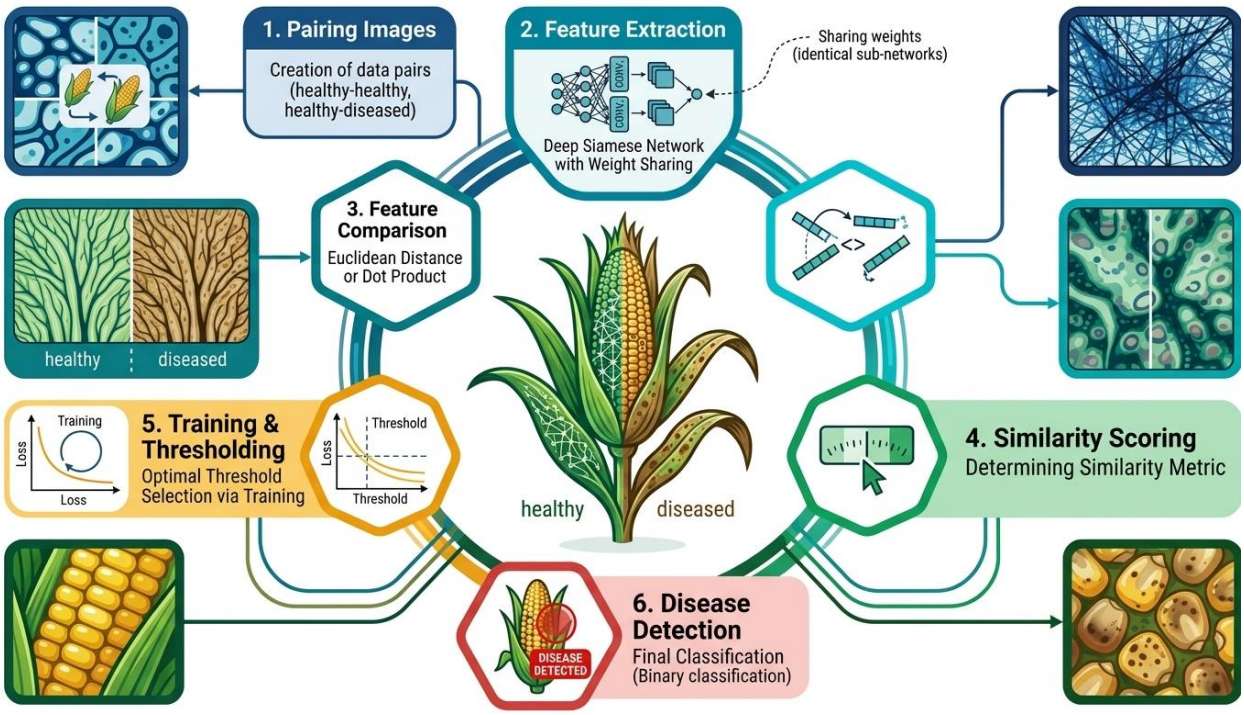


Figure 1: Siamese Neural Network Architecture and Feature Comparison Workflow for Comparative Plant Pathology and Similarity-Based Disease Detection.

2.1 Intrinsic vs. Post-Hoc Interpretability

Intrinsic interpretability means building machine learning models that're clear and understandable from the start. This happens because of how these modelsre designed mathematically. Examples are decision trees, linear regression and generalized additive models. These models are easy to read and explain.. They often cannot handle complex patterns in data. Especially when it comes to natural field imagery, which has details in space and color. That's because these models don't have power to capture high-dimensional patterns (Arrighi et al. 2025).

On the hand post-hoc interpretability works differently. It separates the model training step from the explanation step. After a model is fully trained techniques are used to understand it. These techniques look at neural networks, like DenseNet, ConvNeXt or Vision Transformers. Methods include checking activation maps sending gradients backward through the network or changing parts of the input to see what matters most. The goal is to find which parts of the data affect the output. All of this is done without hurting the model's performance (Venkateswara & Padmanaban 2025).

2.2 Local vs. Global Explanations

Local explanations clarify each model prediction showing why a particular leaf image, such as one with Tomato Early Blight was labeled as diseased by marking the lesion area. Global explanations summarize how the model behaves on the dataset or, across a crop species revealing which features the model prioritizes, how the model activates across different classes and any systematic biases that may come from environmental noise (Somvanshi et al. 2025).

2.3 Model-Specific vs. Model-Agnostic Approaches

Model-agnostic methods look at the machine learning model as a box. They change inputs in a way to see how the output predictions shift. These methods do not need to know what is inside the model. On the hand model-specific methods use

details about the inner workings of the model. They depend on things, like network parameters, feature maps or activation gradients (Dib & Capus 2025).

SHapley Additive exPlanations (SHAP)

Rooted in cooperative game theory, SHAP calculates feature importance by treating input pixels or spectral bands as players in a coalition, allocating fair attribution based on their marginal contributions to the model's output (Fumagalli, 2025). The local additive feature attribution model is expressed as:

$$g(z') = \phi_0 + \sum_{i=1}^{M} \phi_i z_i'$$

where g(z') is the explanation surrogate model, z' belongs to {0,1}^M and represents simplified binary coalition features M is the maximum coalition size ϕ_0 is the baseline model output when no inputs are provided and ϕ_i is a real number representing the Shapley attribution value assigned to feature i. For image classification SHAP divides images into superpixels or uses gradient-based methods (such, as GradientExplainer) on background samples to estimate expected model outputs (Rhouma, 2025).

Local Interpretable Model-agnostic Explanations (LIME)

LIME constructs local explanations by perturbing an input instance x (e.g., masking superpixels) and training an interpretable surrogate model $g \in G$ (such as a sparse linear model) on the perturbed samples. The objective function minimizes classification loss while penalizing surrogate complexity:

$$\text{Explanation}(x) = \arg\min_{g \in G} \mathcal{L}(f, g, \pi_x) + \Omega(g)$$

where $\mathcal{L}$ measures the divergence between the complex model f and the surrogate g, $\pi_x(z)$ defines an exponential distance proximity measure between perturbation z and x, and $\Omega(g)$ penalizes surrogate model complexity (Yavaşlı, 2026).

Gradient-weighted Class Activation Mapping (Grad-CAM and Grad-CAM++)

Grad-CAM computes spatial attribution heatmaps by calculating the gradients of the score for class c (Y^c) with respect to feature activation maps A^k of the final convolutional layer. Neuron importance weights α_k^c are derived via spatial average pooling:

$$\alpha_k^c = \frac{1}{Z} \sum_{i=1}^{U} \sum_{j=1}^{V} \frac{\partial Y^c}{\partial A_{i,j}^k}$$

where $Z = U \times V$ represents the spatial dimensions of the feature map. The class-specific activation map is generated using a Rectified Linear Unit (ReLU) function:

$$L_{\text{Grad-CAM}}^c = \text{ReLU}\left(\sum_k \alpha_k^c A^k \right)$$

Grad-CAM++ extends this formulation by incorporating higher-order partial derivatives (second and third gradients), enhancing spatial localization when multiple pathogenic lesions or co-occurring diseases appear on a single leaf (Hasić et al., 2026).

Table 1: Comparative Analysis of Core Explainable AI Methods in Phytopathology

XAI Method	Paradigm & Scope	Mathematical Basis	Primary Output Format	Key Strengths in Phytopathology	Operational Limitations
Grad-CAM	Model-Specific; Local	First-order gradients from final conv-layer	Coarse spatial activation heatmap	Highly efficient; accurately isolates primary infection focus	Low spatial resolution; misses fine structural details
Grad-CAM++	Model-Specific; Local	Higher-order gradient weighted averages	High-resolution heatmaps for	Superior localization for multiple scattered spots or rusts	Sensitive to gradient saturation in

			multi-target zones		extremely deep models
LIME	Model-Agnostic; Local	Perturbation sampling & local linear surrogates	Superpixel segmentation mask overlays	Compatible with non-differentiable & multi-modal inputs	High computational overhead; sensitive to superpixel boundaries
SHAP	Model-Agnostic / Specific; Local & Global	Cooperative game theory Shapley values	Pixel/Feature attribution vectors & interaction plots	Rigorous theoretical foundation; detects feature synergies	Sampling approximations can be slow on high-res images
Integrated Gradients	Model-Specific; Local	Path integral of gradients from baseline to input	Pixel-level feature attribution maps	Satisfies axiomatic completeness & implementation invariance	Baseline choice (e.g., black image) directly impacts attributions
Focus Score	Model-Specific; Local/Global	Spatial overlap between focus map & target object	Quantitative reliability score (0.0 to 1.0)	Quantifies explainability; filters out background noise	Requires reference object bounding or segmentation masks

3. Computer Vision Architectures and Visual XAI for Leaf-Level Disease Diagnosis

Computer vision models used in diagnostics include traditional Convolutional Neural Networks, lightweight mobile designs, modern Vision Transformers and hybrid approaches. Even though deep classifiers often show accuracy on benchmark datasets such as PlantVillage, evaluations, after the fact using explainable AI methods show that these models interpret visual inputs in different ways (Upadhyay et al., 2025).

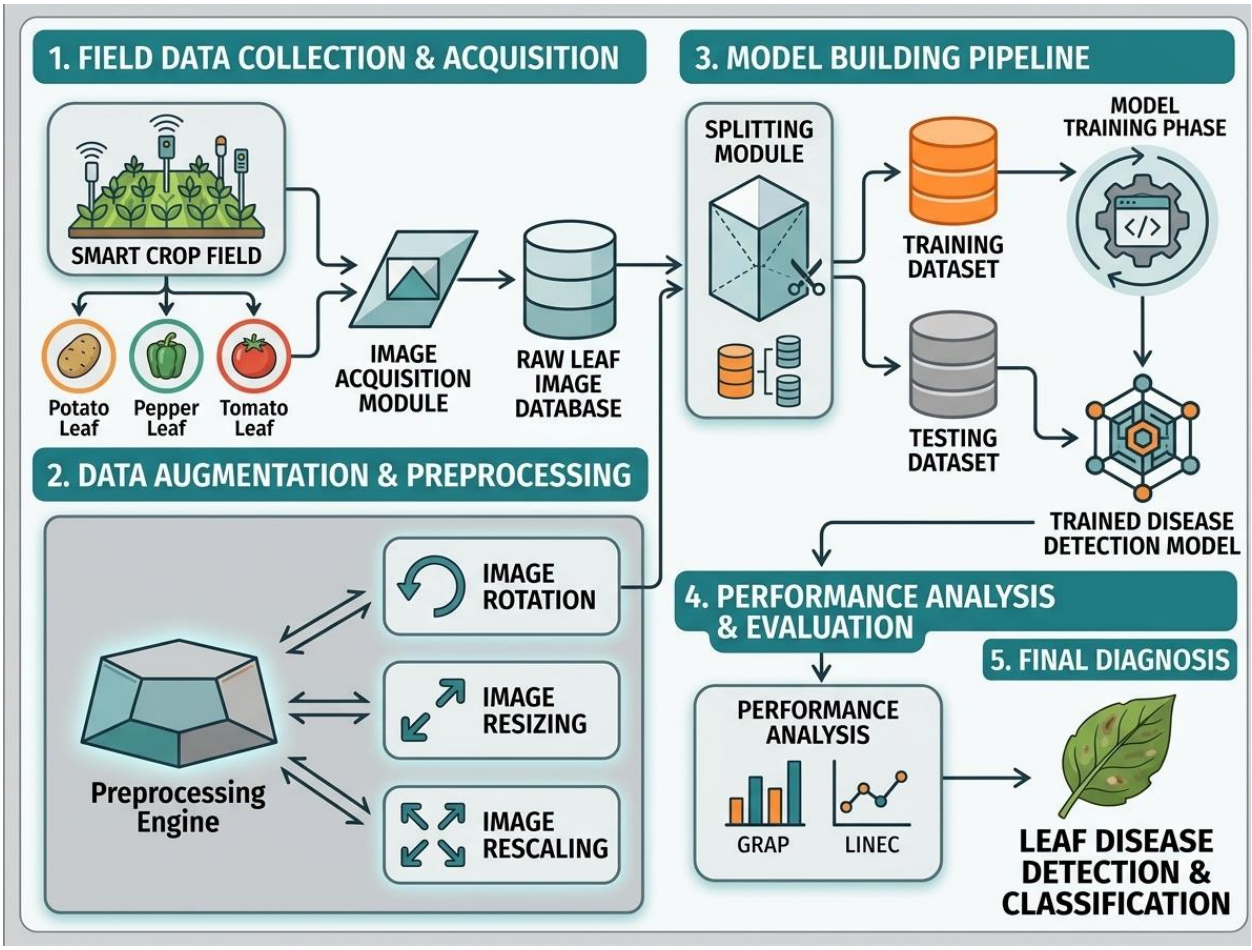


Figure 1: End-to-End Machine Learning Pipeline for Crop Foliar Disease Acquisition, Preprocessing, Model Training, and Diagnostic Evaluation.

3

.1 Architectural Trade-offs and the Accuracy-Explainability Paradox

Comparative tests across crops such as maize, potato, pepper and tomato show that modern lightweight models, for example ConvNeXt-Tiny and MobileNetV2 and optimized deep networks, such as EfficientNet-B4 and DenseNet-121 achieve validation accuracies between 97.8% and 100%. However, XAI analyses indicate that classification accuracy alone does not guarantee biologically sound decision-making. Older deep architectures, such as VGG16 often rely on background soil conditions, leaf margin silhouettes or lighting artifacts. In contrast modern architectures such, as restrict activations almost exclusively to chlorotic halos, necrotic centers and pustules (Junaidi et al. 2025).

3.2 Quantitative Evaluation Metrics for Visual Attribution

To evaluate visual explanations beyond subjective qualitative review, researchers employ rigorous quantitative metrics:

- **Deletion Score**: Measures the decline in classification probability as top-attributed pixels are progressively zeroed out. A rapid drop indicates the model relied on genuinely informative diagnostic features.
- **Insertion Score**: Tracks the increase in classification confidence as high-attribution pixels are added to a neutral baseline image.

• **Infidelity Metric**: Quantifies the mean squared difference between predicted output changes and feature attributions under small input perturbations.

• **Focus Score**: Calculates the ratio of class activation energy located within expert-annotated lesion boundaries relative to total image activation (Zhang et al., 2025).

Table 2: Performance and Interpretability Metrics Across Deep Learning Architectures on Benchmark Datasets

Model Architecture	Target Crop / Pathology Context	Dataset Scale & Conditions	Classification Accuracy (%)	Primary XAI Methods Applied	Quantitative Interpretability & Alignment	Primary Diagnostic Mechanics & Observations
ConvNeXt-Tiny	Maize, Pepper, Potato Diseases	8,479 Segmented Foliar Images	99.0% – 100.0%	Grad-CAM	High spatial focus on lesion regions	Activations precisely track lesion borders; suppresses leaf background noise.
MobileNetV2	Maize Leaf Blight & Rust	Controlled Field Datasets	97.6% – 99.7%	Grad-CAM, Focus Score	High Focus Score efficiency; low latency	Optimized for edge deployment; occasional focus shift to prominent leaf veins.
EfficientNet-B4	Multi-Species Leaf Dataset	PlantVillage Benchmark	99.4%	Grad-CAM, LIME, SHAP	Alignment Score: 4.3/5.0	Balanced feature extraction; parameter efficient.
DenseNet-121	Watermelon / Maize Leaf Pathology	Mixed Field Datasets	97.85% (Test)	Grad-CAM, Score-CAM	High spatial fidelity on fungal lesions	Feature reuse mechanisms retain lesion border details across deeper layers.
CFNET (Custom Deep)	Multi-Crop Cross-Species Domain	Distorted Field Imagery	79.0% – 85.0% (Cross-Species)	Grad-CAM++, SHAP, LIME	Robust under image distortion	Retains localized focus under lighting variations and domain shifts.

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VGG16 / VGG19	Multi-Species Foliage	PlantVillage Datasets	97.0% – 98.9%	Grad-CAM, LIME	Moderate/Poor Focus Score	Prone to learning background artifacts, leaf edges, and lighting variations.

4.
Multi-Spectral, Hyperspectral, and UAV Remote Sensing for Early Pre-Symptomatic Detection

Detecting diseases after visible foliar damage occurs limits intervention options, leaving chemical rescue treatments as the primary recourse. Transitioning to early pre-symptomatic detection requires tracking physiological disruptions before visible lesions develop (Özden, 2026).

4.1 Biophysical Bases of Early Spectral Detection

Pathogen colonization triggers distinct physiological changes that modify spectral reflectance signatures:

- **Photosynthetic Breakdown**: Chlorophyll *a* and *b* degradation alters visible light absorption, inducing reflectance shifts in the green (530–580 nm) and red-edge (680–740 nm) spectrum.
- **Cellular Structural Collapse**: Fungal hyphae colonizing spongy mesophyll tissue alter near-infrared (NIR: 750–1100 nm) light scattering.
- **Transpiration Stress**: Stomatal closure and vascular blockages disrupt leaf energy balances, altering surface temperature profile signals in thermal infrared wavelengths.

Hyperspectral sensors mounted on Unmanned Aerial Vehicles (UAVs) collect continuous narrow-band data across hundreds of spectral channels. However, the high dimensionality of hyperspectral data cubes introduces computational complexity, band redundancy, and risk of overfitting (Hong et al., 2026).

4.2 XAI for Spectral Feature Selection and Intercropping Disambiguation

- Explainable AI helps pick the wavelengths by selecting only those that give useful biological information and dropping extra spectral bands that do nothing. In my view the latest systems that combine Detection Transformers (DETR) with Greedy Political Optimization (EGPO) and Capsule Spatial Shift Neural Networks (CSSNet) use Explainable AI to spot the specific spectral bands that signal disease:

- **Maize Leaf Spot & Rust**: Key diagnostic bands identified at 540 nm, 580 nm, 720 nm, and 740 nm.
- **Pea Powdery Mildew**: Critical bands isolated within 550–600 nm and 710–740 nm.
- **Cucumber Anthracnose**: Highest attributions concentrated at 550 nm, 600 nm, 720 nm, and 740 nm.

In farming systems like when crops are grown together (for example corn and beans or peas and cucumbers) the plants leaves and stems overlap a lot. This makes it hard to tell the plants apart. Models called DETR that use ways to pick important parts of the data and other tools for classifying plants do very well. They get perfect results with an average of 99.998% correct. After the models make their predictions, methods, like LIME, SHAP and Grad-CAM show that the models are using signs of plant health. These methods show that the models match the areas where plantsre sick with a score of 99.997% compared to the areas marked by experts (Ewieda et al. 2026).

5. Spatiotemporal Forecasting and Multi-Omics Mechanistic Integration

Managing agricultural epidemics needs to go beyond leaf checks at a single moment. Managing agricultural epidemics must now use predictive, models. By mixing disease forecasting, with multi-omics data we can track how pathogens

spread and better understand how plants defend themselves (Lou et al., 2026).

5.1 Spatiotemporal Forecasting via Graph Neural Networks and Digital Twins

Pathogen propagation depends on conditions like canopy humidity how long leaves stay wet and the air temperature. It also depends on wind patterns in the region. How close fields are to each other. Standard time-series models usually have trouble handling these non-linear relationships across space (Jones & Barbetti 2012).

To better model these dynamics researchers use temporal digital twins. These combine Convolutional Long Short-Term Memory networks known as ConvLSTM with Graph Neural Networks or GNNs. In this setup agricultural fields are treated as nodes in a graph, written as G = (V, E). The edges between nodes, represented by e_ij carry information about distance between fields, wind direction and similarities in climate. Each node holds past data on disease occurrence along with measurements, over time (Khusnitdinova et al., 2026).

Post-hoc SHAP analysis applied to spatiotemporal GNN models identifies key environmental drivers:

- **Consecutive Leaf Wetness Duration (> 8 hours)**: Exhibits the highest positive SHAP value for spore germination probability.
- **Canopy Relative Humidity (> 85%)**: Serves as a primary driver for temporal spore propagation.
- **Spatial Proximity to Active Infection Centers**: Represents the main structural edge attribute influencing field risk (Garrett et al., 2014).

5.2 Multi-Omics Integration and Biological Discovery via XAI

While remote sensing tracks field-scale disease dynamics, multi-omics frameworks reveal underlying host resistance pathways and pathogen interaction mechanisms. Integrating genomics, transcriptomics, metabolomics, and proteomics clarifies plant-pathogen-microbiome interactions.

Explainable AI moves machine learning from black-box phenotype prediction to verifiable hypothesis generation:

- **Genome-Wide Resistance Gene Annotation**: Frameworks like R-Predictor combine protein language-model embeddings with Random Forest classifiers to predict resistance (*R*) genes and Leucine-Rich Repeat (LRR) structural domains. Applying feature attribution models to transcriptomic data isolates upregulated candidate *R*-genes for downstream validation (Schroth et al., 200).
- **Cross-Kingdom Interaction Biomarkers**: In soybean multi-omics studies under environmental stress, Random Forest models integrated with SHAP interaction analysis outperform standard linear models. SHAP interaction scores identify cross-kingdom modules linking host metabolomics to rhizosphere bacteria, isolating the isoflavone derivative *daidzin*, gamma-aminobutyric acid (*GABA*), and beneficial taxa such as *Paenibacillus* and *Sphingopyxis*.
- **Microbiome Dynamics**: Graph neural networks like SIMBA-GNN model complex host-pathogen-microbiome interaction networks. Applying SHAP feature attribution identifies functional bacterial groups capable of suppressing soil-borne pathogens like *Fusarium oxysporum*, supporting microbiome-assisted breeding and targeted biofertilizer applications (Dhavale et al., 2025).

Table 3: Multi-Omics and Spatiotemporal XAI Frameworks for Plant Protection

System Domain	Primary Model Architecture	Integrated Data Modalities	Applied XAI Techniques	Discovered Biological & Agronomic Mechanics
Spatiotemporal Epidemiology	ConvLSTM-GNN Hybrid	Satellite thermal imagery, local weather networks, spatial graphs	Polynomial-SHAP, Temporal Attention	Identifies leaf wetness duration (> 8 hr) and wind vector corridors

				as primary outbreak triggers.
***R*-Gene Annotation**	R-Predictor + Random Forest	Protein language embeddings, transcriptomic RNA-seq	TreeSHAP, Feature Importance	Prioritizes non-canonical LRR-domain resistance genes in grapevine and rice.
Microbiome Integration	SIMBA-GNN / GNN Models	Rhizosphere 16S rRNA sequencing, metabolomics	SHAP Interaction Values, GNNExplainer	Isolates *Sphingopyxis* and *Paenibacillus* taxa as key drivers of host immune priming.
Crop Climate Stress Modeling	Spatiotemporal CNN + ANN / SNN	Soil chemistry, regional weather, multi-spectral drones	SHAP, LIME	Maps non-linear interactions between nitrogen application rates and pathogen susceptibility.

6. Integrated Disease Management (IDM) and Real-World Field Deployment

Translating XAI from experimental settings into agricultural operations requires embedding explainable models into field-ready decision support systems (DSS) and precision spray machinery (Wang et al., 2026).

6.1 Variable Rate Application and Autonomous Precision Spraying

Conventional chemical treatments often apply broad-spectrum fungicides uniformly across fields, increasing input costs, accelerating chemical resistance, and compounding environmental risks. Combining XAI attribution maps with precision agricultural machinery enables Variable Rate Application (VRA) systems:

- UAVs or tractor-mounted cameras capture foliar imagery across field zones.
- Lightweight edge networks (e.g., MobileNetV2, ConvNeXt-Tiny) process images using activation mapping algorithms like Score-CAM or Grad-CAM to generate spatial infection grids.
- Generated attribution maps are converted into GIS prescription files for variable-rate sprayers. Spray nozzles actuate over infected canopy zones, modulating chemical dosage based on localized severity while skipping healthy foliage (Min et al., 2026).

6.2 Edge Deployment on Resource-Constrained Hardware

Deploying XAI in field settings requires efficient real-time execution on low-power devices (e.g., mobile phones, onboard UAV compute units) operating without continuous cloud connectivity. Structural optimizations enable real-time performance on edge hardware:

- **Attention Pruning**: Strategies like Least Important Attention Pruning (LeIAP) evaluate attention head weight contributions in Vision Transformers, removing redundant parameters without compromising spatial localization.
- **Sparse Matrix-Matrix Multiplication (SPMM)**: Accelerates inference latency on mobile processors, enabling real-time attribution generation at high frame rates (> 30 FPS).
- **User-Centric Visual Interfaces**: Field interfaces display classification confidence alongside superpixel or heatmap overlays highlighting identified lesions. This provides clear, interpretable diagnostic information for extension personnel and farmers (Fones et al., 2020).

Conclusion

This review shows that Explainable Artificial Intelligence has grown from an add-on into a key part of modern plant disease work and precise crop care. By making deep learning predictions clear with tools like SHAP, LIME, Grad-CAM and

Integrated Gradients XAI closes the trust gap that once stopped farmers from using black-box model results. The evidence here reveals three steps. First comparing architectures shows the accuracy-explainability paradox: high test accuracy alone does not mean the model is reasoning well. Older networks often focus on soil, leaf edges or lighting glitches while newer models such as ConvNeXt-Tiny and EfficientNet-B4 find real disease features like halos, dead centers and pustules. New metrics such as Deletion, Insertion, Infidelity and Focus Score give repeatable tests for this. Second XAI helps pick spectral bands finding key wavelengths (540, 580, 720 and 740 nm) for maize leaf spot and rust. SHAP on GNN models pulls out key outbreak drivers like leaf wetness longer than eight hours canopy humidity above 85 % and wind patterns. Third combining data types turns machine learning from simple prediction to idea creation uncovering unusual resistance genes and helpful microbes like Paenibacillus and Sphingopyxis that boost plant defense. In practice techniques such as attention pruning, sparse matrix math and user-friendly visual tools now let farmers generate XAI comments at over 30 frames per second on field devices enabling smart spraying that applies more pesticide where damage is high and skips healthy leaves. Still problems remain: SHAP can be slow on detailed images LIME can be sensitive to how it cuts up the picture and Integrated Gradients depends on the baseline choice. Future work should focus on tests that span many species uncertainty-aware XAI methods, privacy-friendly shared learning and long-term checks that show XAI-guided actions truly improve yield and profits. Embedding biology-based XAI models into disease management plans will be crucial, for safe, fair and climate-smart food security worldwide.

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