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A Review on Image-Based Methods for Plant Disease Identification in Diverse Data Conditions

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***Abstract*—Image-based plant disease identification methods have demonstrated potential in enhancing crop protection through early detection. However, the development of this field faces several challenges, such as the scarcity of high-quality annotated data, significant intra-class variation and high inter-class similarity among plant diseases, and the limited generalization ability of current models under diverse domain conditions. We extensively investigated 110+ latest papers on plant disease identification, aiming to present a timely and comprehensive overview of the most recent advances in the field, along with impartial comparisons of strengths and weaknesses of the existing works. Specifically, we begin by reviewing traditional machine learning and deep learning methods, which form the foundation for many current models. We then introduce a taxonomy of transfer learning methods, including instance-based, mapping-based, and network-based methods, and analyze their effectiveness in enhancing classification performance by leveraging prior knowledge under data-constrained scenarios. Subsequently, we examine recent advances in few-shot learning methods for plant disease identification, categorizing them into model-based, metric-based, and optimization-based methods, and evaluate their capabilities in addressing data scarcity and improving identification accuracy. Finally, we summarize the current limitations and outline promising future research directions, with the aim of guiding continued development in this area.**

***Keywords*—Few-shot learning; transfer learning; deep learning; crop protection; early detection; data scarcity**

I. INTRODUCTION

Plant disease identification has emerged as a significant area of research. Timely identification of plant diseases is critical for reducing crop losses and minimizing the use of pesticides [1]. Image-based plant disease identification has emerged as a fast, accurate, and reliable method for early detection [2],[3]. These methods typically involve several stages, such as image acquisition, image processing, feature extraction, and classification.

However, image-based methods face critical challenges. Variations in noise, background, and lighting in plant disease datasets often affect identification accuracy [4]. In addition, the diversity of tasks, such as identifying citrus diseases [5], tomato diseases [6], and wheat diseases [7], combined with the presence of grafted, hybrid, and genetically modified plants, exacerbates issues of data scarcity and class imbalance in plant disease identification. These challenges underscore the need for new image-based techniques, such as few-shot learning (FSL) [8], [9], transfer learning (TL) [10], [11].

Previous studies have explored various methods for plant disease identification. For example, support vector machines (SVMs) [12], convolutional neural networks (CNNs) [13], TL[14], and generative adversarial networks (GANs) [15]. However, existing surveys are predominantly architecture-centric [3],[16], offering limited guidance when data conditions, rather than model choice, are the primary bottleneck. In practice, field performance is more often constrained by domain shift, class imbalance, and scarce labels than by marginal architectural differences. To ground our review, we conducted a structured search across IEEE Xplore, Scopus, Web of Science, and Google Scholar covering 2019 to 2025, complemented by backward and forward citation tracing to capture seminal earlier work. The search queries combined keywords including plant disease, early detection, leaf disease identification, transfer learning, domain adaptation, and few-shot learning. From over 230 retrieved studies, we retained 116 directly relevant papers on image-based plant disease identification.

To address the identified gap, we adopt a scenario-driven taxonomy organized by three data regimes: (i) tasks with sufficient samples, (ii) tasks with limited samples but abundant related task data, and (iii) tasks with limited samples and no related data. The objective is to map method families to each regime. We synthesize prior work, identify recurring limitations, and provide scenario-specific recommendations for method selection under realistic field conditions. For navigation, an overview diagram is placed at the beginning of Section II (Fig. 1), linking data regimes to the technique families reviewed in Sections II-IV.

II. MACHINE LEARNING OR DEEP LEARNING FOR PLANT DISEASE IDENTIFICATION

When a sufficient amount of data is available, both machine learning (ML) and deep learning (DL) methods have proven effective in various plant disease classification tasks. In this section, a classification method is proposed that combines traditional ML, DL, and their fusion. Fig. 1 illustrates the classification methods reviewed in this study, providing practical guidance for plant disease identification under varying data scenarios.

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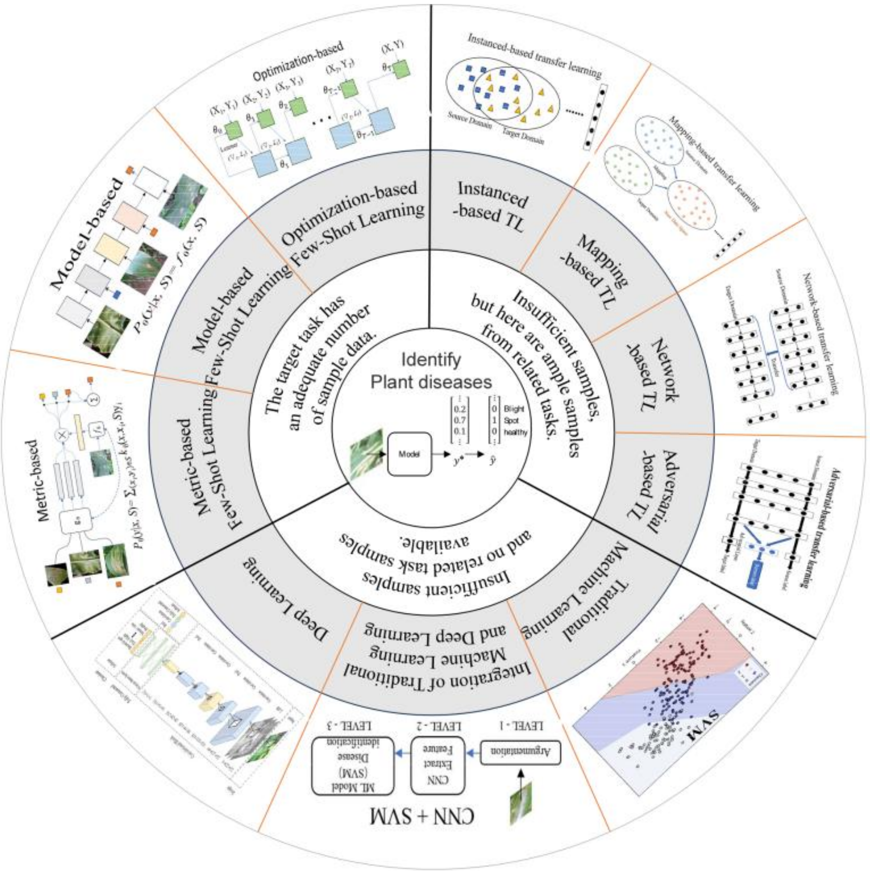

Fig. 1. Scenario-driven taxonomy of image-based plant-disease identification methods under diverse data conditions. The diagram maps three data regimes (sufficient data, limited data with related sources, and limited data without related sources) to representative technique families. (ML, DL and their fusion; transfer learning; few-shot learning).

A. Traditional Machine Learning Methods

Traditional ML methods rely on extracting features such as color, texture, and shape, making the models interpretable. Support Vector Machines (SVM) are particularly effective in handling high-dimensional data [17], while the K-Nearest Neighbors (KNN) algorithm is known for its simplicity and reliability [18]. Additionally, Naive Bayes (NB) classifiers are efficient when processing large datasets [19]. Furthermore, ensemble learning methods like Random Forests (RF) and Gradient Boosting Trees combine multiple weak learners to improve overall performance and robustness [20].

Logistic Regression (LR), NB, and Discriminant Analysis (DA) are often used to simplify complex problems by assuming feature independence, which reduces high-dimensional data to simpler forms. Appeltans *et al*. [21] trained an LR classifier to detect five classes of leek white tip disease, achieving an overall accuracy of 96.74%. However, LR tends to perform poorly in cases involving nonlinear or multi-feature problems, especially when multicollinearity among features is present [22]. DA assumes that data follows a normal distribution and that different groups have equal covariance. Mahmud *et al*. [23] used DA for real-time detection of strawberry PM disease in the field by extracting texture features with color co-occurrence matrices. This method achieved a maximum accuracy of 95.45%. However, DA may not perform well if the data does not meet the assumption of normal distribution [24]. NB works well with different types of data distributions. For instance, Prashar *et al*. [19] used NB combined with a firefly optimization method to identify 494 rice leaf images from five disease categories. However, NB may suffer from reduced accuracy when dealing with features not present in the training data or when ignoring dependencies between features.

SVM, KNN, and Decision Trees (DT) are non-parametric models that do not rely on specific data distribution assumptions or linear relationships among features. KNN works well for small datasets with low-dimensional image features [18]. Devi *et al*. [25] combined Harris corner detection, Histogram of Oriented Gradients, and KNN for peanut disease classification. This method achieved an accuracy of 97.67%. SVMs may face challenges with high-dimensional data due to the "curse of dimensionality" [26]. To address this, Javidan *et al*. [27] used Principal Component Analysis to reduce feature dimensions and applied ReliefF to select key features. RF improves model accuracy by combining the results of multiple DTs. Basavaiah *et al*. [20] compared RF and DT classifiers for plant disease detection. RF achieved a higher accuracy of 94%, while DT reached 90%. Table I summarizes traditional ML methods for plant disease identification.

TABLE I. SUMMARY OF TRADITIONAL ML METHODS FOR PLANT DISEASE IDENTIFICATION

Methods	Dataset	Type of features	Accuracy (%)	Disadvantages
RF [20]	Tomatoes, self-built	Text, color, and shape	94.00	Requires large datasets.
OWs+KNN [18]	Strawberries, self-built	Spectral	93.33	Sensitive to irrelevant features.
SLIC_SVM [17]	Tea, self-built	Shape and textural	98.50	Depends on hyperparameters.
LDA+LR [21]	White, self-built	Hyperspectral	96.74	Limited on high-dimensional.
CCM+DA [23]	Strawberries, self-built	Color and textural	95.45	Not suitable for nonlinear data.
NB+Firefly [19]	Paddy, self-built	Color and textural	98.64	Conditional independence.
SVM+FOA [26]	Tomatoes, PlantVillage	Text, color, and shape	91.10	Slow convergence.

B. Deep Learning Methods

DL enables the automatic extraction of hierarchical representations from large and complex datasets. Methods such as CNN, recurrent neural network (RNN), and Transformer effectively capture intricate patterns and features in plant imagery, offering significant advantages over traditional ML methods.

CNNs are powerful tools for extracting image features through layers of convolution, pooling, and fully connected operations. They can improve performance by increasing network depth, but deeper networks often make training more challenging. ResNet [28] addresses this issue by introducing residual connections, which facilitate gradient flow, allowing the training of much deeper models. On the PlantVillage dataset, a widely used public dataset, the PDICNet model based on ResNet-50 achieved an accuracy of 99.73% [13]. In contrast, DenseNet [29] connects each layer to every other layer in a feed-forward way, improving feature sharing and reducing redundancy. Multi-headed DenseNet was tested on the PlantVillage and achieved an accuracy of 98.17% [30].

Unlike ResNet and DenseNet, MobileNet is designed to reduce the number of parameters and computational cost. However, its accuracy may be lower for more complex datasets, as noted by Bi *et al.* [31]. They improved the MobileNet and achieved an accuracy of 73.50%. Multi-kernel depthwise separable convolutions are employed to reduce the number of model hyperparameters. Lite-MDC [32] utilizes only 2.20M parameters and achieves an accuracy of 99.78% on PlantVillage. These methods are compatible with mobile and embedded systems, where computational efficiency is critical. By focusing on diseased areas and reducing the influence of background noise, attention mechanisms contribute to improved classification accuracy [33]. The rE-GoogLeNet model adds the ECA attention mechanism into the Inception module and achieves an accuracy of 99.58% [34]. XSE-TomatoNet [35] combines SE blocks with multi-scale feature fusion to enhance the classification performance of EntricNet-B0.

For real-time applications, improved models such as YOLOv5s [36] and DM-YOLO [37] have been proposed to achieve faster inference while maintaining high detection accuracy. However, despite their efficiency in spatial object detection, these models are limited in capturing temporal dependencies across image sequences. To address this, RNNs have been employed for analyzing time-lapse images and video data, enabling the modeling of dynamic changes in plant growth and disease progression [38].

Vision Transformers (ViTs) have demonstrated strong performance in plant disease identification by modeling long-range dependencies. A recent study reported an optimized ViT architecture that attained state-of-the-art performance on PlantVillage [39]. To improve inference efficiency and reduce model complexity, recent studies have begun replacing traditional Transformer modules with Mamba-based architectures. LF-Mamba [40] improves the decoder's spatial resolution and enhances its ability to extract complex disease features, while significantly reducing the number of parameters. Table II summarizes DL-based methods for plant disease identification.

TABLE II. SUMMARY OF DL METHODS FOR PLANT DISEASE IDENTIFICATION

Methods	Dataset	Accuracy (%)	Parameters (M)	Disadvantages
Multi-headed DenseNet [30]	PlantVillage [41]	98.17	\	Higher memory requirements.
RIC-Net [42]	PlantVillage	99.55	19.10	Complex structure.
RE-GoogLeNet [34]	Rice, self-built	99.58	9.18	Difficult to optimize.
PDICNet [13]	PlantVillage	99.73	\	Difficult to optimize.
XSE-TomatoNet [35]	Tomato, PlantDoc	99.11	\	Requires high input resolution.
MobileNet [31]	Apple, self-built	73.50	\	Lower detection accuracy.
Lite-MDC [32]	PlantVillage	99.77	2.20	Unable to localize disease regions .
YOLOv5s [36]	MSMSVDD	93.10	8.30	Less effective for small objects.
DM-Yolo [37]	Tomato, self-built	92.50	50.07	Lower training stability.
G-RecConNN [38]	Banana, self-built	93.60	\	Vanishing gradient issues.
Optimized ViT [39]	PlantVillage	99.77	13.02	More computational resources.
LeafMamba [40]	FGVC8	92.50	0.99	Limited capability in local feature.

C. Hybrid Methods

Hybrid ensemble methods leverage the complementary strengths of different architectures to improve image feature extraction, mitigate overfitting caused by feature bias, and enhance generalization [53]. To balance performance and efficiency, recent studies have explored combining CNN-based feature extractors with traditional classifiers, integrating CNNs' spatial feature learning with the interpretability of classical methods [43],[44]. Meanwhile, many hybrid methods reduce model complexity by replacing parts of complex architectures with lightweight components, while maintaining or even enhancing predictive performance [45]. For example, SSD_Mobile-NetV2 [46] uses only 50.9% of the parameters compared to SSD_VGG, yet achieves improvements in precision, recall, F1-score, and mean Average Precision (mAP) by 4.37%, 3.3%, 3.8%, and 8.79%, respectively. Furthermore, CNNs are often employed to replace or supplement parts of Transformer architectures, providing more efficient local feature modeling and faster inference in real-time or resource-constrained plant disease detection scenarios. ConvViT [47], which combines CNNs with Transformer, outperforms models such as ResNet, ViT, and ResMLP by improving accuracy by 4.53% while reducing the number of parameters and FLOPs by more than 10%.

SoyaTrans [48] utilizes CNNs to extract local features and a Transformer module to capture global dependencies. With only 5.2 million parameters, it achieves an accuracy of 98.00% on the PlantVillage dataset. This result demonstrates that integrating multiple learning paradigms can outperform models based on a single architecture. Table III summarizes the latest performance of hybrid methods in plant disease identification tasks.

TABLE III. SUMMARY OF RECENT PERFORMANCE OF HYBRID METHODS IN PLANT DISEASE IDENTIFICATION

Ensemble Methods	Dataset	Accuracy (%)	Parameters (M)
CNN+Transformer [47]	PlantVillage	99.84	59.00
VGG19+InceptionV3 [49]	PlantVillage	98.66	\
VGG16 + RF [43]	PlantVillage	94.00	0.26
KNN+ Transformer [44]	PlantVillage	99.93	\
SoyaTrans [48]	PlantVillage	98.00	5.20
VGG-ICNN [50]	PlantVillage	99.16	23.20
CNN + RNN [51]	AI maize dataset	97.85	0.4
Ensemble models [52]	New PlantVillage	99.89	\

D. Discussion and Summary

Traditional ML, DL, and hybrid methods provide effective solutions for plant disease classification. The choice of method depends on the specific challenges of the task, such as data availability, feature complexity, and computational resources. Traditional ML methods are lightweight and interpretable due to their reliance on handcrafted features. However, their effectiveness is limited by feature quality and poor robustness under varying field conditions. DL methods automatically extract features from raw data. They are powerful at capturing complex disease patterns and usually achieve higher accuracy than ML when sufficient labeled data is available. However, they are data- and resource-intensive, less interpretable, and often struggle with robustness under real-world field conditions. Hybrid ML-DL methods combine the strengths of both paradigms. DL models are used for robust feature extraction, while traditional ML algorithms provide lightweight and interpretable decision-making. This balance reduces reliance on manual features and lowers computational cost compared with full DL pipelines. However, their effectiveness is constrained by the need for precise feature-model integration and limited robustness to previously unseen crops and disease types [54].

III. TRANSFER LEARNING FOR PLANT DISEASE IDENTIFICATION

TL allows models trained on one plant species to be applied to related species. It helps address limited data and domain variability, especially under class imbalance [55]. However, a comprehensive review specifically focused on “agricultural TL” remains lacking [56]. This section reviews three major TL methods, namely instance-based, mapping-based, and network-based.

A. Mapping-Based Transfer Learning

Mapping-based TL reduces the distribution gap between source and target domains by learning a shared feature space or an explicit mapping function. MViT [57] employs an adversarial framework augmented with the Wasserstein distance to learn domain-invariant representations, projecting source and target samples into a common latent space with closely matched distributions. Maximum Mean Discrepancy [58] offers a theoretically grounded measure of domain shift by aligning the mean embeddings of source and target features in a reproducing-kernel Hilbert space. CLA [59] first performs self-supervised contrastive pre-training, then applies a domain-adaptation layer that explicitly aligns the resulting feature distributions. CORrelation Alignment [60] efficiently matches the second-order statistics of source and target features, delivering low computational overhead and good scalability. Attention-based alignment [61] further narrows the domain gap by highlighting discriminative regions while suppressing irrelevant background noise.

For cross-species plant disease identification, adversarial domain adaptation is used to learn domain-invariant representations. A representative method is DANN [62], which performs well under pronounced domain shifts, including highly non-linear settings and large cross-domain datasets. Other strategies reduce domain discrepancy by explicitly constraining the diagnostic model. FMDA [63] minimises the “distance” between source and target, thereby lowering domain divergence. Using unlabelled target data without explicit feature alignment can exacerbate domain mismatch. Unsupervised domain adaptation methods [64] learn shared feature spaces from abundant unlabelled target images, aligning source and target domains through non-adversarial means. Zero-shot TL [65] builds a discriminative, transferable embedding that bridges source and target domains even when their class sets do not overlap.

B. Network-Based Transfer Learning

Network-based TL focuses on modifying the architecture itself so that it can more effectively adapt to new tasks or domains. These methods exploit the learned by a pre-trained backbone, and enhance identification performance through optimizing the architecture [66]. In addition to direct architectural adjustments, several studies have reported further gains in overall accuracy, generalization, and overfitting resistance by employing multi-model fusion or model ensembling [67]. INC-VGGN [68] integrates a pre-trained VGGNet with an Inception module, combining VGG's ability to capture deep hierarchical representations with Inception's multi-scale feature extraction, thereby improving the network's capacity to model fine-grained details. SLViT [69] merges a Transformer encoder with a CNN, striking a balance between recognition performance and computational cost. The incorporation of attention mechanisms has opened an additional optimization avenue. For example, Sudhesh *et al.* [70] introduced an attention module into a DenseNet121 with an RF framework, reinforcing the network's focus on disease-relevant regions.

Unlike single-stage TL, two-stage TL introduces an intermediate adaptation phase that further tailors a network to the target task. Es-MbNet [71], for example, re-trains on the target data, leading to a marked performance gain, after an initial weight initialization stage. A similar method keeps the first ten layers of a pre-trained VGG-16 network fixed, appends two inception blocks, and then fine-tunes the modified architecture with target data, reaching 99.23% accuracy [72]. In addition, knowledge distillation is emerging as an effective transfer-learning technique. By distilling the feature representations of a pre-trained Vision Transformer into a lightweight student model, this method significantly reduces model complexity while maintaining competitive performance [73].

C. Instance-Based Transfer Learning

Instance-based TL fine-tunes models that have been pre-trained on large-scale datasets such as ImageNet and reuses them as feature extractors, thereby enabling efficient knowledge transfer to a target task [74]. For example, a pre-trained VGG16 optimized with stochastic gradient descent with momentum (SGDm) achieved 98.33% accuracy in distinguishing healthy fruit from fruit infected by the Mediterranean fruit fly [75]. A pre-trained MobileNetV2 reached 99.30 % accuracy in detecting tomato leaf diseases on the PlantVillage [76]. A fine-tuned VGG-16 attained 95.00% classification accuracy across 11 tomato disease classes [77]. Even on very small datasets, the approach remains effective. Yu *et al*. [78] fine-tuned a pre-trained ResNet-18 on a dataset of only 120 images and achieved 99.53 % accuracy, while Liu *et al*. [79] reported 99.45% accuracy for apple-disease recognition using a pre-trained Inception-V3 model.

TABLE IV. SUMMARY OF TL METHODS FOR PLANT DISEASE IDENTIFICATION (%)

Model Structure Basis	**Source Domain**	**Target Domain**	**Accuracy**	**Recall**	**F1**	**Precision**
MViT [57]	PlantVillage	PlantDoc [80]	70.00	69.00	67.00	68.00
CPAM-DSAN [61]	Dataset300	Rice, self-built	95.25	95.25	95.34	95.38
Transformer [73]	ImageNet	Rice, self-built	92.00	91.00	89.00	88.00
ResNet18 [78]	ImageNet	Soybean, self-built	99.53	99.55	99.54	99.53
Inception-V3 [79]	ImageNet	PlantVillage	99.45	99.10	99.00	98.84
MobileNetV2 [76]	ImageNet	PlantVillage	99.30	\	\	\
VGG19 [67]	ImageNet	rice, self-built	93.00	89.90	90.50	92.40
XceptionNet [70]	\	Rice, self-built	93.87	85.00	85.00	85.00
VGG16 [77]	ImageNet	tomato, public	95	93.55	94.00	94.55
ResNet50 [81]	2018 AI challenge	2018 AI challenge	97.30	\	\	\
VGG16 [75]	ImageNet	Citrus, self-built	98.33	99.33	99.34	99.35
VGG19 [68]	ImageNet	PlantVillage	91.83	\	\	\
VGG16 [72]	ImageNet	Tomato，self-built	99.23	99.29	99.20	99.12
Es-MbNet [71]	ImageNet	PlantVillage	99.61	98.08	98.08	\
VGG16 [66]	ImageNet	Rice and wheat, self-built	97.99	\	\	\
DANet [82]	CPD P1, self-built	CPD P2, self-built	96.75	\	\	\
STA-GAN [83]	ImageNet	Cucumber, self-built	98.97	\	\	\
AlexNet [84]	ImageNet	PlantVillage	96.63	91.00	91.00	92.00
DTL-SE-ResNet50 [85]	AI Challenger 2018	Vegetable, self-built	97.24	92.58	94.85	\

D. Discussion and Summary

The choice of TL paradigm ultimately reflects trade-offs between resource availability, domain similarity, and the complexity of the target task. Instance-based TL fine-tunes pre-trained models with minimal changes, making it lightweight and suitable for resource-limited tasks when domains are closely aligned. Its drawback is strong dependence on domain similarity and risk of negative transfer under large gaps. Mapping-based TL aligns source and target features via statistical measures, adversarial training, or attention. It is effective when related source data are abundant but target data are scarce, though it often adds complexity, unstable training, and low interpretability under large domain shifts. Network-based TL adapts architectures for deeper transfer, yielding strong performance in complex or fine-grained tasks with large domain differences, but at the expense of high computational and data demands. Table IV summarizes various transfer learning techniques and their effectiveness in plant disease identification, highlighting the source and target domains, accuracy, recall, Precision, F1 scores, and model architectures.

IV. FEW-SHOT LEARNING FOR PLANT DISEASE IDENTIFICATION

ML, DL, and TL methods typically require a large amount of labeled data for model training, but in practical applications, obtaining such data can be very challenging or expensive. FSL Methods aim to address the issue of learning and generalizing in the absence of labeled samples.

A. *Model-Based Few-Shot Learning*

The limited availability of labeled samples often results in significant class imbalance, which poses a major challenge for plant disease identification models. To address this issue, researchers have explored synthetic data generation methods to enhance prediction performance, such as Variational Autoencoders [86],[87], GANs [88], [89], and Diffusion Models [90], [91] are widely used to generate new samples. For example, Singh *et al*. [92] used a Conditional GAN to synthesize maize leaf images for data augmentation, which enhanced classification performance compared with using real images alone. Texture Reconstruction Loss Cycle GAN [93] to generate realistic citrus Huanglongbing leaf data. This method improved the average accuracy of the classification network by 2.76%.

To improve model robustness, CNN_BIT [94] integrates a CNN with BiT, combining their feature extraction capabilities to address a few-shot learning task involving only 20 images per class. Some methods combined generative models with discriminative models. Generating more diversified plant disease images through training to improve the identification model's performance [95]. Sharma *et al*. [96] developed a conditional deep convolutional GAN (ClGan) with an improved loss and paired it with a compact classifier (ClGanNet) for maize leaves. It achieved 99.04% test accuracy and strong parameter efficiency. However, these methods struggle with limited adaptability and poor generalization under task distribution shifts.

B. *Metric-Based Few-Shot Learning*

Metric-based methods aim to learn a similarity metric to measure the similarity between samples. Prototypical Networks perform class prototype computation and distance-based classification [97]. Common distance metrics such as Euclidean distance and cosine similarity are widely used to compare feature representations between support and query samples in few-shot learning. A common strategy is to train the CNN-based feature extractor with supervised contrastive objectives, which pull together embeddings from the same class while pushing apart those from different classes under episodic sampling [98]. Some methods further enhance this approach by integrating triplet loss with efficient class-boundary shallow learners, improving classification performance in low-data scenarios [99]. Alternatively, Circle Loss [100] was introduced to measure sample similarity by optimizing the relative distances among positive, anchor, and negative samples in the embedding space, leading to better feature discrimination. MAFDE-DN4 [101] enhances inter-class separability in the embedding space by introducing additional discriminative distances for each class. However, these methods rely heavily on well-structured embeddings and are limited by intra-class variability and sensitivity to distance metrics.

C. *Optimization-Based Few-Shot Learning*

Optimization-based methods find the optimal decision boundary to distinguish different classes on a limited sample of instances. Meta-learning (learn-to-learn) methods [102] fall under this category, training a meta-learner to quickly adapt to new tasks using only a few training samples. Through transfer optimization, parameters or features of pre-trained models can be optimized for better generalization ability on few-shot tasks [103]. PMF+FA [104] integrates pre-training, meta-learning, and fine-tuning (PMF) with a novel Feature Attention module. This module highlights discriminative regions within images while suppressing the influence of complex backgrounds and irrelevant objects. However, these methods are hindered by initialization sensitivity, high computational cost from inner-loop updates, and slow convergence in complex, non-convex spaces.

D. *Discussion and Summary*

FSL methods become increasingly useful for annotated data in plant disease identification. Their choice depends on the balance between data scarcity, task diversity, and available resources. Model-based FSL methods design architectures that rapidly adapt to new tasks by leveraging shared knowledge across episodes. They are effective for learning transferable representations and provide strong performance when tasks are diverse, but they often involve complex designs and high training costs. Metric-based FSL methods emphasize similarity between support and query samples using distance functions or embedding spaces. They are lightweight, intuitive, and well-suited for cases where disease features are visually consistent, but their performance degrades when inter-class similarities are high or intra-class variations are large. Optimization-based FSL methods aim to improve task adaptation through specialized training strategies, such as meta-optimization or parameter initialization schemes. They can achieve superior accuracy under scarce data, but are computationally demanding and sensitive to hyperparameter tuning. Table V summarizes the recent performances of FSL methods applied to the identification of plant diseases.

TABLE V. RECENT PERFORMANCES OF FSL IN PLANT DISEASES IDENTIFICATION

Methods	Backbone	Datasets	N-way	K = 1	K = 5	K = 10
Attn-CutMix [102]	Transformer	Cotton, self-built	3	72.90	88.00	\
Inception+SVM [99]	Inception V3	PlantVillage	6	55.30	72.60	77.00
ViT ProtoNet+FA [104]	ViT	PlantDoc, Public	5	\	86.79	\
Swin-B [105]	Transformer	Barley, self-built	5	38.63	66.46	78.15
PruneFSL [106]	Resnet 12	Plantvillage	5	77.97	90.70	\
ResNet18+ProtoNet [97]	ResNet18	PlantVillage	10	72.76	92.12	93.32
MAFDE-DN4 [101]	ResNet 12	PlantVillage	5	57.50	81.41	\
MixNet-XL [100]	MixNet-XL	PlantVillage	6	75.41	91.03	93.97
SC-FSL [98]	Resnet 18	PlantVillage	5	78.55	92.90	\
CNN + SVM [103]	GoogleNet	PlantVillage	38	\	75.20	88.40
STV2F6+PDFC [107]	STV2F6	PlantVillage	5	91.81	95.32	95.50

V. FUTURE DIRECTIONS

Advancements in plant disease recognition technology are expected to continue driving significant progress in agriculture and contributing substantially to crop protection and management. Based on recent trends and developments, several promising directions and opportunities emerge.

1) Future research will increasingly harness multi-modal data by integrating visual imagery, audio signals, spectral information, textual inputs, and environmental parameters. This convergence of diverse data modalities will enable more comprehensive feature extraction, thereby enhancing the accuracy of pest and disease detection and classification. Advanced language models such as Claude, GPT-4, Gemini, and DeepSeek can play a pivotal role by combining visual inputs with descriptive textual data to improve early identification and nuanced assessment of plant health [108]. Additionally, integrating visible-spectrum imagery with infrared sensor data can significantly enhance the precision and timeliness of plant stress detection [109].

2) Few-Shot Domain Adaptation (FSDA): FSDA has demonstrated significant potential for addressing the substantial distribution differences and limited labeled data commonly encountered in real-world scenarios. Future research will focus on improving cross-task generalization, enabling models trained on source domains to effectively transfer to target domains with minimal or no labeled data, thereby alleviating performance bottlenecks caused by data scarcity [110]. Additionally, prototype aggregation methods further enhance robustness in few-shot and cross-domain scenarios by aggregating prototypes from multiple samples or domains, thus capturing finer intra-class structures and subtle differences [111].

3) Diffusion model-based sample generation: Utilizing diffusion models for generating interpretable synthetic samples represents an innovative direction in future research [112]. By generating interpretable synthetic samples, diffusion models provide intuitive visualizations that reveal the critical features learned by models, highlight potential biases, and uncover blind spots in training data. Additionally, in few-shot domain adaptation tasks, diffusion models guided by limited target domain samples can generate high-quality pseudo-samples, effectively expanding the target domain distribution and alleviating label scarcity [113]. Future research will explore designing more semantically consistent and finely controlled conditional diffusion mechanisms, alongside advancements in efficient sampling and low-resource deployment, ultimately driving practical applications in high-value fields such as medical imaging and agricultural remote sensing.

4) Edge computing and mobile applications: With the proliferation of mobile technologies and edge computing infrastructure, plant pest and disease identification tools are expected to become increasingly accessible and widely adopted. Deploying sophisticated recognition models directly onto mobile and edge devices will facilitate real-time disease diagnosis, significantly reducing data transmission costs, minimizing latency, and improving overall responsiveness and usability in agricultural field environments [114].

5) Model interpretability: In agricultural applications such as plant pest and disease recognition, model interpretability is becoming a critical factor for enhancing system reliability and practical usability. Future research will focus on embedding interpretability mechanisms into lightweight models, enabling techniques such as Grad-CAM to function efficiently on mobile and edge devices to support real-time, in-field diagnostics [115]. At the same time, concept-based interpretability methods are expected to advance by identifying high-level semantic features, such as "leaf yellowing" or "marginal decay," which align closely with agricultural domain knowledge and improve the clarity and usefulness of model outputs [116]. Additionally, multimodal interpretability is likely to become a major research direction by integrating image data with sensor information and environmental context.

VI. CONCLUSION

Image-based methods for plant pest and disease classification hold significant potential in improving detection accuracy, which is crucial for early disease prediction and timely intervention. This review explores various approaches in plant disease recognition through image analysis, covering traditional ML, DL, and hybrid methods. We explore their achievements and inherent challenges, such as data imbalance, complex training requirements, and domain adaptability. TL and FSL emerge as effective solutions to address the limited availability of annotated data, each offering distinct advantages and facing unique limitations. TL leverages pre-trained models from related domains to improve plant disease detection, with Mapping-based and Network-based TL showing high accuracy in tasks like tomato and soybean leaf disease classification. However, Instance-based TL is less effective due to issues with data distribution and domain mismatches. FSL trains models with minimal labeled data. Model-based FSL methods, such as those using GANs, generate synthetic data to enhance model generalization. Metric-based FSL, including Prototypical and Matching Networks, excels in classification tasks by learning similarity measures between labeled and unlabeled data. Optimization-based FSL enables rapid adaptation to new tasks but faces challenges such as overfitting and hyperparameter sensitivity.

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