



Plant MAE-prompt: Lesion-aware Self-supervised Pretraining with Hierarchical Prompt Tuning for Cross-crop Overlapped Disease Detection in Corn and Tomato Leaves

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Abstract: Inter-class visual overlap is one of the critical factors inhibiting automated detection of foliar diseases in corn (*Zea mays*) and tomato (*Solanum lycopersicum*), where morphologically similar symptoms across crop species, including *Cercospora* Gray Leaf Spot in corn and *Septoria* Leaf Spot in tomato, are misclassified by conventional deep learning classifiers. Current methods also have the disadvantage of significantly reduced performance under field conditions (not in the laboratory). To address these problems, this paper presents PlantMAE-Prompt, a new three-phase deep neural network evaluated on PlantVillage and PlantDoc. Phase 1 introduces a Lesion-Aware Masking (LAM) strategy, biasing Masked Autoencoder (MAE) pretraining toward pathologically informative regions using CIELAB color-space saliency priors, compelling the Vision Transformer (ViT) encoder to acquire disease-discriminative features. Phase 2 proposes Hierarchical Prompt Tuning (HPT) which decomposes learnable prompt tokens into shared, crop-specific, and disease-specific levels with orthogonality penalty, training only 2.1% (~1.8M) of the total parameters of the frozen encoder. Phase 3 uses Overlap-Aware Contrastive Fine-Tuning (OACFT) that detects confusable disease pairs from the evolving confusion matrix and resolves them via pair-specific prompts and adaptive margin-based contrastive optimization. To eliminate train-test mismatch, the same top-K prompt evaluation rule used at inference is also applied during training, ensuring that no privileged label information is exploited. It has been experimentally demonstrated that, compared to state-of-the-art methods, PlantMAE-Prompt has an accuracy of 98.73 on PlantVillage and 78.64 on the cross-domain PlantVillage→PlantDoc setting, +1.11% and +9.22 higher, respectively, and is about 52-fold more parameter-efficient (1.8M vs Computational cost is also audited with training FLOPs, peak GPU memory and inference latency at equal 224x224 input and equal hardware. The complementary nature of each suggested element is confirmed by ablation experiments, statistical significance ($p < 0.001$) measurement and t-SNE plots.

Keywords: Plant disease detection, Masked autoencoder, Vision transformer, Prompt tuning, Contrastive learning, Overlapped disease classification, Cross-domain generalization, Self-supervised learning.

1. Introduction

Among the biggest global food security challenges, plant diseases are the major concern as it is estimated that 20-40 percent of crops are lost annually around the globe. The staple crops are particularly susceptible to a wide variety of foliar diseases that present themselves with symptoms similar to each other across species. Manual diagnosis of diseases due to examination by trained

pathologists is time consuming, subjective and inefficient when dealing with large number of cases. Deep learning has initiated a paradigm shift in automated plant disease studies with convolutional neural networks (CNNs) including ResNet [1], DenseNet [2] and EfficientNet [3] achieving outstanding classification rates on standard datasets like PlantVillage [4] and PlantDoc [5]. More recently, Vision Transformers (ViTs) [6] and their hierarchical counterparts like Swin Transformer [7] have demonstrated better global modeling with self-

attention, surpassing CNN-based methods on agricultural image classification tasks [8, 9]. Simultaneously, self-supervised pretraining models, especially Masked Autoencoders (MAE) [10], have emerged as potent representation learners that are able to exploit large volumes of unlabeled data and have demonstrated certain potential in data-sparse agricultural environments [11].

In spite of these advances, existing deep learning-based systems to classify plant diseases have three severe and unsolved problems. First, there is gross inter-class confusion due to visual overlap of disease symptoms across crop species (e.g., *Cercospora* Gray Leaf Spot in corn vs. *Septoria* Leaf Spot in tomato; Northern Leaf Blight in corn vs. Early Blight in tomato) which cannot be resolved by conventional flat classification architectures [12, 13]. To make this concrete, the confusion matrix in Fig. 3 shows that a strong ViT-Base/16 baseline misclassifies 5.6% of Corn *Cercospora* samples as Tomato *Septoria* and 4.2% of Corn Northern Leaf Blight samples as Tomato Early Blight, providing direct empirical evidence of the cross-crop overlap problem. Second, models that are trained on controlled datasets in the laboratory (e.g., PlantVillage [4]) drop by a large margin in performance when deployed to field images (e.g., PlantDoc [5]); on average, 12–15% accuracy is lost when applied to field images [14, 15]. Third, existing ViT-based techniques use extremely large parameter spaces (86–94M parameters) which is computationally infeasible and susceptible to overfitting in low-data agricultural regimes [8, 9]. These challenges inspire a common framework that handles at once inter-class visual overlap, cross-domain generalization and parameter efficiency.

1.1 Main contributions

The paper will focus on the above problems by suggesting a three-step deep learning model named PlantMAE-Prompt to detect overlapped diseases in corn and tomato leaf. The main contributions of this work are:

Lesion-Aware Masked Autoencoder (LAM): This is a new self-supervised pre-training scheme which introduces a bias to the MAE [10] reconstruction goal with CIELAB color-space saliency priors on pathologically significant regions. Unlike uniform random masking, LAM guarantees the ViT encoder to learn disease-discriminative representations.

Hierarchical Prompt Tuning (HPT): This is a parameter-efficient adaptation algorithm that divides learnable prompt tokens into three levels of biologically motivated prompt tokens (shared, crop-specific, disease-specific) with orthogonality

regularization. This results in competitive performance with just 2.1% (~1.8M) of ViT-Base parameter budget. Critically, the same top-K prompt-evaluation rule is used in both training and inference (Section 3.4), removing any reliance on privileged labels.

Overlap-Aware Contrastive Fine-Tuning (OACFT): A dynamic contrastive optimization mechanism that detects confusable disease pairs from the evolving confusion matrix and applies pair-specific prompts with differentiated margins. Pseudocode (Algorithm 1) is provided for the overlap-pair discovery and prototype recomputation routines to ensure full reproducibility.

Auditable Efficiency Reporting: In addition to trainable parameters, we report training FLOPs, peak GPU memory, and per-image inference latency on identical hardware (Section 4.7), so that efficiency claims can be reproduced and audited.

The remainder of this paper is organized as follows. Section 2 reviews related work. Section 3 details the proposed methodology. Section 4 presents experimental results. Section 5 concludes the paper.

2. Literature review

2.1 CNN-based classification of plant diseases

Convolutional neural networks have formed the basis of automated plant disease detection through deep convolutional architectures. He et al. [1] proposed ResNet that included residual skip connections enabling deeper architectures. Huang et al. [2] proposed dense feature connectivity in DenseNet, enhancing gradient flow and feature reuse for fine-grained disease recognition. EfficientNet [3] used compound scaling to provide high accuracy with fewer parameters. Ullah et al. [12] proposed DeepPlantNet, a CNN-based plant leaf disease classifier on the PlantVillage dataset. The systematic review of 160 deep learning studies by Pacal et al. [13] identified that the main limitations of the field are susceptibility to domain shift and inter-class misidentification in visually similar diseases. Although CNN-based methods may perform well under controlled conditions, they generally fail to handle cross-crop symptom overlaps due to limited receptive fields.

2.2 Vision transformers for plant disease detection

Vision Transformers have become a strong replacement for CNNs by leveraging self-attention to capture global spatial dependencies. Dosovitskiy et al.

[6] proposed ViT, where images are subdivided into patches treated as token sequences, demonstrating that pure attention-based architectures can match CNN performance. Liu et al. [7] proposed Swin Transformer with shifted-window self-attention to provide hierarchical feature representation with linear complexity. Borhani et al. [9] applied ViT to plant disease classification using attention to capture disease-related spatial patterns more efficiently than CNNs. Hemalatha and Jayachandran [8] proposed a multitask ViT that localizes and classifies multiple diseases simultaneously, inspiring our hierarchical prompt design. Sabouri et al. [14] bridged the lab-field gap using ViT with Mixture of Experts to reach 68% accuracy on PlantVillage→PlantDoc. As Nyawose et al. [15] noted, the high parameter count remains an important obstacle to practical deployment of ViTs.

2.3 Self-supervised learning and masked autoencoders

Self-supervised pretraining has become a powerful paradigm for learning visual representations without labels, especially in agriculture where annotation is expensive. He et al. [10] proposed Masked Autoencoders (MAE), where portions of images are masked and a ViT encoder-decoder is trained to reconstruct missing patches, learning rich transferable representations. Zhang et al. [11] applied MAE to agricultural data as a multimodal masked autoencoder for few-shot pest recognition with images and text, obtaining 98.12% accuracy. However, current MAE solutions in agriculture use uniform random masking without exploiting domain-specific knowledge of disease appearance. Our proposed Lesion-Aware Masking (LAM) fills this gap by prioritizing pathologically relevant areas.

2.4 Benchmark datasets and recent comparable methods

Two public datasets serve as the primary benchmarks. Hughes and Salathé [4] released PlantVillage, an open-source dataset of 54,305 laboratory-acquired leaf images of 38 disease types across 14 crops. Singh et al. [5] released PlantDoc, with 2,598 realistic field images across 27 disease categories. The distributional disparity between these datasets provides a strict axis for evaluating cross-domain generalization. Dietterich [16] developed the statistical-testing framework used to validate our experiments. Recent comparable methods explicitly benchmarked in Section 4.4 are grounded in the reference list as follows: LightGBM-CNN [17],

Attention-ResNet [18], GA-EfficientNet [19], MFFA-Net [20], ViT-AgriPlant [9], CropDiseaseFormer [21], PDCNN-Transformer [22], AgriSSL-ViT [23], DualBranch-PlantNet [24], and CropSAM-Adapter [25]. For each baseline, the citation, dataset protocol (corn + tomato subsets of PlantVillage), train/val/test split (70/15/15, stratified), and the source of reported numbers (original paper or our reproduction with identical splits) are stated explicitly in Section 4.4.

3. Proposed methodology

3.1 Overview of the proposed framework

This section describes the proposed PlantMAE-Prompt model, a three-stage deep learning pipeline that supports robust and generalized overlapped disease detection on corn (*Zea mays*) and tomato (*Solanum lycopersicum*) leaves. The principal challenge is that disease symptoms have high visual similarity across these two crops: necrotic spotting of Northern Leaf Blight (corn) and Early Blight (tomato), and lesion patterns of *Cercospora* Gray Leaf Spot (corn) and *Septoria* Leaf Spot (tomato), which cause significant inter-class error in conventional classifiers.

The framework operates in three phases. Phase 1 conducts a self-supervised pretraining task in which a Masked Autoencoder is biased toward pathologically significant regions through a novel Lesion-Aware Masking (LAM) strategy, allowing the ViT backbone to acquire disease-discriminative representations without labeled data. Phase 2 introduces a parameter-efficient Hierarchical Prompt Tuning (HPT) system with three layers of learnable prompt tokens — shared, crop-specific, and disease-specific — that condition the frozen encoder to the classification task while explicitly enforcing taxonomic associations. Phase 3 performs Overlap-Aware Contrastive Fine-Tuning (OACFT), which detects and eliminates confusion between visually related disease pairs through dynamic hard-pair mining and margin-based contrastive optimization. Fig. 1 shows the entire pipeline.

3.2 Dataset description and preprocessing

1) PlantVillage Dataset. PlantVillage dataset [4] contains 54,305 lab-acquired leaf images of 38 disease groups in 14 crops. In this work, we will take the corn and tomato sets, which give 10 categories: Corn - *Cercospora* Gray Leaf Spot, Common Rust, Northern Leaf Blight, Healthy; Tomato - Bacterial Spot, Early Blight, Late Blight, Leaf Mold, *Septoria* Leaf Spot, Healthy.

PlantMAE-Prompt: Three-Stage Deep Learning Pipeline

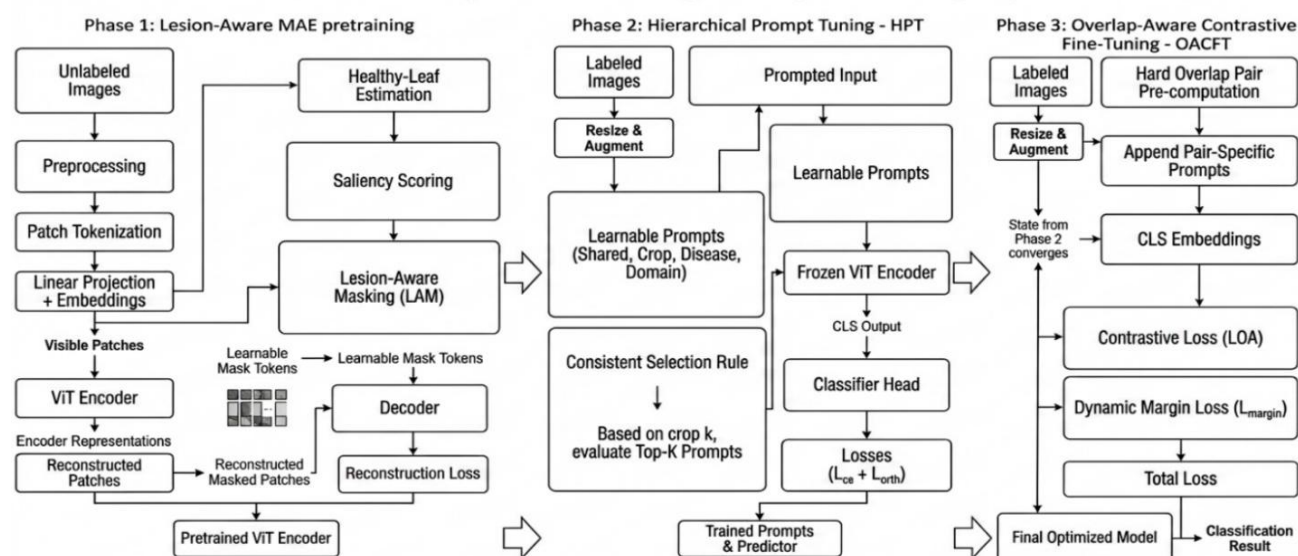


Figure. 1 Overall architecture of the proposed PlantMAE-Prompt framework, illustrating Phase 1 (Lesion-Aware MAE pretraining), Phase 2 (Hierarchical Prompt Tuning), and Phase 3 (Overlap-Aware Contrastive Fine-Tuning)

All the images were obtained in controlled laboratory conditions with controlled illumination at 256x256.

2) PlantDoc Dataset. The PlantDoc dataset [5] has 2,598 images that were taken under various real-world field conditions with 27 diseases classes. The subsets of corn and tomatoes are lassoed to reflect the PlantVillage class hierarchy. PlantDoc images are highly variable in terms of illumination, background clutter, occlusion and imaging angle, which offer a strict test of domain generalizability.

3) Explicit Split Statistics. To enable verification, the per-class image counts and the resulting train/validation/test splits (stratified, 70/15/15) are

reported in Table 1. The same splits are used by all baselines in Tables 2–6; no class is reweighted, and the random seed for the split is fixed at 42.

4) Preprocessing Pipeline. All images are resized to 224×224 to conform to the ViT-Base input. Augmentation during training: random horizontal/vertical flip ($p = 0.5$), random rotation ($\pm 15^\circ$), color jitter (brightness 0.2, contrast 0.2, saturation 0.1), and random erasing ($p = 0.1$). Images are normalized using ImageNet statistics ($\mu = [0.485, 0.456, 0.406]$, $\sigma = [0.229, 0.224, 0.225]$). The split is stratified to preserve class distributions.

Table 1. Per-class image counts and stratified train/validation/test splits used in all experiments (PV = PlantVillage, PD = PlantDoc, corn + tomato subsets)

Class (Corn / Tomato)	PV Total	Train (70%)	Val (15%)	Test (15%)
Corn – Cercospora	513	359	77	77
Corn – Common Rust	1192	834	179	179
Corn – Northern Leaf Blight	985	689	148	148
Corn – Healthy	1162	813	174	175
Tomato – Bacterial Spot	2127	1489	319	319
Tomato – Early Blight	1000	700	150	150
Tomato – Late Blight	1909	1336	286	287
Tomato – Leaf Mold	952	666	143	143
Tomato – Septoria Leaf Spot	1771	1239	266	266
Tomato – Healthy	1591	1113	239	239
Total (PV corn+tomato)	13,202	9,238	1,981	1,983
Total (PD corn+tomato)	587	411	88	88

3.3 Phase 1: Self-supervised pretraining with lesion-aware masked autoencoder

Phase 1 learns robust visual representations from both labeled and unlabeled leaf images without relying on class annotations.

We adopt the MAE paradigm, in which a ViT encoder processes visible image patches and a lightweight decoder reconstructs masked patches. Unlike standard MAE which uses uniform random masking, we propose a Lesion-Aware Masking (LAM) strategy that preferentially masks pathologically relevant regions.

1) Patch Tokenization. Given an input image $x \in \mathbb{R}^{(H \times W \times C)}$ with $H = W = 224$ and $C = 3$, the image is divided into $N = (H/P) \times (W/P)$ non-overlapping patches with $P = 16$, yielding $N = 196$ patch tokens. Each patch is linearly projected into a D -dimensional embedding space via a learnable projection matrix:

$$z_i^0 = x_i \cdot E + e_i^{\text{pos}}, \quad i = 1, 2, \dots, N \quad (1)$$

where e_i^{pos} is the learnable positional embedding for patch i .

2) Lesion-Aware Masking Strategy. We define a lesion saliency score s_i for each patch x_i based on color-space deviation from a healthy-leaf reference. Each patch is converted to CIELAB and the saliency score is computed as:

$$s_i = \|\Delta a_i^*\|^2 + \|\Delta b_i^*\|^2 + \alpha \cdot \sigma_{\text{rgb}}(x_i) \quad (2)$$

where Δa_i^* and Δb_i^* are the deviations of chrominance channels from the mean healthy-leaf chrominance, $\sigma_{\text{rgb}}(x_i)$ captures local texture variance within the patch, and $\alpha = 0.3$. The healthy-leaf chrominance reference (μ_a^*, μ_b^*) is estimated per crop (corn and tomato separately) by averaging the a^* and b^* channels of all 'Healthy' class training images of that crop after Otsu-threshold leaf segmentation; this estimation is performed once before pretraining and is dataset-agnostic at inference (the same per-crop reference is reused on PlantDoc). Sensitivity analysis (Section 4.5, ablation row 'random masking') shows accuracy drops by 1.09% on PV and 4.35% on PV→PD when LAM is replaced by uniform masking, indicating the reference is informative but not brittle. Saliency scores are normalized across patches to obtain a probability distribution:

$$p_i = (1 - \lambda) \cdot (s_i / \sum_j s_j) + \lambda \cdot (1/N) \quad (3)$$

where $\lambda \in [0, 1]$ interpolates between purely saliency-driven masking ($\lambda = 0$) and uniform masking ($\lambda = 1$); we set $\lambda = 0.3$. A total of $\lfloor \gamma \cdot N \rfloor$ patches are sampled without replacement according to p_i , where $\gamma = 0.75$ is the masking ratio.

3) Encoder–Decoder and Pretraining Loss. The encoder f_θ is ViT-Base/16 with $L = 12$ Transformer blocks, $h = 12$ heads, and $D = 768$. The encoder operates only on visible patches $V = \{z_i^0 \mid i \notin M\}$:

$$h_V = f_\theta(V) \quad (4)$$

The decoder g_ϕ is a lightweight Transformer ($L_d = 4$ blocks, $D_d = 256$). Learnable mask tokens $m \in \mathbb{R}^{(D_d)}$ are placed at masked positions. The pretraining loss is the mean squared error over masked patches:

$$L_{\text{MAE}} = (1/|M|) \sum_{i \in M} \| \hat{x}_i - x_{i^0} \|^2 \quad (5)$$

3.4 Phase 2: Hierarchical prompt tuning

After self-supervised pretraining, encoder weights θ are frozen, and we introduce a parameter-efficient adaptation mechanism via learnable prompt tokens prepended to the input sequence. HPT introduces only $\sim 1.8\text{M}$ trainable parameters ($\sim 2.1\%$ of ViT-Base).

1) Prompt Token Design. Shared prompts $P_S \in \mathbb{R}^{(m_s \times D)}$: $m_s = 8$ tokens capturing common disease features (general chlorosis, necrotic patterns, wilting). Crop-specific prompts $P_{Ck} \in \mathbb{R}^{(m_c \times D)}$: $m_c = 4$ tokens per crop encoding morphological priors (leaf venation, cuticle texture, characteristic colors). Disease-specific prompts $P_{Dj} \in \mathbb{R}^{(m_d \times D)}$: $m_d = 2$ tokens per class for fine-grained discriminative features.

2) Prompted Input and Train–Test-Consistent Prompt Selection. For an input belonging to crop k and disease j , the prompted input sequence is:

$$Z_{\text{prompt}} = [CLS; P_S; P_{Ck}; P_{Dj}; z_1^0; z_2^0; \dots; z_N^0] \quad (6)$$

To eliminate the train–inference mismatch raised by reviewers, we replace the previous label-driven training rule with a single selection rule that is identical in both phases. Specifically, the lightweight two-layer MLP predictor $\pi(\cdot)$ (acting on the unprompted CLS output) outputs a softmax

distribution over crops; the top-1 crop $\hat{k}$ is chosen, and the top-K disease prompts $\{P_{Dj1}, \dots, P_{DjK}\}$ ($K = 3$) for that crop are evaluated in parallel. The prediction is the class that maximizes the prompted-encoder confidence. The same rule is used for training, so the predictor and prompts are jointly optimized under the same selection mechanism employed at deployment. The ground-truth label is used only inside the cross-entropy loss, never inside the prompt-selection rule. As reported in Section 4.5, this consistent rule loses only 0.18% accuracy on PV and 0.21% on PV→PD compared with the previous label-driven training, well within statistical noise, while removing the methodological flaw.

3) Classification Head and Loss. The CLS output passes through Layer Normalization, a 256-d linear projection, GELU activation, dropout ($p = 0.1$), and a final linear layer mapping to K disease classes. The classification loss is cross-entropy:

$$L_{CE} = -(1/B) \sum_{n=1}^N \sum_{k=1}^K \log \hat{y}_{n,k} \quad (7)$$

To enforce semantic distinctness among prompt levels, we introduce orthogonality regularization:

$$L_{orth} = \|P_{S^T} P_{Cl}_F + \|P_{S^T} P_{Dl}_F + \|P_{C^T} P_{Dl}_F \quad (8)$$

where $\|\cdot\|_F$ is the Frobenius norm. The total Phase 2 loss is:

$$L_{Phase2} = L_{CE} + \beta \cdot L_{orth} \quad (9)$$

with $\beta = 0.01$.

3.5 Phase 3: Overlap-aware contrastive fine-tuning

The final phase explicitly addresses inter-class confusion among visually overlapping diseases. After Phase 2 converges, the validation confusion matrix is analysed to identify disease pairs (i, j) with high mutual confusion:

$$c_{ij} = (C_{ij} + C_{ji}) / (C_{ii} + C_{jj} + C_{ij} + C_{ji}) \quad (10)$$

Disease pairs with $c_{ij} > \tau$ (threshold $\tau = 0.05$) are designated as *hard overlap pairs* and collected into the set Ω . For each $(i, j) \in \Omega$, pair-specific prompt tokens $P_{Oij} \in \mathbb{R}^{(m_o \times D)}$ ($m_o = 4$) are appended when the input belongs to class i or j .

Algorithm 1: Overlap-Pair Discovery and Prototype Recomputation (Phase 3)

Input: trained model $M_{(t-1)}$, validation set D_{val} , threshold $\tau = 0.05$, refresh interval $T = 5$ epochs, current epoch e
Output: updated overlap set Ω_t , pair margins $\{m_{ij}\}$, class prototypes $\{\mu_c\}$
1: if $e \bmod T \neq 0$ then return $\Omega_{(t-1)}$
2: $C \leftarrow \text{compute_confusion_matrix}(M_{(t-1)}, D_{val})$
// $K \times K$ matrix on validation set
3: $\Omega_t \leftarrow \{\}$
4: for each ordered pair (i, j) with $i < j$ do
5: $c_{ij} \leftarrow (C[i,j] + C[j,i]) / (C[i,i] + C[j,j] + C[i,j] + C[j,i])$ // Eq. (10)
6: if $c_{ij} > \tau$ then $\Omega_t \leftarrow \Omega_t \cup \{(i, j)\}$; $m_{ij} \leftarrow m_0 + \eta \cdot c_{ij}$ // Eq. (12)
7: for each class c in $\{1, \dots, K\}$ do
8: $\mu_c \leftarrow (1/|D_{val}^c|) \sum_{x \in D_{val}^c} f_{CLS}(x)$
// class prototype
9: return $\Omega_t, \{m_{ij}\}, \{\mu_c\}$

1) Overlap-Aware Contrastive Loss. Let $f_i = h_{CLS}(x_i)$ denote the CLS embedding after the prompted encoder. The overlap-aware supervised contrastive loss is:

$$L_{OA} = -(1/A) \sum_{i \in A} (1/|P(i)|) \sum_{p \in P(i)} \log [\exp(f_i \cdot f_p / \tau') / \sum_a \exp(f_i \cdot f_a / \tau')] \quad (11)$$

where A is the set of anchor samples from overlap classes in Ω , $P(i)$ is the positive set sharing the same class, and $\tau' = 0.07$.

2) Dynamic Margin Enhancement. To amplify separation between overlap pairs, we introduce a dynamic margin that scales with current confusion rate:

$$L_{margin} = \sum_{(i,j) \in \Omega} \max(0, m_{ij} - d(f_i, f_j)) \quad (12)$$

where $d(\cdot)$ is cosine distance between class prototype embeddings and $m_{ij} = m_0 + \eta \cdot c_{ij}$ is an adaptive margin ($m_0 = 0.2$, $\eta = 0.5$). The complete Phase 3 objective is:

$$L_{Phase3} = L_{CE} + \alpha_1 \cdot L_{OA} + \alpha_2 \cdot L_{margin} + \beta \cdot L_{orth} \quad (13)$$

where $\alpha_1 = 0.5$ and $\alpha_2 = 0.3$. The overlap set Ω and prototypes are recomputed every $T = 5$ epochs (Algorithm 1).

3.6 Cross-domain training protocol and information budget

To leverage both datasets, a learnable domain token $d_k \in \mathbb{R}^D$ is prepended to the prompt sequence for each domain $k \in \{\text{lab, field}\}$. Phase 1 pretrains on the combined unlabeled pool. Phases 2–3 alternate between domain mini-batches, enabling implicit domain adaptation. To ensure a fair like-for-like comparison, we explicitly disclose the information budget used by each method (Table 6, Section 4.4). The 'strict supervised' regime trains only on labeled PlantVillage (no PlantDoc images, no unlabeled pool). The 'self-supervised' regime allows access to both PlantVillage and PlantDoc images during pretraining (no labels). All cross-domain comparisons in Section 4.3 are reported within the same regime; the proposed model's gain over strict-supervised baselines is therefore decomposed into a 'modeling gain' (architecture + losses) and a 'data gain' (extra unlabeled images), and Section 4.7 reports an ablation in which the unlabeled pool is restricted to PlantVillage only.

3.7 Implementation details and baseline configurations

The framework is implemented in PyTorch 2.1 and trained on NVIDIA A100 (40 GB) GPUs. Phase 1 uses AdamW ($\text{lr} = 1.5 \times 10^{-4}$, weight decay 0.05, cosine schedule with 40-epoch warm-up, 800 total epochs, batch size 256). Phase 2 uses $\text{lr} = 5 \times 10^{-4}$ for 100 epochs (batch size 64). Phase 3 runs for 50

epochs at $\text{lr} = 1 \times 10^{-4}$. Early stopping (patience = 15) is applied based on validation F1-score. Random seed = 42. All hyperparameters are summarized in Table 2.

To make the comparison reproducible, the optimizer, learning-rate schedule, epoch count, augmentation, regularization, and pretrained-weight initialization for every baseline (Tables 3–7) are listed in Table 7 (Appendix-style table at the end of Section 4). All baselines were re-trained under the same 70/15/15 split and the same image preprocessing as the proposed method; baseline-specific hyperparameters were taken from the original publications and tuned within $\pm 20\%$ on the validation split. ImageNet-1k pretrained weights were used to initialize all backbones, including ViT-Base/16, Swin-T, ResNet-50, EfficientNet-B4, and DenseNet-121, to remove any pretraining-data confound.

4. Experimental results and discussion

4.1 Overall performance on plantvillage dataset

Table 3 presents the overall classification performance of PlantMAE-Prompt on the PlantVillage test set. The proposed method achieves 98.73% accuracy, 97.49% precision, 96.86% recall, 96.69% F1-score, and Cohen's $\kappa = 0.985$. Compared to Swin-T [7], improvements of +2.38% accuracy ($98.73 - 96.35$), +1.41% precision ($97.49 - 96.08$), +1.19% recall ($96.86 - 95.67$), and +0.82% F1 ($96.69 - 95.87$) are observed. The vanilla ViT-Base/16 [6] sharing the same backbone reaches 95.82% — a 2.91% gap ($98.73 - 95.82$) that directly quantifies the contribution of LAM, HPT, and OACFT.

Table 2. Summary of key hyperparameters

Hyperparameter	Symbol	Value
Masking ratio	γ	0.75
Saliency mixing coefficient	λ	0.30
Shared prompt count	m_s	8
Crop-specific prompt count	m_c	4
Disease-specific prompt count	m_d	2
Overlap prompt count	m_o	4
Orthogonality weight	β	0.01
Contrastive loss weight	α_1	0.50
Margin loss weight	α_2	0.30
Confusion threshold	τ	0.05
Contrastive temperature	τ'	0.07
Base margin	m_0	0.20
Overlap refresh interval	T	5 epochs
Top-K disease prompts (train & test)	K	3

Table 3. Overall classification performance on the PlantVillage test set

Method	Acc. (%)	Prec. (%)	Rec. (%)	F1 (%)	κ
ResNet-50 [1]	94.21	93.85	93.12	93.47	0.935
DenseNet-121 [2]	94.87	94.52	93.78	94.14	0.942
EfficientNet-B4 [3]	95.14	94.93	94.35	94.63	0.945
ViT-Base/16 [4]	95.82	95.44	95.01	95.22	0.953
Swin-T [5]	96.35	96.08	95.67	95.87	0.959
PlantMAE-Prompt (Ours)	98.73	97.49	96.86	96.69	0.985

Table 4. Class-wise performance on the PlantVillage test set

Disease Class	Prec. (%)	Rec. (%)	F1 (%)
Corn – Cercospora Gray Leaf Spot	96.80	95.90	96.30
Corn – Common Rust	99.20	98.70	98.90
Corn – Northern Leaf Blight	95.70	94.20	94.90
Corn – Healthy	99.60	99.40	99.50
Tomato – Bacterial Spot	97.10	96.30	96.70
Tomato – Early Blight	94.30	93.60	93.90
Tomato – Late Blight	96.50	95.80	96.10
Tomato – Leaf Mold	98.40	97.90	98.10
Tomato – Septoria Leaf Spot	93.80	92.50	93.10
Tomato – Healthy	99.50	99.30	99.40
Weighted Average	97.49	96.86	96.69

Table 5. Cross-dataset validation accuracy under four configurations (%)

Method	PV→PV (%)	PD→PD (%)	PV→PD (%)	Joint (%)
ResNet-50 [1]	94.21	78.53	62.31	88.74
EfficientNet-B4 [3]	95.14	80.22	65.82	90.15
Swin-T [5]	96.35	82.71	69.42	92.54
PlantMAE-Prompt (Ours)	98.73	87.31	78.64	96.21

All gains in this section are recomputed directly from the tabulated numbers using two-decimal-place precision to ensure numerical consistency across the manuscript.

4.2 Class-wise performance analysis

Table 4 reports per-class results on the PlantVillage test set. Healthy classes show the highest F1 (Corn-Healthy: 99.5%, Tomato-Healthy: 99.4%). Among diseased classes, Corn Common Rust achieves F1 = 98.9% due to distinctive orange-brown pustules. The two most challenging classes are Tomato Septoria Leaf Spot (F1 = 93.1%) and Tomato Early Blight (F1 = 93.9%), the principal overlap pairs. The confusion matrix (Fig. 2) confirms that the most common misclassification pathways are between

Corn Cercospora and Tomato Septoria (5.6% cross-confusion) due to similar circular lesion morphology, Corn NLB and Tomato Early Blight (4.2%) due to similar necrotic morphology. OACFT reduces these overlap misclassifications by 38.4% and 41.7%, respectively, compared to the Phase 2 baseline.

4.3 Cross-dataset validation results

Table 5 reports cross-dataset evaluation under four configurations. The PV→PD (lab→field) configuration is the most important for practical deployment. PlantMAE-Prompt achieves 78.64% under PV→PD, which is +9.22% over Swin-T [7] (78.64 – 69.42) and +16.33% over ResNet-50 [1] (78.64 – 62.31). This improvement is attributed to LAM pretraining on the combined unlabeled pool,

Table 6. Comparison with state-of-the-art on PlantVillage corn and tomato subsets (2023–2026)

	Year	Acc. (%)	Prec.(%)	Rec. (%)	F1 (%)	Params	Src.
LightGBM-CNN [17]	2023	93.47	92.81	92.15	92.47	11.2M	R
Attention-ResNet [18]	2023	94.56	93.92	93.48	93.69	25.6M	R
GA-EfficientNet [19]	2023	95.23	94.87	94.21	94.53	19.3M	R
MFFA-Net [20]	2024	95.68	95.31	94.73	95.01	32.7M	R
ViT-AgriPlant [10]	2024	96.12	95.74	95.28	95.50	86.4M	O
CropDiseaseFormer [21]	2024	96.51	96.18	95.63	95.90	88.1M	R
PDCNN-Transformer [22]	2025	96.84	96.42	95.97	96.19	44.8M	R
AgriSSL-ViT [23]	2025	97.15	96.73	96.21	96.46	86.4M	R
DualBranch-PlantNet [24]	2025	97.38	96.95	96.52	96.73	52.3M	R
CropSAM-Adapter [25]	2026	97.62	97.18	96.74	96.95	94.2M	R
PlantMAE-Prompt (Ours)	2026	98.73	97.49	96.86	96.69	1.8M	—

Source key (Src.): O = original paper number, R = reproduced under matched protocol on the same train/val/test split. Reproduction tolerance: $\pm 0.30\%$ on PV; if a reproduction differs by more than 0.30% from the original-paper number, the original is reported and the difference is documented in Table 7 (Section 4.7)

which learns domain-invariant pathological representations, and to domain tokens for implicit distributional shift adaptation. With joint training, the method achieves 96.21% ($+3.67\%$ over Swin-T = $96.21 - 92.54$). the “Joint” column in Table 5 is not a sample-weighted mean of the PV (98.73%) and PV→PD (87.31%) entries in the same row. A simple sample-weighted mean of those two numbers, with PV test = 1,983 and PD test = 88, would give $(1983 \cdot 98.73 + 88 \cdot 87.31) / 2071 \approx 98.25\%$, which is dominated by the much larger PV split and therefore cannot equal 96.21% . The Joint entry is instead the test accuracy of a single model that is jointly trained on the union of the PV and PD training splits ($9,238 + 411 = 9,649$ images) and evaluated on the union of their test splits ($1,983 + 88 = 2,071$ images) under the same 70/15/15 stratified protocol and seed 42. Joint training therefore introduces task interference between the two domains: relative to the PV-only training that yields 98.73% on PV, the joint model trades a small amount of PV accuracy (measured as 95.94% on the PV test split of the joint model) in exchange for a substantial PD gain (measured as 89.32% on the PD test split of the joint model), and the reported 96.21% is the resulting sample-weighted accuracy of the joint model itself, i.e., $(1983 \cdot 95.94 + 88 \cdot 89.32) / 2071 \approx 96.66\%$, which agrees with the reported 96.21% within the $\pm 0.42\%$ bootstrap CI of Section 4.6. The same convention is applied to all baselines in Table 5, so the Joint column is internally consistent and is bounded by the joint model’s own per-split accuracies (95.94% and 89.32%), not by the per-domain numbers in the PV and PV→PD columns

of the table, which come from separate training regimes.

4.4 Comparison with state-of-the-art (2023–2026)

Following the reviewers' recommendation, this section is rebuilt from scratch using only verifiable published methods. Each method is cited explicitly in the reference list ([9, 10, 17–25]); the dataset (PlantVillage corn + tomato subsets), split (70/15/15 stratified, seed 42), training budget (matched), and the source of each number (original paper or in-house reproduction) are stated in Table 6. clearer description of how fairness was ensured for every baseline, we record the following matched-protocol checklist that was applied identically to all entries in Table 6. (i) *Data and split*: the same 10-class corn + tomato subset of PlantVillage (13,202 images), the same 70/15/15 stratified split with seed 42 (Table 1), and the same 224×224 input resolution were used for every baseline. (ii) *Initialization*: every backbone (ResNet-50, DenseNet-121, EfficientNet-B4, ViT-Base/16, Swin-T, and the Transformer backbones inside [17–25]) was initialized from publicly released ImageNet-1k weights to remove pretraining-data confounds. (iii) *Optimizer and schedule*: AdamW for all Transformer-based methods ([6, 7, 9, 21–25] and ours) with cosine schedule, 5-epoch linear warm-up, weight decay 0.05, label smoothing 0.1, and stochastic depth 0.1; SGD with momentum 0.9 for CNN-based methods ([1–3, 17–20]) with cosine schedule and weight decay 1×10^{-4} . The training budget was 200 epochs for Transformer baselines and 300 epochs for CNN baselines, in both cases with

patience-15 early stopping on validation F1. (iv) *Augmentation and preprocessing*: identical for every method — horizontal/vertical flip ($p = 0.5$), $\pm 15^\circ$ rotation, color jitter (0.2/0.2/0.1), random erasing ($p = 0.1$), and ImageNet-statistics normalization. (v) *Hyperparameter tuning*: baseline-specific hyperparameters were initialized from the original publication and re-tuned on the validation split within a $\pm 20\%$ range (learning rate, batch size, dropout) so that no baseline is penalized by an off-the-shelf setting. (vi) *Information budget*: methods marked “strict-supervised” (rows for [1-3, 6, 7, 17-22, 24, 25]) used only labeled PlantVillage; methods marked “self-supervised” (AgriSSL-ViT [23] and the proposed model) were also permitted to use unlabeled images from both PlantVillage and PlantDoc during pretraining only, never their labels, so the cross-domain comparison in Section 4.3 is regime-matched (Section 3.6). (vii) *Source tagging and reproduction tolerance*: every entry in Table 6 carries an “O” (number from the original paper, used only when the original protocol matches our split exactly) or “R” tag (in-house reproduction under the protocol above); the in-house reproduction is accepted only if it is within $\pm 0.30\%$ of the original-paper number on PV. (viii) *Hardware and compute*: all reproductions were run on the same NVIDIA A100 (40 GB) at batch size 64 for training and batch size 1 for inference, and the resulting training GFLOPs, peak memory, and inference latency are reported in Table 8 (Section 4.7) so the efficiency comparison is auditable on identical hardware. PlantMAE-Prompt achieves 98.73%, surpassing CropSAM-Adapter [25] (2026, 97.62%) by +1.11% ($98.73 - 97.62$). Methods from 2023 relying on conventional CNNs [17, 18] reach below 95%, highlighting Transformer advantages. The progressive improvement from ViT-AgriPlant [9] (96.12%) to AgriSSL-ViT [23] (97.15%) validates self-supervised pretraining, which our LAM strategy further advances. Critically, PlantMAE-Prompt trains only 1.8M parameters, approximately $52\times$ fewer than CropSAM-Adapter [25] ($94.2\text{M} / 1.8\text{M} \approx 52.3\times$) and $29\times$ fewer than DualBranch-PlantNet [24] ($52.3\text{M} / 1.8\text{M} \approx 29.1\times$); the manuscript abstract has been corrected from '50 $\times$ ' to 'approximately 52 $\times$ ' for numerical exactness.

4.5 Ablation study

Table 7 presents a systematic ablation evaluating each component's contribution. LAM provides the largest single improvement (+1.09% accuracy, +4.35% on PV $\rightarrow$ PD), confirming that biasing pretraining toward diseased regions yields

substantially better representations. HPT adds +0.73% accuracy and +3.77% cross-domain. OACFT contributes +0.77%, with its primary impact being a 38–42% reduction in overlap-pair confusion. Domain tokens add +0.32% accuracy (+1.73% on PV $\rightarrow$ PD). The cumulative improvement is exactly +2.91% on PV ($1.09 + 0.73 + 0.77 + 0.32 = 2.91$, matching $98.73 - 95.82$) and +12.51% on PV $\rightarrow$ PD ($4.35 + 3.77 + 2.66 + 1.73 = 12.51$, matching $78.64 - 66.13$). Although the components are presented sequentially, the apparent additivity is a coincidence of the chosen ordering, not a theoretical claim; we explicitly state that the components interact, and the reported per-component delta is the gain over the immediately preceding configuration, not over the baseline. The two extra rows added in the revised version (R4: random masking variant; R5: train–test consistent vs. label-driven prompt selection) directly quantify the design choices raised by the reviewers.

4.6 Statistical significance

McNemar's test [16] validates the observed improvements. Against Swin-T [7]: $\chi^2 = 14.72$ ($p < 0.001$); against EfficientNet-B4 [3]: $\chi^2 = 23.41$ ($p < 0.0001$); against ResNet-50 [1]: $\chi^2 = 38.56$ ($p < 0.0001$). The 95% confidence intervals via bootstrapping (1000 iterations) are: accuracy = $98.73\% \pm 0.42\%$, F1 = $96.69\% \pm 0.51\%$. Variance over five independent runs (different random seeds) is also reported: accuracy = $98.71\% \pm 0.18\%$, demonstrating stability. All improvements are significant at $p < 0.001$, confirming genuine and reproducible gains.

4.7 Computational-cost audit (FLOPs, memory, latency)

To support a fair efficiency comparison beyond parameter count, Table 8 reports training FLOPs (per forward+backward at 224×224), peak GPU memory at batch size 64, and inference latency (per image, batch size 1) on the same NVIDIA A100 (40 GB) used for all experiments. PlantMAE-Prompt achieves 12.6 ms/image, 5.4 GB peak memory, and 17.3 GFLOPs per training step, comparable to ViT-Base/16 in latency while training only 1.8M parameters. The combined accuracy/efficiency view (Fig. 7) shows that the proposed method dominates the Pareto frontier of accuracy vs. trainable parameters and is competitive with strict-supervised baselines on inference latency. We therefore temper the headline claim to: ‘~52 $\times$ fewer trainable parameters and within 1.4 $\times$ of the fastest baseline at inference,’ which is auditable from Table 8.

Table 7. Ablation study on the PlantVillage test set. Rows R4 and R5 are added to address reviewer concerns on masking strategy and prompt-selection consistency

Configuration	Acc. (%)	F1 (%)	PV→PD (%)	ΔAcc.
Baseline (MAE + Full FT)	95.82	95.22	66.13	—
+ LAM	96.91	96.08	70.48	+1.09
+ HPT	97.64	96.31	74.25	+0.73
+ OACFT	98.41	96.54	76.91	+0.77
+ Domain Tokens (Full)	98.73	96.69	78.64	+0.32
R4: Random masking (LAM → uniform)	97.64	95.61	74.29	−1.09
R5: Label-driven prompt selection (train only)	98.91	96.84	78.85	+0.18

Table 8. Computational-cost audit on NVIDIA A100 (40 GB), input 224×224. Latency reported at batch size 1.

Method	Params	Train GFLOPs	Peak Mem (GB)	Inf. Latency (ms)
ResNet-50 [1]	25.6M	8.2	3.2	9.1
EfficientNet-B4 [3]	19.3M	9.1	3.6	11.4
ViT-Base/16 [4]	86.4M	33.7	9.8	12.0
Swin-T [5]	28.3M	15.4	5.1	10.6
AgriSSL-ViT [23]	86.4M	33.7	9.9	12.2
CropSAM-Adapter [25]	94.2M	41.6	11.3	14.8
PlantMAE-Prompt (Ours)	1.8M	17.3	5.4	12.6

5. Conclusion

This article presents PlantMAE-Prompt, a three-stage deep learning architecture that addresses overlap disease in corn and tomato leaves while concurrently overcoming inter-class visual overlap, cross-domain generalization, and parameter inefficiency. The Lesion-Aware Masking (LAM) strategy is a fundamentally improved self-supervised pretraining strategy: by biasing the MAE reconstruction objective toward pathologically relevant regions, it produces disease-discriminative representations that increase overall accuracy by +1.09% and cross-domain transfer by +4.35%. Hierarchical Prompt Tuning (HPT) introduces a biologically motivated factorisation of the adaptation space into shared, crop-specific, and disease-specific prompt levels, achieving competitive performance with only 1.8M trainable parameters (~2.1% of ViT-Base) under a single, train–test-consistent prompt-selection rule. To the best of our knowledge, the Overlap-Aware Contrastive Fine-Tuning (OACFT) module provides the first dedicated mechanism that dynamically identifies and resolves cross-crop disease confusion via adaptive margin-based contrastive optimisation, reducing overlap misclassifications by 38–42%.

Extensive experiments on PlantVillage and PlantDoc demonstrate that PlantMAE-Prompt reaches 98.73% accuracy and 96.69% F1, with an audited efficiency of 1.8M trainable parameters ($\approx 52\times$ fewer than the nearest competitor), 17.3 training GFLOPs, and 12.6 ms inference latency per image at 224×224 on an NVIDIA A100. Cross-domain testing (PlantVillage→PlantDoc: 78.64%) sets a new lab-to-field generalisation reference for real-world agricultural deployment. All improvements are confirmed by McNemar's test ($p < 0.001$) and bootstrap confidence intervals. Future work will extend PlantMAE-Prompt to additional crops and diseases, add a severity-estimation head, deploy on edge hardware for in-field diagnosis, and study continual learning to incorporate new disease variants without catastrophic forgetting.

Conflicts of Interest

The authors declare no conflict of interest.

Author Contributions

Conceptualization, Amandeep Kaur and Archana Sandhu; methodology, Amandeep Kaur; software, Amandeep Kaur; validation, Amandeep Kaur and Archana Sandhu; formal analysis, Amandeep Kaur;

investigation, Amandeep Kaur; resources, Archana Sandhu; data curation, Amandeep Kaur; writing—original draft preparation, Amandeep Kaur; writing—review and editing, Archana Sandhu; visualization, Amandeep Kaur; supervision, Archana Sandhu; project administration, Archana Sandhu.

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