

Original Research

Received 18 May 2026

Revised 15 June 2026

Accepted 01 July 2026

Natural Resources for Human Health 2026, Vol. 6 (4s): 134–149

KEYWORDS:

cauliflower; deep learning; plant disease; transfer learning; explainable artificial intelligence; food safety

Cauliflower Disease Identification and Classification: A Comprehensive Review

Preethi B¹, Patil N. S.², Vinutha H. P³

¹Department of Computer Science and Engineering, Bapuji Institute of Engineering and Technology (BIET), P.O. Box No. 325, Shamanur Road, Davangere 577004, Karnataka, India; ORCID: 0009-0008-8595-0326.

²Department of Information Science and Engineering, Bapuji Institute of Engineering and Technology (BIET), P.O. Box No. 325, Shamanur Road, Davangere 577004, Karnataka, India

³Department of Information Science and Engineering, Bapuji Institute of Engineering and Technology (BIET), P.O. Box No. 325, Shamanur Road, Davangere 577004, Karnataka, India

ORCID: Patil N. S., 0000-0002-9372-5486; Vinutha H. P., 0000-0002-4789-8319.

ABSTRACT: Cauliflower (*Brassica oleracea* var. *botrytis*) is a high-value cruciferous vegetable that is susceptible to bacterial, fungal, oomycete and viral diseases, which often have similar visual symptoms. This is an update of the 2024 survey and a critical review of the evidence on cauliflower published up to 11 August 2026, presented as a structured narrative review. Bibliographic records and publisher platforms were systematically examined, references from eligible studies were traced, and research on disease classification, lesion localization, severity estimation, postharvest defect recognition, and field deployment was assessed. The literature available shows a clear evolution from handcrafted descriptors and traditional classifiers to transfer learning, YOLO-based detection, explainable AI, federated and few-shot learning, lightweight networks, and multimodal RGB-depth analysis. The within-dataset accuracy of several transfer-learning studies was above 99%, while the mean average precision of the modified YOLOv8 and the RGB-plus-estimated-depth detector was 91.1% and 92.0%, respectively. While these results are promising, they are limited by the repeated use of the small VegNet data set, the use of augmentation to expand the data set, the lack of consistent validation procedures, the use of ambiguous disease labels, the lack of calibration analysis, and the lack of external testing. Immediate research priorities are identified as multilocation validation, plant-level data partitioning, pathogen-informed ground truth, uncertainty estimation, lesion-level explanation, and computationally efficient edge deployment. The human-health significance of this area is indirect, and more properly related to food availability, product quality, responsible pesticide use, and residue control than to unsupported assumptions that cauliflower diseases directly lead to human disease

1. INTRODUCTION

In precision agriculture, image-based diagnosis is gaining in significance as many plant diseases are first manifested by changes in colour, texture, shape or integrity of the tissue. The 2024 survey indicated that conventional diagnosis relies heavily on visual inspection by trained individuals and can be slow, subjective, expensive, and challenging to scale in areas with limited access to experts. Other diseases such as black rot, downy mildew, bacterial and soft rots, *Alternaria* leaf spot, white rust, powdery mildew, blackleg, ringspot and mosaic disorders were also found to be significant yield and market quality limiting factors of cauliflower (Preethi et al., 2024a).

The image-based symptom recognition is better thought of as a probabilistic phenotyping rather than a definitive etiological diagnosis. Different pathogens, nutrient imbalance, abiotic stress, insect feeding, chemical injury, mechanical damage or senescence may cause similar lesions. Model outputs should thus be considered as ranked estimates for decision support, while ambiguous cases and treatment determining diagnoses should continue to be evaluated by a plant pathologist and if needed, laboratory confirmed.

The connection between cauliflower disease management and human health is primarily through the food system. When crop-protection practices are not appropriate, disease can impact harvestable yield and quality, influence pesticide-use decisions, and impact farm income and food safety. This pathway is demonstrated by recent residue studies. Hanif et al. (2024) found pesticide residues in a sub-sample of cauliflower samples from around Multan, Pakistan, but their dietary-risk assessment did not suggest a risk for an average 60-kg adult under the conditions assessed. In contrast, Paul et al. (2025) found 36.7% of cauliflower and bitter-melon samples in Bangladesh with residues and identified possible noncarcinogenic risk for certain pesticides. These results suggest that monitoring of residues is more appropriate than direct association of human disease with common cauliflower plant pathogens.

The technical literature has grown from image processing, segmentation, statistical descriptors, and traditional machine-learning classifiers to transfer learning using EfficientNet, MobileNet, NASNetMobile, ResNet, DenseNet, and other convolutional neural networks (CNNs). Recent studies have focused on lesion localization using YOLO, privacy-preserving and few-shot learning, explainable feature fusion, lightweight mobile models, and multimodal RGB-depth detection (Sara et al., 2022; Kanna et al., 2023; Uddin et al., 2024; Muntaqim et al., 2025; Gupta et al., 2026; Xue et al., 2026).

Reported accuracy, however, is not equivalent to agronomic reliability. Models can achieve high accuracy on training and test images with the same backgrounds, cameras, plants, acquisition conditions, or augmented parent images, but can suffer from a drop in accuracy when the crop variety, geography, symptom stage, illumination, or device changes. For instance, Mahapatra et al. (2026) achieved a maximum accuracy of 99.38% in the same dataset and a best average accuracy of 82.93% in the cross-dataset evaluation. This is particularly important for cauliflower as many studies use the same small public data set, while field images have overlapping leaves, soil, weeds, shadows, mixed symptoms and lesions at varying scales.

To this end, evidence published from 2021 to 2026 was reviewed with three main goals: (i) to evaluate the maturity of deep learning for cauliflower disease identification and classification, (ii) to identify methodological approaches with the highest potential to improve field generalization, and (iii) to clarify how diagnostic performance can be responsibly linked to sustainable crop protection, food quality, and human-health relevance.

2. MATERIALS AND METHODS

2.1 Review design and scope

Instead of a registered PRISMA systematic review or meta-analysis, a structured narrative review was conducted. The starting point for the 2024 survey was set as the historical one, and peer-reviewed literature up to 11 August 2026 was considered. The review was crop-focused, and cauliflower-specific studies were prioritized in terms of disease identification, classification, defect recognition, localization, and deployment. Multi-crop studies were also considered to include only those that dealt with methodological limitations that were directly applicable to cauliflower, such as cross-dataset generalization, explainability, lightweight inference, or multimodal sensing.

2.2 Literature identification and eligibility

Records in PubMed-indexed and publisher-hosted bibliographic resources were searched with combinations of the terms cauliflower disease deep learning, cauliflower disease classification CNN, cauliflower YOLO disease detection, VegNet cauliflower, cauliflower transfer learning, cauliflower explainable AI, plant disease cross-dataset, plant disease edge deployment, and cauliflower pesticide residue health risk. The publisher platforms that were reviewed were Springer Nature, Elsevier/ScienceDirect, Frontiers, PLOS, EAI, and Taylor and Francis. Eligible primary studies and dataset articles reference lists were also screened to find foundational cauliflower datasets and previous machine-learning studies. Original research articles, dataset papers, and peer-reviewed conference or journal publications were given priority as they contained enough methodological and quantitative data to be scientifically interpreted.

The studies were included in cases where they utilized images of cauliflower leaves, entire plants, curds, or fresh-cut cauliflower to identify disease or defects, along with methodological studies of deployment-related issues pertinent to cauliflower. The publications that lacked enough methodological description were only discussed contextually and were not included in quantitative comparisons. Since the definitions of classes, datasets, augmentation processes, data partitions, and evaluation measures varied significantly across the studies, no pooled effect size was estimated, and meta-analysis did not rank model architectures.

2.3 Data extraction and synthesis

In every study that concentrated on cauliflower, data were retrieved on the task, image source, disease or defect classes, model family, key performance measures, and constraints on interpretation. The values of accuracy were not deemed to be directly comparable unless the task and validation conditions were close enough. Special consideration was made of the independence of test data, repeated use of the same public data, reporting of precision, recall, F1-score, or mean average precision along with accuracy, and field variability, interpretability, privacy, computational efficiency, and external validation.

The current review builds upon the 2024 survey (Preethi et al., 2024a). To be transparent, two related publications by the same group of authors are also mentioned: an article on a Unified Multi-Scale Feature Network to detect and classify cauliflower disease (Preethi et al., 2024b) and a study on the classification of cruciferous-vegetable species and human-health interpretation (Preethi and Vinutha, 2026). These publications are mentioned as related work and are not considered as independent external validation. Compared to the previous survey, the current article includes a clear review methodology, evidence up to 11 August 2026, and critical discussion of lesion localization, cross-dataset robustness, explainability, federated and few-shot learning, RGB-depth fusion, edge deployment, food-safety relevance, and minimum reporting standards.

2.4 Reference verification and quality control

The final publisher page, DOI record, PubMed record, or official journal record, where possible, were compared with publication year, volume, pagination or article number, and digital object identifier. In cases where full text was not available, data extraction was limited to information reported in the verified abstract or publisher record. Where there was a primary record, performance values were not derived based on secondary summaries.

The main text and tables also analyzed citation-reference concordance to make sure that all studies cited had a reference and that all retained references were used in the synthesis. The same author group publications were revealed as related work and were not included in the number of independent evidence of generalization. In cases where primary reports were not sufficiently informative, the restriction was mentioned explicitly instead of being addressed by assumption.

3. RESULTS AND DISCUSSION

3.1 Cauliflower disease phenotypes and imaging targets

Phenotypes of diseases that have direct implications on image analysis were initially studied. *Alternaria* leaf spot is known to cause dark necrotic spots with concentric or target-like rings (Mourou et al., 2023). Black rot is associated with marginal chlorosis and V-shaped lesions that grow inwards and sometimes with vascular darkening (Dániel-Gómez et al., 2022). Downy mildew of cauliflower may result in pale or yellow lesions on the upper leaf surface, and sporulation or discoloration on the underside (Shaw et al., 2021). Bacterial soft rot is associated with pectolytic bacteria such as *Pectobacterium* spp. and is characterized by water-wet tissue breakdown, maceration and loss of structural integrity. (Li et al., 2020). White rust caused by *Albugo candida* results in white or cream blister-like sori, and powdery mildew results in superficial white colonies on Brassica leaves (Nirwan et al., 2023; Mourou et al., 2023). Symptoms of viral mosaic can be mottling, chlorosis, changes in veins, distortion, or stunting (Pouresmaeil et al., 2023). Nutrient deficiency, senescence, insect damage, mechanical damage and spray deposits should be considered as possible visual mimics as the appearance of the symptoms will depend on the stage of the disease, cultivar, environment and camera conditions. The representative images of the 2024 survey are reproduced in figures 1-3.



Figure 1. Representative Brassica leaf image labelled as Alternaria leaf spot in the 2024 survey (Preethi et al., 2024a). Alternaria leaf spot in Brassicaceae commonly appears as dark necrotic lesions with concentric rings (Mourou et al., 2023).



Figure 2. Representative Brassica canopy image labelled as black rot in the 2024 survey (Preethi et al., 2024a). Black rot of Brassica crops is caused by *Xanthomonas campestris* pv. *campestris* and commonly produces marginal chlorosis, V-shaped lesions, and vascular darkening (Dániel-Gómez et al., 2022).

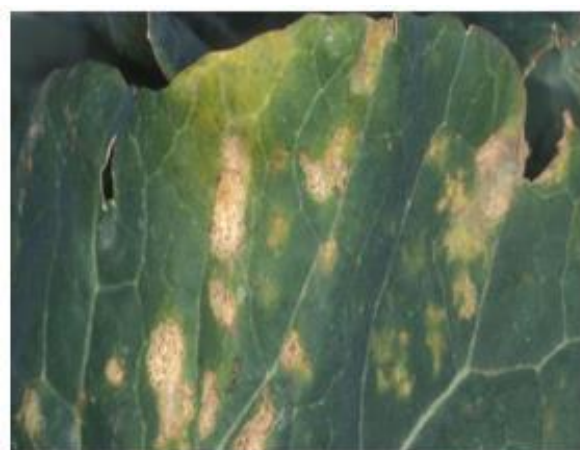


Figure 3. Representative Brassica leaf image labelled as downy mildew in the 2024 survey (Preethi et al., 2024a). Downy mildew of cauliflower is associated with *Hyaloperonospora* spp. and may produce pale or yellow upper-surface lesions with lower-surface sporulation (Shaw et al., 2021).

Disease-resistance breeding is still a valuable supplementary method. Based on molecular markers linked to black-rot resistance and genetic studies of downy-mildew resistance, it is recommended that image-based diagnosis should be used in combination with pathogen-informed breeding and integrated disease management (IDM) (Kalia et al., 2017; Verma and Singh, 2018).

These biological differences dictate the best computer-vision task. If there is only one predominant condition, and the organ of interest has been segmented, then image-level classification is appropriate. Object detection is more suitable when the lesions need to be localized in cluttered field scenes, while semantic or instance segmentation is needed when the area or severity of the lesions needs to be quantified. Temporal models can be helpful if disease progression is observed over multiple observations. Hence, the term disease detection is only used when spatial localization is concerned and is distinguished from whole-image classification. The main disease phenotypes, diagnostic pitfalls, and implications for model design are summarized in Table 1.

Table 1. Major cauliflower disorders, diagnostic caveats, and implications for computer-vision analysis.

Disorder	Typical causal agent or label status	Principal visible cues	Implication for computer vision
Alternaria leaf spot	<i>Alternaria brassicae</i> and <i>A. brassicicola</i>	Dark necrotic lesions, frequently with concentric rings	Texture and lesion-margin cues are useful, but early lesions may resemble injury or senescence.
Black rot	<i>Xanthomonas campestris</i> pv. <i>campestris</i>	Yellow V-shaped lesions advancing inward from leaf margins; vein darkening and necrosis	Lesion geometry and marginal origin are informative, although advanced symptoms overlap with other necrotic disorders.
Downy mildew	<i>Hyaloperonospora brassicae</i> ; older literature may use <i>Peronospora parasitica</i> or <i>H. parasitica</i>	Pale or yellow upper-surface lesions; downy sporulation may occur on the abaxial surface	A single adaxial RGB view may miss diagnostic sporulation; multi-view acquisition can improve evidence.
Bacterial soft rot	<i>Pectobacterium</i> spp. and <i>Dickeya</i> spp.	Water-soaked tissue, soft collapse, maceration, and decay	Appearance changes rapidly with severity; leaf and curd symptoms may require organ-specific models.
White rust	<i>Albugo candida</i>	White pustules, commonly on the lower leaf surface, with corresponding chlorotic areas	Models should distinguish pustules from powdery growth, spray deposits, glare, and debris.
Powdery mildew	<i>Erysiphe cruciferarum</i> and related powdery-mildew fungi	Superficial white powdery growth and progressive chlorosis or senescence	Fine surface texture is important; imaging conditions can strongly affect visibility.
Viral mosaic symptoms	<i>Cauliflower mosaic virus</i> and other viruses	Mottling, chlorosis, distortion, vein clearing, or stunting	Diffuse plant-level symptoms may be poorly represented by bounding boxes; contextual or temporal evidence is useful.
Dataset-defined “bacterial spot rot”	Non-standard or ambiguous label; causal organism is not established by the class name alone	Spot or rot appearance on leaves or curds as labeled in reused datasets	Treat as a dataset class rather than laboratory-confirmed etiology; future datasets should document diagnostic criteria.

Note: Disease names, causal agents, and characteristic symptoms are supported by peer-reviewed Brassicaceae pathology literature (Daniel-Gómez et al., 2022; Mourou et al., 2023; Shaw et al., 2021; Li et al., 2020; Nirwan et al., 2023; Pouresmaeil et

al., 2023). The final column represents a critical synthesis of implications for computer-vision analysis and should not be interpreted as a pathogen-confirmation criterion.

3.2 From handcrafted descriptors to deep transfer learning

The initial studies on cauliflower were based on color and texture processing, k-means segmentation, co-occurrence statistics, and classifiers such as Random Forest, support vector machines, BayesNet, KStar, decision trees, and neural networks. For example, Rajbongshi et al. (2022) experimented with 776 cauliflower images and attained an accuracy of approximately 89% with Random Forest. Although these pipelines are simple and explainable at the feature level, they are very sensitive to the quality of the segmentation and the manually selected descriptors.

CNNs alleviated this reliance by directly learning hierarchical visual features from images. Evidence from cauliflower and other plant-disease research (Chen et al., 2020; Too et al., 2019; Maria et al., 2022; Abdul Malek et al., 2022) explains why the use of ImageNet-pretrained backbones for crop-specific datasets with limited data is done. VegNet provided an organized public dataset of 656 images of bacterial spot rot, black rot, downy mildew, and healthy classes (Sara et al., 2022). Subsequent studies employed EfficientNet, MobileNet, NASNetMobile, ResNet, DenseNet and other networks with augmentation. Kanna et al. (2023) obtained a validation accuracy of 99.90% using EfficientNetB1, while Abdul Azeem et al. (2024) obtained a test accuracy of 99.25% and F1-score of 0.993 using NASNetMobile. These results demonstrate good discrimination within the reported data sets, but do not indicate equal performance under independent field conditions.

So, near perfect performance values should be taken with a grain of salt. These findings suggest that there are learnable visual differences in the available data sets, but do not prove that the data sets are equally reliable when applied to new farms, cultivars, seasons, or imaging devices. If a small data set is being augmented, then the same source image should not be present in the development and test sets as transformed images. A more stringent approach is to split the data into independent plant, field or acquisition episode and then only augment the training subset. This should be clearly documented in future cauliflower research.

3.3 Cauliflower-specific evidence from 2021 to 2026

There are now three different tasks in the cauliflower-specific literature. The first is whole-image disease classification, mainly demonstrated by transfer-learning comparisons on VegNet and other four-class datasets. The second is lesion localization, an adaptation of YOLOv8 to detect and localize bacterial soft or spot rot, downy mildew and black rot in smartphone or handheld images, called Cauli-Det. The third is quality or defect evaluation of edible cauliflower heads and fresh-cut products. These tasks vary in terms of labels, image scale, annotations and evaluation metrics and require separate interpretation.

In various classification studies, EfficientNet-family models have shown good performance. Pradhan et al. (2024) and Malik et al. (2025) obtained 98% and 99.85% accuracy respectively using EfficientNetB3 as the backbone model among eight models tested. However, Arnob et al. (2025) achieved a lower best accuracy of 90.85% using ResNet50. The discrepancies between the studies suggest that the ranking of the models depends on the data partitioning, preprocessing, hyperparameter tuning, and composition of the datasets; at this time, there is no single architecture that can be considered as the best model for cauliflower disease classification.

Research was extended beyond the traditional benchmark classification in 2025 and 2026. Muntaqim et al. (2025) combined federated learning, Reptile-based few-shot learning, and voting among five pretrained networks under non-IID client distributions. The reported ensemble accuracy went from 95% in the two-shot setting to 100% in the five-shot setting. Gupta et al. (2026) suggested the use of Cauli-NET, a lightweight VegScratchNet with MobileNetV2 features and dilated convolution, and achieved 92.63% accuracy in disease or defect identification along with explainable-AI analysis. These studies are not only about benchmark accuracy, but also about adaptation, small-sample learning, privacy, and interpretability.

Another significant advancement was multimodal localization. Xue et al. (2026) proposed HMFNet, which is a combination of RGB images and monocular depth maps produced by Depth Anything V2, with boundary enhancement, self-attention, and wavelet-guided attention. A total of 640 original RGB images of bacterial spot, black rot, downy mildew and healthy plants were used and 1,920 RGB-depth pairs were generated by augmentation. The model achieved 93.2% precision, 87.9% recall, an F1-score of 90.3%, and mAP@0.5 of 92.0%. This result is a computational multimodal fusion since the depth maps were estimated from a single RGB image and not captured using an RGB-D sensor.

In 2024, the same group of authors suggested a Unified Multi-Scale Feature Network (UMFN) for the detection and classification of cauliflower diseases (Preethi et al., 2024b). Due to common authorship, that publication is deemed to be related work and not independent validation. Table 2 presents a comparison of representative studies on cauliflower.

Table 2. Representative cauliflower-focused image-analysis studies, reported performance, and critical interpretation.

Study	Task and data	Model or approach	Principal reported result	Critical interpretation
Orin et al. (2021)	Leaf disease recognition	Image processing and machine learning	Baseline automated recognition	Early benchmark with limited evidence of external field validation.
Rajbongshi et al. (2022)	776 images; four classes	K-means, handcrafted features, and classical classifiers	Random Forest approximately 89% accuracy	Performance depends on segmentation and engineered descriptors.
Maria et al. (2022)	Cauliflower disease recognition; machine-learning and transfer-learning comparison	Random Forest and pretrained CNNs	Random Forest 81.68%; InceptionV3 90.08%	Useful early comparison; dataset independence and external testing remain limited.
Abdul Malek et al. (2022)	Approximately 2,500 images; bacterial soft rot, black rot, buttoning, and white rust	VGG16, VGG19, ResNet50, and InceptionV3	InceptionV3 93.93% test accuracy	Different class ontology from VegNet; field generalization was not established.
Sara et al. (2022)	VegNet; 656 original images; four classes	Public cauliflower dataset	Reproducible cauliflower-specific benchmark	Small dataset that has been reused repeatedly; one disease label is diagnostically ambiguous.
Durjoy et al. (2025)	2,661 images; healthy, insect holes, and black rot	Public multilocation image dataset	Broader acquisition conditions; 3,000 × 3,000-pixel standardized images	Only one disease class plus insect injury; independent pathologist-confirmed testing remains necessary.
Li et al. (2022)	Fresh-cut defects; 4,790 images	Transfer learning	MobileNet 99.27% accuracy; F1 99.24%	Postharvest surface-defect task, not foliar field diagnosis.
Kanna et al. (2023)	VegNet; four classes; augmented dataset	Ten transfer-learning CNNs	EfficientNetB1 validation accuracy 99.90%	High within-study performance; original-image independence and external testing require emphasis.
Pradhan et al. (2024)	Four-class disease classification	EfficientNetB3, DenseNet121, VGG19, and ResNet50	EfficientNetB3 98% accuracy	Result remains specific to the reported data split and experimental protocol.
Uddin et al. (2024)	656 smartphone-captured images;	Modified YOLOv8 (Cauli-Det)	Precision 93.2%; recall 82.6%; mAP 91.1%	Meaningful localization advance; lower recall indicates

	three classes; object localization			missed lesions remain important.
Abdul Azeem et al. (2024)	VegNet; 656 original images; four classes	Fine-tuned transfer learning	NASNetMobile 99.25% test accuracy; F1 0.993	Small public dataset; external and cross-device validation are still needed.
Malik et al. (2025)	Cauliflower disease classification	Eight transfer-learning models	EfficientNetB3 99.85% accuracy	Benchmark accuracy should not be interpreted as cross-domain robustness.
Arnob et al. (2025)	VegNet classification	VGG16, Inception v3, ResNet50, and custom CNN	ResNet50 90.85% accuracy	Different outcome from other VegNet studies illustrates protocol and implementation sensitivity.
Muntaqim et al. (2025)	Non-IID clients and two- to five-shot settings	Federated learning, Reptile few-shot learning, and five-model voting	Reported 95-100% accuracy across two- to five-shot settings	Promising simulated heterogeneity; requires validation across genuinely independent institutions.
Gupta et al. (2026)	Small-sample leaf and edible-head defect classification	Cauli-NET feature fusion and explainable AI	Accuracy 92.63%	Interpretability is useful; independent-site and cultivar-level testing are still required.
Xue et al. (2026)	640 RGB images; model-generated monocular depth maps; 1,920 augmented pairs; detection	HMFNet multimodal fusion	Precision 93.2%; recall 87.9%; F1 90.3%; mAP@0.5 92.0%	Computationally estimated depth is promising but is not equivalent to hardware RGB-D acquisition; external field validation is needed.
Preethi et al. (2024b)	Cauliflower disease detection and localization	Unified Multi-Scale Feature Network	Reported improvement in precision, recall, and mAP within the original study	Related publication from the present author group; treated as contextual evidence rather than independent external validation.
Preethi and Vinutha (2026)	Three-class broccoli, cabbage, and cauliflower species classification	Deep learning predictive model	Contextual cruciferous-classification result	Not a disease-diagnosis benchmark; retained only for transparent scope differentiation.

Note: Each study is cited in the first column and listed in the reference section. Dataset and localization details were cross-checked against the VegNet data article (Sara et al., 2022), the multilocation image dataset (Durjoy et al., 2025), and Cauli-Det (Uddin et al., 2024). Performance values are study-specific and are not directly comparable across different datasets, tasks, or validation protocols.

In 2026, two of the authors of the present review carried out a separate study on three-class classification of broccoli, cabbage and cauliflower (Preethi and Vinutha, 2026). This investigation is not a benchmark for cauliflower disease, but is mentioned for scope differentiation because it is a classification of cruciferous-vegetable species.

3.4 Classification is not localization or severity estimation

Whole image classification classifies the image, but does not provide information about the location of the lesion, the amount of tissue involved, or the presence of multiple disorders. These differences are relevant to integrated disease management, as users need to be confident that a model is responding to the symptoms of the tissue and not to background cues, and management decisions may be based on severity. To overcome this, Uddin et al. (2024) proposed a modified YOLOv8 model, Cauli-Det, which was trained using 656 images of cauliflower. The study reported 93.2% precision, 82.6% recall, and 91.1% mAP. The primary benefit is that it moves from a global class label to a spatially localized prediction.

The concept of localization should be expanded to quantitative estimation of severity. Bounding boxes are used to approximate the position of the lesions but are not fine enough to measure the percentage of affected tissue. Segmentation at the pixel level can be used to estimate lesion-to-leaf area, and ordinal or continuous severity labels can be used to correlate image-derived measurements with agronomic decision thresholds. Evaluation should be suitable, including intersection-over-union or Dice-type measures for segmentation, mean average precision over a range of intersection-over-union thresholds for detection, and agronomically meaningful error bands for severity estimates. Datasets for early diagnosis should also be able to distinguish between presymptomatic, mild, moderate and severe images, as opposed to all diseased images being the same.

3.5 Dataset shift, leakage risk, and external validation

The main constraint is still the design of the datasets. VegNet allowed for reproducible comparison, but repeated analysis of the same 656 source images implies that many published accuracy values are not independent replications on new biological material. Class balance, near duplicate images, augmentation, backgrounds, and acquisition devices may be shortcuts that a model learns rather than disease pathology. This problem is not unique to cauliflower. Controlled resources like PlantVillage have helped to develop algorithms, and also shown the difference between lab images and field images (Mohanty et al., 2016).

A newer public resource has 2,661 images of cauliflower leaves, split into three classes: healthy (934), insect-hole (639), and black-rot (1,088). The images were captured under different weather, temperature, illumination and capture devices at two locations in Bangladesh from November 2024 to January 2025 by Durjoy et al. (2025). The dataset expands acquisition diversity beyond VegNet, but only one disease category and one insect-injury category. It does not therefore obviate the need for external testing by a pathologist in multiple countries and diseases.

Cross-dataset testing is a more challenging estimate of generalization. Under cross-dataset testing, Mahapatra et al. (2026) tested an attention-based CNN on multiple plant-disease datasets and found that the best average accuracy was 82.93% compared to 99.38% in the best intra-dataset setting. The methodological implication is directly relevant, although the crops were not cauliflower: performance must be demonstrated when backgrounds, acquisition conditions, and data sources change. A meaningful external test for cauliflower should involve at least one farm, season, region, or device that did not provide any images for model development.

Reports should include the number of original images before augmentation, the number of independent plants and farms (if applicable), the unit used for partitioning the data, the method used to identify near duplicates, the exact proportions of the training, validation, and test sets, and the distribution of classes within each partition. The final model should be tested once on a locked test set, and a confidence interval or repeated-seed results are more informative than a single accuracy value. Open code, trained weights, and versioned datasets should be made available whenever possible, in terms of licensing and ethics.

3.6 Explainability, calibration, and trustworthy decision support

Explainable artificial intelligence (XAI) is becoming more popular to visualize image regions that affect prediction. Grad-CAM and similar techniques can be used to determine if a CNN is reacting to symptomatic tissue or irrelevant background patterns. Grad-CAM++ has been recently used in plant-disease studies in lightweight architectures (Mazumder et al., 2024), and feature fusion with XAI is used in cauliflower-specific Cauli-NET (Gupta et al., 2026). Hybrid CNN-transformer models have also been used in conjunction with explanation methods, which integrate local texture analysis with global attention (Srinivasan et al., 2026; Jawed et al., 2026).

Heat maps are not a measure of trustworthiness on their own. Explanations should be compared to lesion annotations or expert assessments, particularly if symptoms are small or diffuse. Calibrated confidence is also needed for field decision-support systems. The meaning of a nominal probability of 0.99 should be the same in all acquisition conditions, otherwise users may over-trust uncertain predictions. Future studies should include calibration error or reliability diagrams, assess abstention when confidence is low, and explore out-of-distribution detection for unfamiliar diseases, nutrient deficiencies, and non-disease damage.

3.7 Lightweight, federated, and multimodal deployment

Constraints that are not considered in benchmark experiments are introduced in practical deployment. Smartphones and edge devices have constrained memory, energy and latency budgets, and connectivity in rural areas can be intermittent. Lightweight backbones like MobileNet and EfficientNet can help lower computational expenses, and recent multi-crop studies have explicitly mentioned latency and edge feasibility (Hasani et al., 2026). Rahaman et al. (2026) trained a customized MobileNetV3Large model on a hybrid field and public dataset with cauliflower, which achieved 99.37% test accuracy for 26 plant-disease classes and deployed the model in an Android application. This study demonstrates the usefulness of using field images in conjunction with a portable architecture, but external evaluation of the crop is still required.

Another way to scale is federated learning, which enables farms or institutions to train together without centralizing raw images. Muntaqim et al. (2025) showed that federated and few-shot learning can be synergized for cauliflower under heterogeneous client distributions. The next step is validation on truly independent institutions (cultivar, camera, climate, crop management) and not only on simulated data partitions. The cost of communication, client imbalance, leakage of privacy due to model updates, and robustness to mislabeled local data also need to be measured.

Multimodal representations can help to make the system more robust when the RGB appearance varies due to illumination or background clutter. To enhance the boundaries of the lesions and minimize background noise, Xue et al. (2026) fused RGB images with monocular depth maps generated by a model. Additional structural or physiological data can be obtained from multispectral, hyperspectral, thermal, or hardware-acquired depth data, but the complexity of the data and cost and calibration of the sensors can restrict their use at the farmer scale. Therefore, each modality should be compared to a carefully tested RGB-only baseline. Table 3 provides an overview of the deployment relevance of these methods and the validation that still needs to be done.

Table 3. Methodological advances and validation priorities for next-generation cauliflower disease systems.

Priority	Representative evidence	What it addresses	What still needs validation
Cross-dataset evaluation	Mahapatra et al. (2026)	Measures performance under dataset shift rather than within one source	Multi-farm cauliflower testing with locked external datasets.
Localization rather than global labels	Uddin et al. (2024); Xue et al. (2026)	Shows where lesions occur and supports severity-oriented analysis	Small-lesion recall, multiple co-occurring diseases, and segmentation-based severity.
Explainable AI	Mazumder et al. (2024); Gupta et al. (2026); Srinivasan et al. (2026)	Audits whether predictions are driven by symptom regions	Quantitative comparison of explanations with expert lesion annotations.
Lightweight/edge inference	Mazumder et al. (2024); Hasani et al. (2026); Rahaman et al. (2026)	Supports mobile/offline deployment and lower compute cost	Device-specific latency, energy, memory, and field usability.

Federated/few-shot learning	Muntaqim et al. (2025)	Addresses data scarcity, heterogeneity, and raw-data sharing constraints	True multi-institution clients, communication cost, privacy and label noise.
Multimodal sensing	Xue et al. (2026)	Adds model-generated geometric information when RGB is sensitive to illumination and clutter	Incremental value relative to RGB-only models and validation with hardware-acquired depth or spectral data.
Calibration and abstention	Recommended future standard	Prevents over-confident use of uncertain predictions	Reliability curves, OOD detection and thresholds validated with end users.

Note: Representative evidence includes Mahapatra et al. (2026), Uddin et al. (2024), Xue et al. (2026), Mazumder et al. (2024), Gupta et al. (2026), Srinivasan et al. (2026), Hasani et al. (2026), Rahaman et al. (2026), and Muntaqim et al. (2025). The final column presents a critical synthesis of the remaining validation requirements.

3.8 Food-safety and human-health implications

The connection between plant-disease AI and human health is indirect. Maintaining yield and market quality helps to ensure food availability, and early and more specific diagnosis can help to make more targeted crop-protection decisions. There is also the potential for reduced unnecessary chemical applications with better discrimination, but this benefit must be quantified. A diagnostic model cannot ensure reduced pesticide use as management is dependent on disease severity, local recommendations, economics and farmer behavior.

The studies of cauliflower residues illustrate the importance of responsible crop protection. Hanif et al. (2024) found residues in 20% of 40 samples from the Multan area, but the study-specific dietary-risk calculation did not show a risk for an average 60-kg consumer. Paul et al. (2025) found residues in 36.7% of cauliflower and bitter-gourd samples collected from Bangladesh, with the majority of the detected residues being above the European Commission maximum residue limits, and the authors indicated potential noncarcinogenic risk in their hazard assessment. Dong and Hu (2023) also demonstrated that the dissipation of residues and dietary risk are dependent on the chemical, crop, and preharvest interval. These findings, combined, suggest a connection between AI-assisted diagnosis and validated disease-management recommendations and residue-aware pesticide stewardship.

Postharvest quality provides a second food-system pathway. Li et al. (2022) employed transfer learning for surface defect detection of fresh-cut cauliflower and achieved an accuracy of 99.27% using MobileNet. Postharvest defect recognition is different from field disease diagnosis, but automated quality inspection can be used to sort and minimize the movement of visibly affected products. Future research may link preharvest disease history, postharvest imaging, microbial safety testing, and storage results to see if image-based decisions result in measurable improvements in food safety or shelf life.

3.9 Research priorities and reporting recommendations

Evidence quality should be given priority over marginal improvements obtained on a familiar benchmark. Future datasets should include prospective sampling across regions, seasons, cultivars, growth stages and imaging devices, and plant- or field-level partitioning. Annotations should include location of lesion, severity of disease, other diseases present, and other non-disease mimics. Evaluation should involve external testing, class specific metrics, calibration, uncertainty and quantitative comparison of explanation maps with expert lesion annotations. A minimum reporting framework is provided in Table 4.

Table 4. Minimum reporting checklist for field-relevant cauliflower disease artificial-intelligence studies.

Reporting domain	Minimum information	Why it matters
Dataset provenance	Original image count, farms/locations, season, cultivar, camera/device, class definitions	Reveals biological and acquisition diversity.

Data partitioning	Split unit (image/plant/plot/farm), ratios, random seed, duplicate checks	Reduces leakage and clarifies independence of the test set.
Augmentation	Exact transforms and confirmation that augmentation occurs after splitting	Prevents transformed copies from contaminating evaluation.
Ground truth	Expert criteria; laboratory confirmation where diagnosis is ambiguous	Improves label validity.
Metrics	Accuracy plus macro F1; per-class precision/recall; mAP/IoU for detection; confidence intervals	Avoids over-reliance on a single aggregate metric.
External validation	At least one unseen location/season/device or a cross-dataset test	Best evidence of real-world generalization.
Calibration/uncertainty	Reliability or calibration metric; low-confidence abstention rule	Supports safe decision support.
Explainability	XAI method and, ideally, overlap with expert lesion regions	Tests whether the model uses biologically plausible evidence.
Deployment efficiency	Parameters, model size, hardware, latency; energy if feasible	Determines mobile/edge feasibility.
Reproducibility	Versioned dataset, code/weights, preprocessing and hyperparameters where licensing permits	Enables independent replication.
Downstream impact	Time-to-diagnosis, management change, pesticide-use change, yield/cost/food-safety outcome where claimed	Connects AI performance to agricultural and human-health value.

Note: This checklist was developed from recurring methodological limitations and reporting practices documented by Mohanty et al. (2016), Uddin et al. (2024), Mahapatra et al. (2026), Hasani et al. (2026), Srinivasan et al. (2026), and Xue et al. (2026). It is proposed as a minimum reporting framework for future cauliflower disease-AI studies.

Parameter count, model size, hardware, latency, energy consumption (if possible), and offline capability should also be reported in deployment studies. Federated learning should be evaluated on real distributed data and communication and privacy analysis should be provided. Multimodal systems should be able to measure the added value of depth, spectral or thermal information in terms of diagnosis, as well as the cost of the information. If sustainability or human-health benefit is claimed, evidence must be provided downstream, including reduction in time to diagnosis, reduction in unnecessary pesticide use, yield, cost per diagnosis, or compliance with residue-management recommendations.

Plant pathologists and end users should be engaged in model development. Ground-truth labels are best when derived from expert diagnosis and, if symptoms are not clear, laboratory confirmation. Farmer facing systems should convey the probable diagnosis, level of confidence and location of the lesion, and suggest expert confirmation where the diagnosis is not clear or the management implications are significant. The goal is not to supplant agronomic knowledge, but to offer a reproducible triage and decision-support layer.

3.10 Limitations of this review

There are some limitations to the present review that should be noted. The search strategy was not registered in a systematic-review protocol or meta-analysis, and the targeted search strategy may not have identified all relevant publications. The synthesis is thus subject to limitations of database coverage, language, indexing, and publication bias. A formal risk-of-bias instrument was not used. Furthermore, there was significant variation in disease labels, original image counts, augmentation methods, data partitions, evaluation metrics, and task definitions, which made quantitative analysis across all models impossible and made it difficult to defend the ranking of model architectures.

The evidence base for cauliflower is dominated by repeated analyses of a relatively small number of public images, especially VegNet, which reduces the biological and statistical independence of studies. There is also limited independent replication for publications that will be published in 2025 and 2026. The 2024 UMFN publication by the same group of authors was not considered as external validation. Therefore, the present review should be viewed as a critical synthesis of evidence available as of 11 August 2026, and not as evidence that any reviewed system is ready for autonomous disease diagnosis or pesticide recommendation.

4. CONCLUSIONS

The evidence available shows that the disease recognition in cauliflower has evolved from handcrafted features and traditional classifiers to transfer learning, YOLO-based lesion localization, federated few-shot learning, explainable feature fusion, lightweight mobile architecture, and RGB analysis with model-generated depth information. These methods have been shown to be able to differentiate cauliflower symptom and defect classes with high reported performance under defined experimental conditions. But the evidence has not yet shown the same level of reliability in unseen farms, cultivars, seasons, devices, disease stages and visually similar non-disease conditions.

Independent generalization is thus a more significant research goal than incremental accuracy within the dataset. Future research should consider plant-, plot-, or farm-level partitioning, prospective multilocation validation, pathogen-informed ground truth, post-split augmentation, calibrated uncertainty and abstention, and localization or segmentation when severity assessment is needed. While federated, few-shot, and lightweight approaches tackle data scarcity, privacy, and deployment constraints, Cauli-Det and HMFNet represent the shift from global labels to spatially meaningful predictions. The most compelling reason for this research within the Natural Resources for Human Health is the ability to produce resilient food, ensure food quality, and make more precise decisions about crop protection. Before wider public health benefits are attributed, agricultural, economic and food-safety benefits should be measured directly.

Declarations

Funding:

Acknowledgements:

Author contributions:

Conflict of interest:

Ethics statement:

Data availability

Declaration of generative AI and AI-assisted technologies

References

- [1] Abdul Azeem, N., Sharma, S., Verma, A., 2024. Automatic cauliflower disease detection using fine-tuning transfer learning approach. *SN Computer Science* 5, 817. <https://doi.org/10.1007/s42979-024-03185-6>.
- [2] Abdul Malek, M., Reya, S.S., Zahan, N., Zahid Hasan, M., Uddin, M.S., 2022. Deep learning-based cauliflower disease classification. In: Uddin, M.S., Bansal, J.C. (Eds.), *Computer Vision and Machine Learning in Agriculture*, Volume 2. Springer, Singapore, pp. 171-186. https://doi.org/10.1007/978-981-16-9991-7_11.

- [3] Arnob, A.S., Kausik, A.K., Islam, Z., Khan, R., Bin Rashid, A., 2025. Comparative result analysis of cauliflower disease classification based on deep learning approach VGG16, Inception v3, ResNet, and a custom CNN model. *Hybrid Advances* 10, 100440. <https://doi.org/10.1016/j.hybadv.2025.100440>.
- [4] Chen, J., Chen, J., Zhang, D., Sun, Y., Nanehkaran, Y.A., 2020. Using deep transfer learning for image-based plant disease identification. *Computers and Electronics in Agriculture* 173, 105393. <https://doi.org/10.1016/j.compag.2020.105393>.
- [5] D aniel-G omez, M., Reeves, E., Meadows, I.M., 2022. Practical and comprehensive diagnostic guide for black rot of brassicas. *Plant Health Progress* 23(3), 369-375. <https://doi.org/10.1094/PHP-08-21-0109-DG>.
- [6] Dong, B., Hu, J., 2023. Dissipation patterns, residue analysis, and risk evaluation of hexaflumuron in turnip and cauliflower under Chinese growth conditions. *Environmental Science and Pollution Research* 30, 85534-85544. <https://doi.org/10.1007/s11356-023-28011-z>.
- [7] Durjoy, S.H., Shikder, M.E., Shoib, M.M.H., Bijoy, M.H.I., 2025. Cauliflower leaf diseases: A computer vision dataset for smart agriculture. *Data in Brief* 60, 111594. <https://doi.org/10.1016/j.dib.2025.111594>.
- [8] Gupta, S., Tripathi, A.K., Wankhade, A.V., 2026. Feature fusion based deep dilated convolution network and explainable intelligence for defect identification in small-sample cauliflower crops. *Engineering Applications of Artificial Intelligence* 173, 114497. <https://doi.org/10.1016/j.engappai.2026.114497>.
- [9] Greer, S.F., Surendran, A., Grant, M., Lillywhite, R., 2023. The current status, challenges, and future perspectives for managing diseases of brassicas. *Frontiers in Microbiology* 14, 1209258. <https://doi.org/10.3389/fmicb.2023.1209258>.
- [10] Hanif, M.N., Haq, T., Akhtar, M.N., Hussain, A., Matloob, A., 2024. Risk assessment of pesticide residues in cauliflower grown in vicinity of Multan City, Pakistan. *Sarhad Journal of Agriculture* 40(4), 1164-1171. <https://doi.org/10.17582/journal.sja/2024/40.4.1164.1171>.
- [11] Hasani, Z., Fondaj, J., Bytyqi, D., Misini, S., 2026. Comparative evaluation of deep learning models for plant disease classification with edge-aware performance analysis. *PLOS ONE* 21(6), e0349901. <https://doi.org/10.1371/journal.pone.0349901>.
- [12] Jawed, M.M., Tufail, F.A., Ahmed, M.Z., Suji, A.R., Nallusamy, P., Raja, K.T., 2026. A hybrid deep learning framework using convolutional and transformer models for robust plant disease classification. *Scientific Reports* 16, 9704. <https://doi.org/10.1038/s41598-026-38209-z>.
- [13] Kalia, P., Saha, P., Ray, S., 2017. Development of RAPD and ISSR derived SCAR markers linked to Xca1Bo gene conferring resistance to black rot disease in cauliflower (*Brassica oleracea* var. *botrytis* L.). *Euphytica* 213, 232. <https://doi.org/10.1007/s10681-017-2025-y>.
- [14] Kanna, G.P., Jagadeesh Kumar, S.J.K., Kumar, Y., Changela, A., Wo zniak, M., Shafi, J., Ijaz, M.F., 2023. Advanced deep learning techniques for early disease prediction in cauliflower plants. *Scientific Reports* 13, 18475. <https://doi.org/10.1038/s41598-023-45403-w>.
- [15] Li, X., Fu, L., Chen, C., Sun, W., Tian, Y., Xie, H., 2020. Characteristics and rapid diagnosis of *Pectobacterium carotovorum* ssp. associated with bacterial soft rot of vegetables in China. *Plant Disease* 104(4), 1158-1166. <https://doi.org/10.1094/PDIS-05-19-1033-RE>.
- [16] Li, Y., Xue, J., Wang, K., Zhang, M., Li, Z., 2022. Surface defect detection of fresh-cut cauliflowers based on convolutional neural network with transfer learning. *Foods* 11(18), 2915. <https://doi.org/10.3390/foods11182915>.
- [17] Mahapatra, P., Panda, M., Dash, S.K., Sahu, U.K., 2026. Advancing plant disease classification using an attention-based CNN for intra-dataset and cross-dataset training. *Scientific Reports* 16, 10925. <https://doi.org/10.1038/s41598-026-45464-7>.
- [18] Malik, N., Chhikara, R., Yadav, G., Sharma, P., Sisodia, N., 2025. Advanced deep learning techniques for cauliflower plant disease detection. *Procedia Computer Science* 259, 1326-1335. <https://doi.org/10.1016/j.procs.2025.04.087>.
- [19] Maria, S.K., Taki, S.S., M a, M.J., Biswas, A.A., Majumder, A., Hasan, F., 2022. Cauliflower disease recognition using machine learning and transfer learning. In: Somani, A.K., Mundra, A., Doss, R., Bhattacharya, S. (Eds.), *Smart Systems: Innovations in Computing. Smart Innovation, Systems and Technologies*, Vol. 235. Springer, Singapore, pp. 359-375. https://doi.org/10.1007/978-981-16-2877-1_33.
- [20] Mazumder, M.K.A., Mridha, M.F., Alfahood, S., Safran, M., Abdullah-Al-Jubair, M., Che, D., 2024. A robust and light-weight transfer learning-based architecture for accurate detection of leaf diseases across multiple plants using less amount of images. *Frontiers in Plant Science* 14, 1321877. <https://doi.org/10.3389/fpls.2023.1321877>.

- [21] Mohanty, S.P., Hughes, D.P., Salathé, M., 2016. Using deep learning for image-based plant disease detection. *Frontiers in Plant Science* 7, 1419. <https://doi.org/10.3389/fpls.2016.01419>.
- [22] Mourou, M., Raimondo, M.L., Lops, F., Carlucci, A., 2023. Brassicaceae Fungi and Chromista Diseases: Molecular Detection and Host-Plant Interaction. *Plants* 12(5), 1033. <https://doi.org/10.3390/plants12051033>.
- [23] Muntaqim, M.Z., Smrity, T.A., Kafi, H.M., Miah, A.S.M., Al Farid, F., Karim, H.A., Rahman, A., 2025. Federated learning meets few-shot learning: A voting ensemble based combined approach to cauliflower leaf disease classification across Non-IID data distributions. *Array* 28, 100516. <https://doi.org/10.1016/j.array.2025.100516>.
- [24] Nirwan, S., Sharma, A.K., Tripathi, R.M., Pati, A.M., Shrivastava, N., 2023. Resistance strategies for defense against *Albugo candida* causing white rust disease. *Microbiological Research* 270, 127317. <https://doi.org/10.1016/j.micres.2023.127317>.
- [25] Orin, T.Y., Mojumdar, M.U., Siddiquee, S.M.T., Chakraborty, N.R., 2021. Cauliflower leaf disease detection using computerized techniques. In: 2021 IEEE 6th International Conference on Computing, Communication and Automation (ICCCA), pp. 730-733. <https://doi.org/10.1109/ICCCA52192.2021.9666437>.
- [26] Paul, M.C., Ahmed, M.W., Prodhan, M.D.H., Dutta, N.K., Ahmed, M.T., Abdullah, M.M., Islam, M.A., Khan, M.S.I., 2025. Pesticides in widely consumed vegetables in Bangladesh and its health risk. *Food Additives & Contaminants: Part B* 18(1), 1-11. <https://doi.org/10.1080/19393210.2024.2404924>.
- [27] Pouresmaeil, M., Dall'Ara, M., Salvato, M., Turri, V., Ratti, C., 2023. Cauliflower mosaic virus: Virus-host interactions and its uses in biotechnology and medicine. *Virology* 580, 112-119. <https://doi.org/10.1016/j.virol.2023.02.008>.
- [28] Pradhan, N.R., Ghosh, H., Rahat, I.S., Janjhyam Venkata Naga Ramesh, Yesubabu, M., 2024. Enhancing agricultural sustainability with deep learning: A case study of cauliflower disease classification. *EAI Endorsed Transactions on Internet of Things* 10(1). <https://doi.org/10.4108/eetiot.4834>.
- [29] Preethi, B., Vinutha, H.P., Patil, N.S., 2024a. A survey on deep learning-based disease identification and classification on cauliflower vegetable. *YMER* 23(4), 702-716.
- [30] Preethi, B., Vinutha, H.P., Patil, N.S., 2024b. Unified Multi-Scale Feature Network (UMFN) for accurate detection and classification of cauliflower diseases. *Computer Fraud and Security* 2024(12). <https://doi.org/10.52710/cfs.682>.
- [31] Preethi, B., Vinutha, H.P., 2026. A deep learning-based predictive model for cruciferous vegetable classification with a literature-based interpretation of human health relevance. *Journal of Experimental Biology and Agricultural Sciences* 14(2), 39-46. <https://jebas.org/ojs/index.php/jebas/article/view/3761> (accessed 11 August 2026).
- [32] Rahaman, J., Paul, P., Chowdhury, A., Quamruzzaman, M., 2026. A customized MobileNetV3Large-based deep learning framework for plant disease detection. *Discover Artificial Intelligence* 6, 110. <https://doi.org/10.1007/s44163-025-00733-8>.
- [33] Rajbongshi, A., Islam, M.E., Mia, M.J., Sakif, T.I., Majumder, A., 2022. A comprehensive investigation to cauliflower diseases recognition: An automated machine learning approach. *International Journal on Advanced Science, Engineering and Information Technology* 12(1), 32-41. <https://doi.org/10.18517/ijaseit.12.1.15189>.
- [34] Sara, U., Rajbongshi, A., Shakil, R., Akter, B., Uddin, M.S., 2022. VegNet: An organized dataset of cauliflower disease for a sustainable agro-based automation system. *Data in Brief* 43, 108422. <https://doi.org/10.1016/j.dib.2022.108422>.
- [35] Shaw, R.K., Shen, Y., Zhao, Z., Sheng, X., Wang, J., Yu, H., Gu, H., 2021. Molecular breeding strategy and challenges towards improvement of downy mildew resistance in cauliflower (*Brassica oleracea* var. *botrytis* L.). *Frontiers in Plant Science* 12, 667757. <https://doi.org/10.3389/fpls.2021.667757>.
- [36] Srinivasan, S., Ranjith Kumar, A., Nagashree, B.A., Tanwar, J., Singh, V.P., Moorthy, U., 2026. Multi-class classification of plant leaf diseases using a hybrid deep neural transformer system and explainable AI techniques. *Scientific Reports* 16, 18161. <https://doi.org/10.1038/s41598-026-48103-3>.
- [37] Too, E.C., Yujian, L., Njuki, S., Yingchun, L., 2019. A comparative study of fine-tuning deep learning models for plant disease identification. *Computers and Electronics in Agriculture* 161, 272-279. <https://doi.org/10.1016/j.compag.2018.03.032>.
- [38] Uddin, M.S., Mazumder, M.K.A., Prity, A.J., Mridha, M.F., Alfarhood, S., Safran, M., Che, D., 2024. Cauli-Det: enhancing cauliflower disease detection with modified YOLOv8. *Frontiers in Plant Science* 15, 1373590. <https://doi.org/10.3389/fpls.2024.1373590>.
- [39] Verma, A., Singh, Y., 2018. Inheritance of downy mildew resistance and its relationship with biochemical traits in cauliflower (*Brassica oleracea* L. var. *botrytis*). *Crop Protection* 106, 132-138. <https://doi.org/10.1016/j.cropro.2017.12.024>.

- [40] Xue, J., Li, T., Wu, P., Xie, Z., Liu, Z., Wei, M., Yuan, X., Wang, X., Zhang, Z., 2026. Integration of boundary enhancement and wavelet-guided attention in a hierarchical multimodal network for *Brassica oleracea* var. *botrytis* disease detection. Journal of King Saud University - Computer and Information Sciences 38, 308. <https://doi.org/10.1007/s44443-026-00667-w>.