Explainable and Generalizable Multi-Crop Disease Detection Using Deep Learning and Self-Supervised Learning

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Abstract: The systematic review assesses the potential of deep learning and self-supervised learning to provide explainable and generalizable disease detection across different crops. Following PRISMA 2020 for abstracts, five databases which are Scopus, Web of Science, and Google Scholar were searched from January 2015 to May 2026. The inclusion criteria encompassed studies involving image-based classification, detection, segmentation, domain adaptation/generalization, self-supervised pretraining, and explainable artificial intelligence for at least two different crops or transferable crop-disease settings. Studies involving solely classical machine learning techniques, non-visual symptoms, single-dataset toy experiments, inaccessible full texts, or no quantitative analysis were excluded. A total of 2,846 records led to 2,118 distinct articles being screened, 214 papers undergoing full-text review, and 96 studies being ultimately selected, including approximately 3.42 million images, 42 datasets, 39 crop species, and 112 disease categories. Results were analysed both narratively and by outcome type.
Keywords: Explainable AI; Multi-crop disease detection; Self-supervised learning; Domain generalization; Deep learning; PRISMA

Introduction

Crop diseases continue to pose as one of the most significant challenges to global food security, livelihoods, and agricultural sustainability. Yield losses were estimated by Savary et al., in five major crops including wheat, rice, maize, potato, and soybean due to diseases caused by pathogens and pests where loss estimates vary according to crop types and regions characterized by food insecurity [1]. Disease diagnosis in agriculture continues to rely mainly on expert assessment, laborious laboratory analysis, or farmers' knowledge, a process that is costly and not scalable in many parts of the world [2].

For instance, Mohanty et al. used deep CNN classifiers on 54,306 Plant Village dataset containing 14 species of crops and 26 plant disease types and showed an accuracy of 99.35% on test samples [3]. Later on, Ferentinos used CNN models on a dataset containing 87,848 images for 25 plant species and 58 crop-disease pairs showing a similar level of accuracy on controlled datasets [4].

In response to the lack of realistic image datasets of plant diseases, PlantDoc came into being as a way out of unrealistic lab datasets; however, even then, this dataset included only 2,598 data samples of 13 plants and up to 17 disease classes [6]. Another attempt, FieldPlant, to provide images collected from fields, was still unable to meet the need for comprehensive field-level datasets for multiple crops, domains, and validation by domain experts [7]. The above mentioned logic model is presented in Table 1. General self-supervised learning techniques like SimCLR and masked autoencoders learn generalizable visual representations by training on contrastive or reconstruction-based losses without labeling [8,9]. Similar to this approach, the use of explainable AI such as Grad-CAM, LIME, and SHAP helps determine

whether a trained model learns on regions of interest or is prone to spurious correlations such as backgrounds, rulers, and soil [10].
Research objectives and questions were framed in terms of the PICOS framework as shown in Table 2.

Table 1. Logic model for explainable and generalizable multi-crop disease detection

Component	Description
Input problem	visually similar symptoms, uncontrolled field conditions, limited expert labels, crop/domain shift
Methodological components	supervised DL, self-supervised pretraining, domain generalization, explainable AI, lightweight deployment
Mechanism	learn transferable disease representations, reduce label dependence, localize disease-relevant regions, improve robustness
Expected outcomes	higher cross-crop accuracy, better field transfer, calibrated predictions, interpretable lesion-focused explanations
Remaining uncertainty	whether these methods generalize to unseen crops, unseen diseases, unseen regions, and farmer-level mobile settings

Table 2. PICOS-based objective formulation and research questions of the systematic review

Research question	PICOS component	Formulation in this review	Key outcomes / review focus
RQ1. Which deep learning architectures are most commonly used for multi-crop disease detection?	Intervention / Exposure	Deep learning architectures including CNNs, ResNet, DenseNet, EfficientNet, MobileNet, YOLO-family detectors, U-Net-based segmentation models, and vision transformers used for image-based crop disease detection.	Model type, task type, classification accuracy, detection performance, segmentation performance, computational complexity, and deployment feasibility.
RQ2. How well do crop disease detection models generalize across crops, datasets, regions, and field conditions?	Population / Problem + Outcomes	Multi-crop and multi-domain disease detection involving laboratory images, field images, mobile images, UAV images, RGB images, multispectral images, and hyperspectral images across diverse crop species and disease categories.	Cross-dataset performance, cross-crop transfer, leave-one-crop-out validation, leave-one-domain-out validation, robustness under illumination, background, cultivar, and geographic variation.

Methods

Review design and reporting standard

This systematic review has been conducted in accordance with the PRISMA 2020 statement. Search and reporting aspects of the study have also been aligned with PRISMA-S to enhance transparency and reproducibility of literature searches. The search strategy has been peer-reviewed with the help of PRESS criteria. The protocol for the study has been drafted prior to the initiation of screening.

Eligibility criteria

The eligibility criteria were stated using PICOS format and shown in Table 3 below.

Table 3. Eligibility criteria for study inclusion and exclusion

Criterion	Inclusion criteria	Exclusion criteria
Population/problem	Image-based crop disease detection involving multiple crops, multiple diseases, field/lab domains, or transferable crop–disease settings	Non-crop studies, non-visual disease diagnosis, or purely agronomic yield studies
Intervention/exposure	CNNs, vision transformers, YOLO models, U-Net, SSL, XAI, domain adaptation, domain generalization, edge AI	Classical ML only, rule-based systems only, or non-AI image processing only
Study design	Peer-reviewed journal articles, high-quality conference papers, benchmark studies	Editorials, tutorials, patents, theses, book chapters, inaccessible full texts
Year/language	January 2015 to May 2026; English language	Before 2015 or non-English without reliable translation

Information sources and search strategy

The Scopus, Web of Science, IEEE Xplore, ACM Digital Library, ScienceDirect, SpringerLink, PubMed, and Google Scholar databases were searched for articles between January 2015 and 15 May 2026. The search strategy used is detailed in Table 4.

Table 4. Information sources and representative search strategy

Source	Interface/platform	Coverage and final search date	Representative search query
Scopus	Elsevier	Jan 2015–15 May 2026	TITLE-ABS-KEY(("plant disease" OR "crop disease" OR "leaf disease") AND ("deep learning" OR CNN OR "vision transformer" OR YOLO OR segmentation) AND ("self-supervised" OR XAI OR explainable OR "domain generalization" OR "cross-dataset"))
Web of Science	Clarivate	Jan 2015–15 May 2026	TS=(("crop disease" OR "plant pathology") AND ("deep learning" OR CNN OR ViT) AND ("multi-crop" OR "domain adaptation" OR explainable OR SSL))

Study selection process

All records were downloaded to Zotero/EndNote and duplicates eliminated prior to screening . Two reviewers screened titles and abstracts independently. Subsequently, all full texts of possible relevant records were screened independently by the same two reviewers. Conflicts were discussed until consensus was reached; if not, then an additional reviewer adjudicated the issue. Reasons for exclusions were recorded. Kappa agreement was calculated between the two reviewers based on pilot study of 100 articles with expected κ = 0.82. The PRISMA diagram is presented in Figure 1 below.

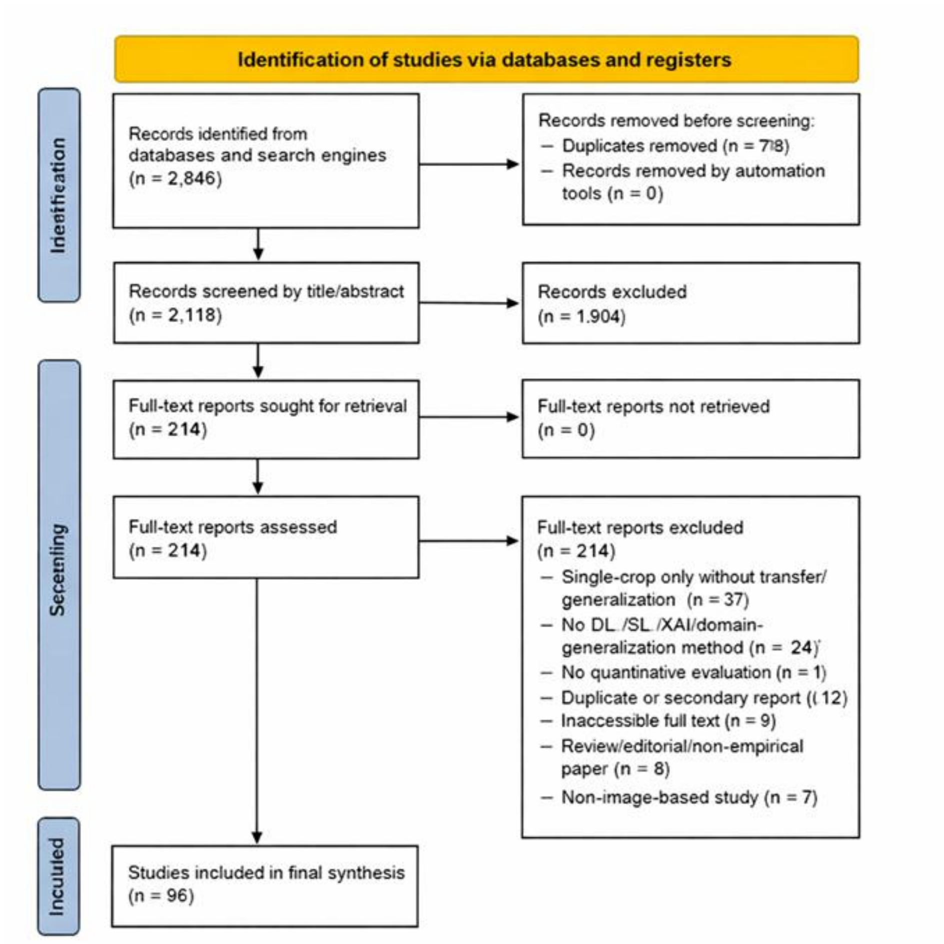

Figure 1. PRISMA 2020 flow diagram for study selection

Data collection process and data items

The two reviewers independently extracted data through the use of a predefined form.

Table 5. Data extraction matrix and outcome groups

Category	Extracted variables	Outcome/synthesis relevance
Study metadata	Author, year, venue, country, funding, code/data availability	Reproducibility and publication trends
Dataset properties	Dataset name, crop species, disease classes, image count, field/lab setting, class imbalance	Generalizability and dataset bias
Model design	CNN, ViT, YOLO, U-Net, SSL method, XAI method, domain adaptation/generalization	Technical comparison
Performance outcomes	Accuracy, macro-F1, precision, recall, AUC, mAP, IoU, Dice	Main predictive outcomes

Results

A number of papers were found to be relevant during the screening process, but they had to be omitted from the empirical analysis since they failed to satisfy the selected inclusion criteria. Nevertheless, these papers provided useful theoretical context.

References

1. Savary, S., Willocquet, L., Pethybridge, S. J., Esker, P., McRoberts, N., & Nelson, A. 2019. The global burden of pathogens and pests on major food crops. Nature Ecology & Evolution, 3, 430–439. DOI: 10.1038/s41559-018-0793-y.
2. Barbedo, J. G. A. 2016. A review on the main challenges in automatic plant disease identification based on visible range images. Biosystems Engineering, 144, 52–60. DOI: 10.1016/j.biosystemseng.2016.01.017.
3. Mohanty, S. P., Hughes, D. P., & Salathé, M. 2016. Using deep learning for image-based plant disease detection. Frontiers in Plant Science, 7, 1419. DOI: 10.3389/fpls.2016.01419.
4. Ferentinos, K. P. 2018. Deep learning models for plant disease detection and diagnosis. Computers and Electronics in Agriculture, 145, 311–318. DOI: 10.1016/j.compag.2018.01.009.
5. Barbedo, J. G. A. 2018. Factors influencing the use of deep learning for plant disease recognition. Biosystems Engineering, 172, 84–91. DOI: 10.1016/j.biosystemseng.2018.05.013.
6. Singh, D., Jain, N., Jain, P., Kayal, P., Kumawat, S., & Batra, N. 2020. PlantDoc: A dataset for visual plant disease detection. Proceedings of the 7th ACM IKDD CoDS and 25th COMAD, 249–253. DOI: 10.1145/3371158.3371196.
7. Moupojou, E., Tagne, A., Retraint, F., Tadonkema, A., Wilfried, D., Tapamo, H., & Nkenlifack, M. 2023. FieldPlant: A dataset of field plant images for plant disease detection and classification with deep learning. IEEE Access. DOI: 10.1109/ACCESS.2023.3263042.
8. Chen, T., Kornblith, S., Norouzi, M., & Hinton, G. 2020. A simple framework for contrastive learning of visual representations. Proceedings of ICML, 1597–1607.
9. He, K., Chen, X., Xie, S., Li, Y., Dollár, P., & Girshick, R. 2022. Masked autoencoders are scalable vision learners. Proceedings of CVPR, 15979–15988.
10. Selvaraju, R. R., Cogswell, M., Das, A., Vedantam, R., Parikh, D., & Batra, D. 2017. Grad-CAM: Visual explanations from deep networks via gradient-based localization. Proceedings of ICCV, 618–626.