Overview of Low-Cost Plant Phenotyping Methods for Individual Plants

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***Abstract*—Low-cost plant phenotyping for individual plants is increasingly important for plant digital twins, breeding, and continuous crop monitoring. This review surveys representative studies on image-based plant phenotyping from 2015 to 2025 and organizes them into two major categories: deep-learning-based trait estimation from red green blue (RGB)/red green blue depth (RGB-D) images and low-cost three-dimensional (3D) phenotyping based on multi-view reconstruction. These literatures indicate that deep learning methods are advantageous for rapid, automated, and high-throughput estimation of specific traits, but they often depend on annotated data and may show limited cross-scenario generalization. In contrast, 3D reconstruction methods usually provide richer structural information and broader trait coverage, but they require more complex acquisition workflows and higher computational burden. Therefore, low-cost plant phenotyping should be understood not only in terms of sensor price, but also in terms of the overall trade-off among sensing, computation, labor, and deployability. Finally, this review summarizes current challenges and identifies future directions, including cost-aware benchmarking, lightweight image-based models, robust field 3D reconstruction, and tighter integration with plant digital twin systems.**

I. INTRODUCTION

Global food demand continues to increase under the combined pressures of population growth, climate change, and resource constraints, making food security one of the most pressing challenges facing modern agriculture [1]. Addressing this challenge requires not only increasing crop productivity but also improving the resilience and stability of agricultural systems. In this context, accelerating plant breeding programs has become a crucial strategy for developing high-yielding, stress-tolerant, and resource-efficient crop varieties [2, 3].

Plant development is shaped by the complex interaction between genotype and environment ($G \times E$). A comprehensive understanding of plant growth and morphology is therefore essential for both cultivation management and precise breeding decisions. However, phenotypic data acquisition remains a major bottleneck in modern breeding pipelines. Traditional phenotyping methods rely heavily on manual measurement, which is time-consuming, labor-intensive, and costly, rendering them impractical for large-scale breeding programs or continuous growth monitoring [4, 5].

Compared with destructive sampling and specialized phenotyping platforms, image-based approaches offer significant advantages in terms of portability, non-destructiveness, and operational simplicity. This non-invasive method enables the efficient capture of high-quality data while preserving natural plant growth conditions, facilitating repeated and continuous observation. These capabilities are particularly significant for the emerging field of plant digital twins. Digital twins, virtual representations of physical plants, require continuous, non-destructive data streams to simulate, monitor, and predict plant growth in real-time. Vision-based phenotyping, powered by computer vision and deep learning, provides the critical technical foundation for feeding these digital twin systems with accurate morphological data [5–7].

Nevertheless, for digital twins to be widely adopted in real-world breeding and agricultural scenarios, the "low-cost" aspect must be emphasized beyond just sensor price, as efficient data collection can often be achieved using common cameras and compact sensors [8]. It must encompass computational efficiency, deployment simplicity, annotation burden, and robustness under diverse field conditions.

Against this background, this review aims to examine low-cost image-based phenotyping approaches for individual plants, with a focus on key morphological traits such as leaf number, leaf area, and plant height. We categorize the current methodologies into direct deep learning analysis and three-dimensional (3D) reconstruction techniques, summarizing their progress, advantages, and limitations. By clarifying which methods are truly scalable and economical, we aim to provide insights into the future of intelligent agricultural management and the practical realization of plant digital twins.

II. IMAGE-BASED PLANT PHENOTYPIC DATA ACQUISITION

The reviewed studies can be classified according to the stage at which phenotypic traits are recovered. The first route estimates traits directly from two-dimensional (2D) visual observations, and has evolved from single-task regression or segmentation to multi-task, multimodal, and foundation-model-based phenotyping. The second route reconstructs plant structure before trait extraction, and has evolved from the classical approach, which combines structure from motion

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(SfM) and multi-view stereo (MVS), to time-series 3D analysis, point-cloud learning, and multi-sensor comparisons. This classification helps distinguish methods that prioritize inference efficiency from those that prioritize structural completeness and broader trait coverage.

To investigate the current research status of plant phenotypic data acquisition based on visual data, a literature search was conducted using keywords such as "low-cost", "3D reconstruction", "deep learning", and "plant phenotypes" across Google Scholar, Elsevier, Web of Science, and Semantic Scholar. Relevant publications from 2015 to 2025 were screened and collected for analysis, as illustrated in Fig. 1.

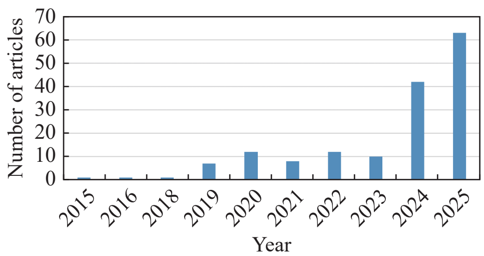

Fig. 1 Number of relevant publications on low-cost image-based plant phenotypic data acquisition from 2015 to 2025 across Google Scholar, Elsevier, Web of Science, and Semantic Scholar.

A. *Methods Based on Deep Learning*

Traditional image analysis generally relies on manually designed preprocessing operations and handcrafted feature extraction steps to derive useful information from images. In plant phenotyping, early preprocessing commonly includes intensity adjustment, noise reduction, and the segmentation of plants of interest from the background [9–10]. Such procedures are important for improving image quality and enabling subsequent phenotypic analysis. However, conventional rule-based methods are often constrained by fixed thresholds and handcrafted features, which limits their ability to adapt to changes in illumination, background complexity, plant morphology, and imaging conditions [10]. As a result, deep learning has become increasingly important in plant image analysis, since it can automatically learn discriminative features from data and provide more robust performance under complex and variable conditions.

Deep learning has achieved significant breakthroughs in image classification, notably with the successful demonstration of deeper convolutional neural networks (CNNs) during the ImageNet large scale visual recognition challenge (ILSVRC) in 2012 [11]. CNNs, a subclass of deep learning networks that use shared weights in a convolutional kernel, have proven to be more effective than fully connected multilayer perceptrons at encoding hierarchical patterns in data, particularly in images and videos. This effectiveness has led to substantial performance improvements in image classification tasks [12–13]. In the field of agriculture, CNNs are widely employed for various image analysis tasks, including disease detection, weed identification, and counting. Through deep learning approaches, especially the use of CNNs, agricultural researchers can process and analyze farmland image data more accurately and efficiently [5, 14]. This not only aids in the early detection of crop diseases and mitigating the effects of weeds on crops but also provides a fast and reliable method for crop monitoring.

Through segmentation and tracking analysis, computers can automatically and accurately calculate organ area, measure length and width, and dynamically monitor growth and movement [5, 15]. Table 1 shows that neural-network-based plant trait estimation has evolved from 2D traits such as leaf counting and area estimation to multi-trait estimation, field trajectory analysis, and automated 3D phenotyping. In particular, recent studies published from 2023 to 2025 demonstrate clear progress in multi-modal learning, foundation-model adaptation, and high-throughput 3D phenotype analysis.

B. *Methods Based on 3D Reconstruction*

As a complex organism, a plant involves the synergistic functioning of multiple organs, necessitating an analysis of the whole plant [27]. Generally, analyzing the phenotype of the entire plant solely based on a single picture or angle proves challenging for obtaining comprehensive phenotypic data throughout the entire growth and development process. To achieve a more thorough understanding of plant growth, most research approaches aim to capture as complete a 3D geometry of the plant as possible, involving geometric modeling of the entire aerial part of the plant [28–29]. The subsequent discussion focuses on research into 3D phenotyping techniques for plants.

3D measurements of plants have undergone tremendous development in recent decades. In comparison to traditional 2D images, 3D measurements offer more accurate estimates of coordinates and distances, along with the capability to determine the precise orientation of the object. This makes it easier to extract information about the three-dimensional phenotypic structure of plants [30].

There are various techniques for obtaining the 3D information of plants, one of which involves directly capturing the 3D point cloud of plants through sensors, including depth imaging methods and light detection and ranging (LiDAR) systems [31–32]. These methods can acquire high-precision point cloud structures of plants, but they often require complex and expensive instrumentation and may be limited by environmental conditions. Another method is to reconstruct the three-dimensional structure of plants using multi-view stereo vision techniques, which typically require relatively simple equipment, lower cost, and fewer environmental constraints. This approach is suitable for obtaining phenotypic data of individual plants and providing corresponding phenotypic parameters for crop models. Multi-view stereo vision reconstructs plant structures from images captured at multiple viewpoints through 3D reconstruction algorithms, offering a relatively efficient and flexible way to obtain plant phenotypes.

For extracting 3D information from multi-view plant images, the most widely used approach is the combination of SfM [33] and MVS [34] for 3D reconstruction. SfM can be

Table 1 Neural network trait estimation study.

Data source	Plant trait	Methodology	Result	Plant species	Reference
CVPPP leaf counting datasets	Leaf number	Hierarchical correlation propagation and bootstrap backpropagation	Compared with ground-truth leaf counts, the method achieved |DiC| = 0.74 and MSE = 1.2.	*Arabidopsis*	[16]
Greenhouse crop images and hanging-scale measurements	Fresh weight and leaf area	CNN-based regression	Compared with manual hanging-scale and leaf-area measurements, the estimated leaf area showed $R^2 = 0.95$.	Bell pepper	[17]
Leaf images acquired with clamp-assisted stretching	Leaf area	U-Net-Attention segmentation and image processing	Compared with manual leaf-area measurements, the average segmentation accuracy reached 96.77%, and the average error rate of leaf-area estimation was 0.65%.	Rapeseed	[18]
Plant phenotyping benchmark datasets	Leaf counting, segmentation, and disease classification	Foundation model adaptation with low-rank adaptation (LoRA) and decoder tuning	Compared with task-specific state-of-the-art models on benchmark datasets, the adapted foundation models achieved competitive performance across multiple phenotyping tasks.	*Arabidopsis*, tobacco, and benchmark plants	[19]
Red green blue (RGB)/red green blue depth (RGB-D) images of greenhouse or hydroponic lettuce across different growth stages and the complete growth cycle	Fresh weight, dry weight, plant height, diameter, leaf area, and geometric/color/texture phenotypic indices	Two-stage CNN using RGB-D images, multi-modal fusion deep learning with U-Net segmentation and multi-branch regression, deep learning-based computational model, and lightweight DeepLabv3+ with MobileNetV2 and regression model	For biomass and morphological traits, the reported performance reached $R^2 = 0.89–0.968$, with NRMSE values of 5.62%–7.92%; segmentation achieved mIoU = 0.982 and accuracy = 0.998; and for geometric, color, and texture phenotypic indices, the average error was less than 0.55% for geometric traits and less than 1.70% for color and texture traits.	Lettuce	[20–23]
Darkroom RGB images of soybean plants	Plant height, node number, internode length, main stem length, stem curvature, and branching angle	Multi-target object detection and directed search	Compared with manual phenotype measurements, the Pearson correlation coefficients for the extracted stem-related traits ranged from 0.9084 to 0.9925, and the maximum mAP for stem nodes and scale markers reached 94.36%.	Soybean	[24]
RGB images under field conditions	Number of leaves, number of stalks, and growth trajectory	Point-Line Net with Mask R-CNN and lightweight keypoint detection	Compared with manually annotated field images, the object detection accuracy reached mAP50 = 81.50%.	Maize	[25]
Top-view RGB-depth images with morphometric descriptors	Leaf fresh weight, leaf dry weight, leaf area, and plant height	Morphometric descriptor extraction with random forest and least absolute shrinkage and selection operator (LASSO) regression	Compared with measured biomass and morphological traits, random forest and LASSO achieved high estimation accuracy; for different harvest rounds, R^2 values were generally above 0.65 and MAPE was below 8.00%.	Hydroponic romaine lettuce	[26]

Note: |DiC| is the absolute value of the difference between the predicted count and the ground-truth count, measuring the model's counting error per sample. MSE is the average of the squared differences between predicted and actual values, measuring the mean squared deviation of the estimator from the true value. R^2 is the proportion of the variance in the dependent variable that is predictable from the independent variables, ranging from 0 to 1, with higher values indicating better model fit. NRMSE is the root mean square error normalized by the range (max-min) or the mean of the observed values, allowing comparison of model accuracy across datasets with different scales. mIoU is the average of the intersection over union ratios computed across all semantic classes, used to evaluate the segmentation accuracy of a model. mAP is the mean of the average precision scores across all object classes, commonly used to evaluate the overall accuracy of object detection models. mAP50 is the mean average precision calculated when the intersection over union threshold between predicted and ground-truth bounding boxes is set to 0.5. MAPE stands for the mean absolute percentage error.

implemented using images acquired by a single camera, which makes it more convenient and cost-effective for recovering plant 3D structures than stereo vision systems requiring multiple synchronized cameras. Furthermore, a wide range of software tools is currently available for 3D reconstruction, point cloud processing, and structural trait analysis [35]. Detailed information on representative studies of 3D trait estimation is presented in Table 2. As shown in this table, current 3D phenotyping studies mainly adopt three types of technical routes: RGB image-based multi-view reconstruction, point-cloud-based trait extraction, and dedicated sensing or phenotyping platforms. Multi-view RGB methods, including SfM-based and MVS-based pipelines, are widely used because they can be implemented with relatively low-cost devices such as digital cameras and smartphones, and they have demonstrated strong performance in estimating traits such as plant height, leaf length, leaf width, and leaf area. Their main limitation is that they often depend on controlled acquisition conditions,

Table 2 3D trait estimation study.

Data source	Plant trait	Methodology	Result	Plant species	Reference
Multi-view images with scale reference	Plant height	MicMac digital phenotyping software and SfM methodology	Compared with manual plant height measurements, accuracy reached 98.7%, with $R^2 = 0.99$, RMSE = 1.1 cm, and MAE = 0.85 cm.	Brussels sprouts, savoy cabbages, cauliflowers, sunflowers, and sugar beets	[36]
Multi-view digital camera images	Leaf area, leaf length, and leaf width	Bundler and MVS for dense point cloud generation	Compared with manual measurements, leaf area showed RE < 5% and $R^2 = 0.99$, while leaf length and width both showed $R^2 > 0.95$.	Cucumber, eggplant, green pepper, and hot pepper	[37]
Greenhouse images under natural light	Leaf number, plant height, and leaf length	VisualSFM and CloudCompare octree method	Compared with reference measurements, the extracted traits achieved RMSE = 8.6 mm and $R^2 = 0.98$.	Wheat seedling	[38]
Multi-view beet images	Plant height, leaf length, total leaf area, and bulb volume; Root length and maximum diameter	3DF Zephyr Aerial and CloudCompare; 3DF Zephyr Aerial and point-cloud-based trait extraction	Compared with manual measurements, plant height and leaf length achieved $R^2 = 0.88$ and 0.83, with RMSE = 5.2 cm and 1.77 cm, respectively; root length and maximum diameter achieved $R^2 = 0.995$ and 0.971, with RMSE = 0.178 and 0.244, respectively.	Beet	[39–40]
Multi-view smartphone images	Leaf area, leaf length, leaf width, and leaf inclination	VisualSFM and region-growing leaf segmentation	Compared with manual measurements, leaf area accuracy reached 96.8%; the average errors of leaf length and width were below 4%, and the leaf inclination error was 2.9°.	*Maranta arundinacea* and *Dieffenbachia picta*	[41]
MVS-Pheno platform images	Plant height, leaf width, and leaf area	Commercial MVS-based reconstruction and organ/plant-level trait extraction	Compared with manual measurements, plant height, leaf width, and leaf area achieved $R^2 = 0.99$, 0.87, and 0.93, respectively.	Maize seedlings	[42]
Rotating-table multi-view images	Plant height, leaf length, relative leaf area, and leaf width	VisualSFM	Compared with manual measurements, plant height, leaf length, relative leaf area, and leaf width achieved $R^2 = 0.991$, 0.989, 0.926, and 0.963, respectively.	Maize	[43]
MVS-Pheno v2 maize-ear images	Branch length, branch angle, and number of branches	MVS-SfM, PointNet++, and shortest-path-based skeleton extraction	Compared with manual measurements, branch length, branch angle, and branch number achieved $R^2 = 0.9897$, 0.9317, and 0.9587, respectively.	Maize ear	[44]
Kinect and smartphone multi-view images	Plant height, petiole angle, leaf length, and leaf width	Conditional and K-nearest-neighbor filtering, random sample consensus (RANSAC), iterative closest point (ICP), and 3D reconstruction; MVS-SfM and locality preserving matching (LPM) algorithm	Compared with manual measurements, the Kinect-based method achieved $R^2 = 0.984$ for plant height and 0.919 for petiole angle, while the smartphone-based method achieved $R^2 = 0.9775$, 0.9785, and 0.9487 for plant height, leaf length, and leaf width, respectively.	Soybean	[45–46]
Point cloud data acquired by the Wiwarm plant analyzer	Internode length	PointNet++ and Euclidean-distance-based point cloud segmentation	Compared with corresponding 2D methods, the 3D point-cloud-based method provided more accurate internode length estimation.	Cucumber	[47]
Top-view RGB sequences and multi-view 3D point clouds	Spatio-temporal 3D modeling, segmentation, and biomass trait quantification	MVS-based time-series point cloud registration; multi-view 3D reconstruction and machine learning	Time-series point cloud registration enabled daily segmentation and growth monitoring, while reconstructed point clouds supported trait extraction and biomass estimation.	Lettuce	[48–49]
LiDAR, MVS, and depth-image 3D point clouds	3D canopy traits, point cloud quality, and sensor performance comparison	Comparative evaluation of LiDAR, MVS reconstruction, and depth image synthesis	The comparison showed that LiDAR, MVS, and depth-image-derived point clouds had different strengths across maize growth stages in terms of accuracy, density, and platform suitability.	Maize canopy	[50]

sufficient viewpoints, and computationally intensive reconstruction procedures. By contrast, active sensing systems and dedicated platforms can provide more stable geometric information and are advantageous for complex structural phenotyping, but their hardware cost and deployment requirements are usually higher. In addition, recent work has increasingly integrated 3D reconstruction with point-cloud learning and skeleton-based analysis to improve the extraction of organ-level and architectural traits. Overall, these studies indicate that the advantages and limitations of 3D trait estimation methods should be evaluated not only in terms of accuracy, but also in terms of sensing cost, reconstruction complexity, automation level, and adaptability to realistic phenotyping environments.

III. Discussion

The reviewed literature shows that low-cost plant phenotyping for individual plants has developed along two complementary technical routes. Deep-learning-based methods estimate traits directly from 2D images and are especially suitable for rapid, automated, and high-throughput analysis of specific targets such as leaf number, leaf area, biomass, and plant height. Their main advantage lies in operational efficiency: once trained, these models can be deployed with relatively simple image acquisition devices and can support scalable trait estimation. However, their performance is strongly influenced by annotation quality, training data diversity, and domain shifts caused by changes in lighting, background complexity, plant morphology, and growth conditions. As a result, many methods perform well under controlled conditions but remain less robust in open-field or cross-species scenarios.

In contrast, 3D reconstruction-based methods recover plant geometry before phenotypic measurement and therefore provide richer structural information, broader trait coverage, and stronger interpretability. They are particularly advantageous when the target application requires organ-level morphology, spatial architecture, or subsequent integration with crop models and plant digital twins. Nevertheless, these methods are not automatically low-cost in a broader sense. Although many of them use affordable acquisition devices such as smartphones or RGB cameras, they often require multi-view image capture, careful viewpoint control, longer processing time, and more demanding reconstruction pipelines. Their final utility is also highly dependent on reconstruction quality under occlusion, leaf overlap, motion, and illumination variation. Therefore, compared with 2D deep learning methods, 3D reconstruction methods often trade simpler labeling requirements for higher acquisition and computational complexity.

A key insight of this review is that "low-cost" should be understood as a system-level property rather than merely a hardware attribute. A truly low-cost phenotyping method should be evaluated jointly in terms of hardware affordability, computational burden, deployment complexity, and annotation effort. Under this broader view, some RGB-based deep learning methods are low-cost in sensing and deployment but costly in annotation and retraining, while some multi-view 3D methods are low-cost in sensing hardware but expensive in processing time and workflow control. This explains why existing studies often report "low-cost" advantages without being directly comparable. The lack of unified cost-aware benchmarks remains a major gap in the literature.

Several additional research gaps can be identified. First, many studies focus on a limited set of plant species or controlled experimental environments, which restricts the generalizability of the conclusions. Second, current evaluation is still dominated by phenotypic accuracy, whereas cost-related indicators such as processing time, device accessibility, portability, and manual intervention are rarely reported in a standardized way. Third, although multimodal learning, foundation-model adaptation, and automated 3D analysis have shown promising results, their actual cost-effectiveness for routine phenotyping remains insufficiently discussed. Finally, the connection between low-cost phenotyping and downstream digital twin applications is still weak in most studies, even though structural and temporal phenotypic data are precisely what digital twins require for dynamic growth simulation and decision support.

Overall, the future of low-cost plant phenotyping is likely to depend on the integration of lightweight sensing, robust cross-scenario learning, efficient 3D reconstruction, and digital-twin-oriented trait analysis. Methods that can balance trait richness, computational efficiency, operational simplicity, and robustness under realistic environments will be more valuable than methods optimized for accuracy alone.

IV. Conclusion

This review examined low-cost plant phenotyping methods for individual plants from two major perspectives: direct trait estimation from 2D images and trait extraction from reconstructed 3D structures. The comparison shows that deep learning methods are more advantageous for fast, automated, and scalable estimation of selected traits, whereas 3D reconstruction methods are more suitable for obtaining richer structural phenotypes and supporting crop modeling or digital twin applications. Importantly, the review highlights that low-cost plant phenotyping should not be judged solely by sensor price, but by the overall trade-off among hardware affordability, computational demand, deployment complexity, and annotation effort.

Current research still faces several open challenges, including limited cross-species generalization, insufficient robustness under field conditions, the absence of standardized cost-aware benchmarks, and the weak connection between phenotyping pipelines and downstream digital twin systems. Future work should therefore focus on four directions: developing unified evaluation frameworks for low-cost phenotyping; reducing annotation dependence through weakly supervised, transfer-learning, or foundation-model-based methods; improving robust and efficient 3D reconstruction under occlusion and environmental variability; and integrating phenotypic acquisition more tightly with plant digital twin modeling, growth simulation, and decision-making applications.

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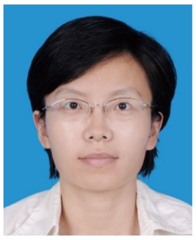

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