

Three-dimensional phenotyping: Technological advances and applications in genomics-assisted crop breeding

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ABSTRACT

With rapid advancements in breeding technologies, phenomics, and artificial intelligence, crop breeding is progressively entering an era of greater precision and efficiency. In this context, three-dimensional (3D) phenotyping techniques—leveraging multidimensional spatial resolution capabilities—have overcome the limitations of two-dimensional (2D) phenotyping in breeding analyses, enabling precise characterization of crop spatial interactions, spatial distribution of plant architecture, and complex 3D structural traits. Recent breakthroughs in computer technology for 3D reconstruction and 3D segmentation have provided robust technical support for crop 3D phenotypic analysis. Furthermore, effective integration of extracted 3D phenotypic data with genotypic data serves as a powerful tool for future research on crop gene function and genomics-assisted breeding. This review systematically examines major advances in 3D phenotyping techniques and their representative applications, with particular emphasis on innovations in 3D phenotyping and analytical methodologies. In parallel, we describe the latest interdisciplinary advances in 3D phenotyping within crop functional genomics research and genomics-assisted breeding. We objectively evaluate the advantages and limitations of 3D phenotyping compared with 2D approaches to assist breeders in selecting appropriate technologies. Finally, we propose future perspectives to promote deeper integration of phenomics and breeding technologies. Despite existing conceptual and technical challenges, it is foreseeable that cross-disciplinary integration of phenomics and genomics will offer promising prospects for crop breeding.

Key words: crop 3D phenotyping, artificial intelligence, deep learning, genomics-assisted breeding, crop 3D reconstruction

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INTRODUCTION

With the continuous growth of the global population and intensification of climate change, global agriculture is facing unprecedented challenges. Research indicates that by 2050, global food

production will need to increase by 25%–70% relative to current levels to meet future population demands (Hunter et al., 2017). Therefore, accelerating the development of crop varieties with high yield, superior quality, and strong stress resistance has become essential. However, screening extensive breeding

materials in conventional breeding processes is not only time-consuming and labor-intensive but also limited in efficiency and precision, leading to considerably greater breeding difficulties. In recent years, the rapid development of digital phenotyping techniques has provided important technical support to address this challenge. Current mainstream phenotyping approaches primarily utilize sensors such as red, green, and blue (RGB) cameras, multispectral cameras, thermal infrared cameras, and chlorophyll fluorescence cameras to acquire crop phenotypic information on specific planes. Although substantial progress has been achieved in biomass estimation and photosynthetic capacity assessment (Buitrago et al., 2016; Pérez-Bueno et al., 2019; Bai et al., 2023), considerable limitations persist regarding crops' complex three-dimensional (3D) morphological structures. Crops exhibit complex 3D morphology with broad individual variation. Their 3D traits, such as canopy architectural compactness and leaf angle distribution, can more accurately reflect dynamic growth and environmental responsiveness (Pieruschka and Schurr, 2019). However, conventional 2D phenotypic representations cannot accurately quantify spatial organ topology or structural characteristics. For instance, common leaf area measurements involve flattening leaves to obtain projected area, but this approach is inherently imprecise because of leaf wrinkling and curling. Similarly, spatial features such as branching angles present differently across viewing perspectives, and components perpendicular to the imaging plane cannot be measured; these aspects clearly demonstrate the limitations of trait quantification solely based on 2D images. Additionally, mutual occlusion among plants and between plant organs during 2D phenotyping affects the accuracy of phenotypic analysis while complicating data processing.

In recent years, the development of 3D technologies has provided a novel research paradigm for crop phenotypic analysis. Based on high-resolution data acquired from 3D sensors—including binocular images, multiview images, and light detection and ranging (LiDAR) 3D point cloud data—researchers can construct up to millimeter-precision crop 3D models that enable precise quantification of organ-level spatial topology and dynamic growth parameters, providing crucial data support for the construction of digital twin models of crop growth (Akhtar et al., 2024). From a technological evolution perspective, 3D phenotyping techniques have progressed from conventional methods (structure-from-motion, multiview stereo, stereo vision, time-of-flight, and structured light methods; Paulus, 2019) to deep-learning-based approaches. These technologies possess distinct advantages across application scenarios: structure-from-motion and multiview stereo technologies offer flexibility but involve computational complexity; stereo vision technology is cost-effective but requires high image quality; time-of-flight technology provides real-time capabilities but with limited precision; and structured light technology achieves high measurement accuracy but requires strict environmental conditions. Novel 3D reconstruction methods, exemplified by neural radiance fields (NeRF) and 3D Gaussian splatting (3DGS), have received widespread attention. Breakthroughs in rendering accuracy are driving crop phenotyping research toward greater precision. For instance, NeRF has been used to generate dense point clouds of tomatoes (*Solanum lycopersicum*) from multiview RGB images

(Choi et al., 2024). Similarly, 3DGS has been utilized to construct 3D models of rapeseed, enabling high-precision yield estimation (Shen et al., 2025).

After acquisition of crop 3D data, efficient and high-precision analytical approaches for trait extraction are equally crucial. In crop 3D phenotypic analysis, one or more preprocessing steps are typically required; 3D segmentation represents the most fundamental and widely applied step, whose accuracy directly impacts the precision of trait quantification (Yang et al., 2024a). Conventional segmentation methods include algorithms based on region growing and graph cuts, whereas deep-learning-based methods such as PointNet++ (Qi et al., 2017) and 3D U-Net (Çiçek et al., 2016) demonstrate superior adaptability and accuracy when processing complex crop structures. Following segmentation, the quantification of 3D traits transforms spatial data into biologically meaningful features, which can be categorized into three hierarchical levels: linear morphological metrics such as plant height, leaf length, and stem diameter; shape-descriptive metrics, including shape metrics, volume, and leaf area; and topological structure metrics encompassing topological structure quantification, angular distribution, canopy characteristics, and growth dynamics.

Three-dimensional phenotyping provides spatially resolved information on crop organs for modern breeding. Its integration with other technologies, such as genomics, to enhance breeding efficiency and precision is particularly important. Research on crop functional genes leveraging 3D phenotyping techniques primarily involves quantitative trait locus (QTL) mapping and genome-wide association studies (GWASs), which identify genetic loci controlling traits by associating phenotypic and genotypic data. These methods have been utilized to investigate diverse aspects of crop structure, development, and responses to environmental factors (Huang et al., 2010; Wang et al., 2023). In genomics-assisted crop breeding, mainly through marker-assisted selection and genomic selection, predictive models are constructed using 3D phenotypic data to enable efficient selection in early generations, thereby accelerating breeding processes and facilitating phenome–genome technology-guided breeding practices.

Although 3D phenotyping techniques have achieved preliminary progress in crop research, systematic syntheses and in-depth discussions remain limited regarding key issues such as precise capture of crop 3D morphological structures, deep integration of phenomic and genomic data, and large-scale phenotype–genotype association analyses. Most published reviews focus on 2D phenotypic feature analysis (Li et al., 2014, 2020; Walter et al., 2015; Singh et al., 2021), with related discussions often confined to phenotyping techniques themselves and demonstrating weak connections with functional genomics research (Paulus, 2019; Akhtar et al., 2024; Zuo et al., 2024). To our knowledge, this is the first review article to systematically integrate 3D phenotypic analysis, crop functional genomics research, and genomics-assisted breeding applications. The framework of this review is structured as follows. We first systematically examine the latest advances in 3D phenotyping techniques and discuss analysis of key phenotypic features derived from 3D data. We then investigate strategies and methodologies applied to genetic improvement while critically evaluating the readiness levels and adoption barriers of

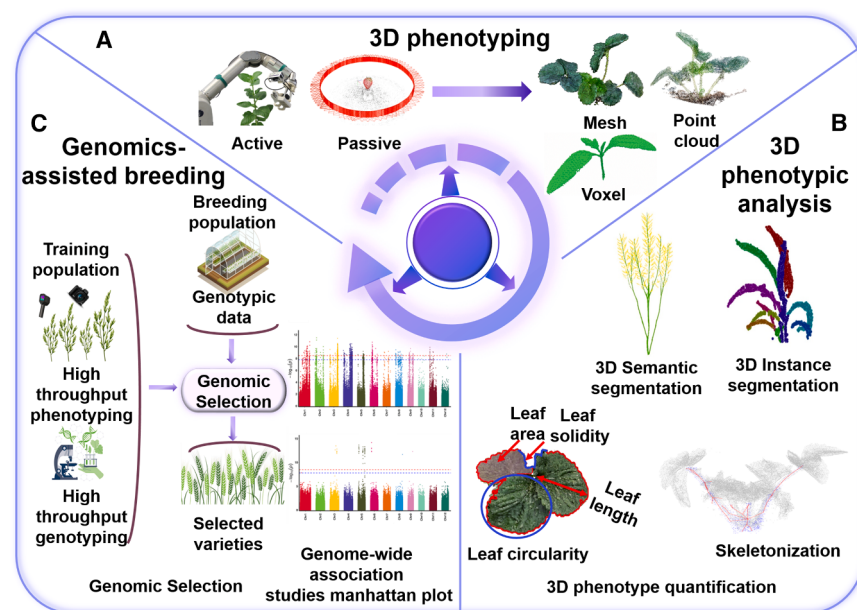


Figure 1. Integrated workflow of crop 3D phenotyping and genomics-assisted breeding.

This schematic illustrates the technical road map for integrating phenomics with genomics.

(A) Three-dimensional phenotyping uses active and passive 3D sensors to construct digital crop models, including mesh, point cloud, and voxel representations.

(B) The 3D phenotypic analysis pipeline progresses from 3D segmentation to precise quantification of traits across linear, shape, and topological dimensions.

(C) Application of these high-precision 3D traits in genomics-assisted breeding strategies, such as genome-wide association studies and genomic selection, enables identification of genetic loci undetectable through conventional 2D methods and thus facilitates efficient selection of superior varieties.

these technologies in practical breeding programs. Finally, we propose solutions to existing technical bottlenecks and outline future development directions, aiming to establish a theoretical framework and technical road map for 3D phenotyping-driven genomics-assisted breeding. The overall framework of the paper is illustrated in Figure 1.

THREE-DIMENSIONAL (3D) PHENOTYPING

Acquisition of crop 3D phenotypic data primarily relies on noninvasive imaging technologies, which can be broadly categorized into conventional algorithm-based methods and deep-learning-based approaches. In current research, conventional algorithm-based 3D phenotyping methods are predominant; they primarily achieve 3D data collection through established algorithms such as geometric feature analysis, photometric consistency constraints, and geometric model construction. In contrast, deep-learning-based crop 3D phenotyping technologies demonstrate greater developmental potential. These methods automatically learn complex 3D structural features of crops via neural network training, without manual design of geometric models or feature extraction, thus exhibiting greater robustness and environmental adaptability when processing complex scenes. However, such methods typically depend heavily on large-scale, high-quality annotated datasets and high-performance computing resources. At present, the computer vision field has developed various advanced 3D deep learning technologies. Effective application of these general 3D technologies to agriculture-related fields and management of challenges specific to crop scenarios remain directions requiring in-depth exploration.

Table 1 and Figure 2 summarize applications of major 3D phenotyping techniques, including sensor types, applicable plant species, 3D model representations, and their respective advantages and limitations. From the perspective of

technological development, crop 3D representations were primarily point-cloud-based before 2020; acquisition technologies were dominated by conventional methods, and deep learning played a supporting role. Since 2020, with rapid advances in deep learning technologies and the emergence of novel 3D representation methods such as NeRF (Mildenhall et al., 2021) and 3DGS (Kerbl et al., 2023), 3D phenotyping techniques have demonstrated two major developmental trends. First, adoption of deep-learning-based RGB image approaches has made 3D phenotyping more accessible and reduced dependence on complex hardware and expensive sensors (Li et al., 2023b). Second, exploration of implicit representation-based 3D reconstruction has enabled generation of higher-fidelity crop 3D models. Specific applications of sensors and algorithms are introduced in the following sections.

Conventional 3D phenotyping

Conventional 3D phenotyping techniques can be divided into active and passive methods on the basis of sensor data acquisition principles. Active methods utilize active sensors (time-of-flight cameras and structured light cameras; Paoli et al., 2020; Phang et al., 2021) to emit and receive signals for generation of 3D data; processing algorithms typically include time-of-flight algorithms and structured light algorithms. Passive methods rely on passive sensors (monocular cameras, stereo cameras, or multiview camera systems; Li et al., 2015; Gao et al., 2023; Yu et al., 2024) to capture 2D images under natural or existing light sources. They subsequently derive crop 3D geometric information through visual algorithms such as structure-from-motion, multiview stereo, and stereo vision.

Active 3D measurement methods

Time-of-flight technology resolves crop 3D structural information by measuring the time difference between emission and reflection of short pulse signals (typically infrared or laser) (Debnath et al., 2023); LiDAR is a typical example. Considering differences in crop type, required precision, practical

Technology	Advantages	Disadvantages	Suitable scenarios	Sensor	3D representation	Environment	Crops
Time of flight	real-time acquisition; low cost	low resolution, unable to capture fine details (e.g., leaf veins or stem texture); sensitive to strong outdoor light and interference	rapid overall 3D capture in greenhouses or labs for high-throughput plant phenotyping	LiDAR	point cloud	laboratory	maize and sorghum (Thapa et al., 2018), canola (Panjvani et al., 2019), maize (Forero et al., 2022)
				LiDAR	point cloud	field	maize (Qiu et al., 2019), cotton (Sun et al., 2018)
				time-of-flight camera	point cloud	laboratory	maize (Li and Tang, 2017), peanut (Liu et al., 2023)
Structured light	high accuracy; low texture dependency; suitable for capturing fine geometric details	complex deployment and calibration; high cost; requires a controlled environment	detailed 3D capture of small plant parts under lab conditions	structured light camera	point cloud	laboratory	cabbage, cucumber and tomato (Nguyen et al., 2015), Chinese cabbage (Shu et al., 2024)
Structure from motion and multiview stereo	captures both overall structure and fine details; flexible and applicable outdoors; effective in large-scale reconstructions	requires high-quality images and optimal camera angles; sensitive to insufficient viewpoint overlap and shadows; not suitable for real-time applications	field-scale plant 3D reconstruction using unmanned aerial vehicles or mobile platforms, capturing detailed and overall plant structures	multiview reconstruction system	point cloud	field	maize and soybean (Zhu et al., 2020), lettuce (Ge et al., 2025)
				multiview reconstruction system	point cloud	laboratory	maize (Wu et al., 2020, 2024), cotton (Hao et al., 2024)
Stereo vision	real-time measurement; low cost; suitable for outdoor natural lighting	high texture dependency; depth limited by camera baseline/resolution	real-time dynamic plant growth monitoring and leaf motion tracking on mobile platforms under natural outdoor light	binocular camera	point cloud	laboratory	<i>Pachira glabra</i> (Peng et al., 2022)
				binocular camera	point cloud	field	sorghum (Xiang et al., 2021), apple trees (Zhao et al., 2023), orchard trees (Zhang et al., 2024)
Deep learning	high reconstruction accuracy; rich detail and realistic models; capable of capturing subtle morphological features in plants; low cost	requires high computational resources; slow training; non-real-time	high-precision offline analysis for research and breeding; complex trait research	monocular camera	point cloud	laboratory	potted plants (Zhao et al., 2022a)
				multiview reconstruction system	implicit representation	laboratory	walnut (Huang et al., 2024b)
				multiview reconstruction system	implicit representation	field	tomato (Choi et al., 2024); pitahaya, grape, orange, and fig (Hu et al., 2024); sugar beet, maize, and soybean (Esser et al., 2023)

Table 1. Applications of crop 3D phenotyping techniques.

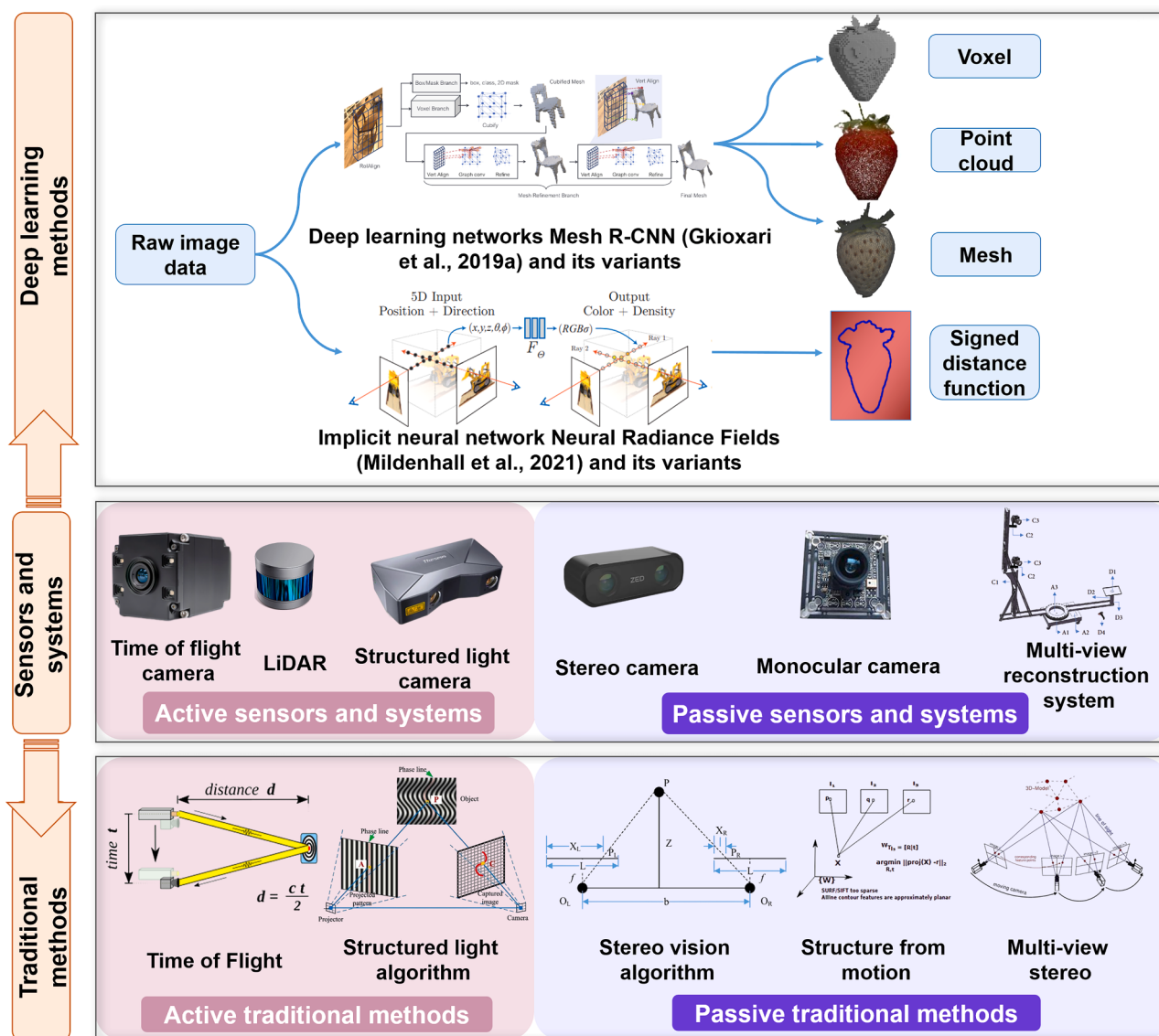


Figure 2. Overview of sensors, systems, and algorithmic approaches employed in crop 3D phenotyping.

The figure categorizes technologies into conventional methods at the bottom and deep-learning-based approaches at the top. The middle section displays common active sensors, including time-of-flight cameras, LiDAR, and structured light cameras, as well as passive sensors (e.g., stereo cameras, monocular cameras, and multiview reconstruction systems). Conventional methods often depend on specific sensor configurations. Deep-learning-based approaches illustrate advanced 3D representations, ranging from explicit forms—such as voxels, point clouds, and meshes—to emerging implicit representations such as neural radiance fields, which provide higher fidelity for complex crop structures.

application needs, and equipment cost, researchers have explored and developed various time-of-flight-based 3D phenotyping schemes. For instance, in stem measurement, researchers utilized time-of-flight cameras to acquire raw point cloud data of maize (*Zea mays*) stems. In conjunction with density histogram and radius filtering methods, this approach constituted a stem localization method with an average positioning error of 24 mm (Vázquez-Arellano et al., 2018). To improve the precision of data acquisition while reducing costs, consumer-grade time-of-flight cameras such as Azure Kinect have also been employed. Multiview (e.g., six-view) image acquisition combined with improved iterative closest point algorithms has been successfully applied to phenotypic measurement of fine structures such as rapeseed leaves and siliques, achieving submillimeter precision

(Teng et al., 2021). With regard to acquisition efficiency, viewpoint-planning-based time-of-flight data collection strategies have been explored. This approach can obtain richer effective point clouds while collecting the same amount of—or less—scan data, improving efficiency and precision of phenotypic measurements such as seedling leaf area, with leaf area measurement $R^2 > 0.99$ (Wei et al., 2024). Research indicates that time-of-flight technology offers strong real-time performance and low cost but has limited resolution and difficulty capturing fine crop features such as leaf veins or stem details. Additionally, it is sensitive to environmental light intensity and interference, rendering it essentially unusable under strong outdoor illumination. Therefore, it is most suitable for scenarios that require rapid acquisition of overall 3D crop morphology,

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such as high-throughput phenotyping in greenhouses or laboratory environments.

Structured light technology, based on triangulation principles, calculates depth information for each pixel by analyzing the deformation relationship between projected light patterns and camera-captured images, thus playing an important role in the measurement of 3D crop morphology (Liu and Wang, 2021). Different structured light modes exist according to measurement requirements: dot-matrix, line, and surface. Whereas the latter two are commonly used in industrial fields, dot-matrix structured light is frequently employed in crop 3D phenotyping. Dot-matrix structured light cameras scan crop surfaces point by point under a precise displacement mechanism control, making them suitable for high-precision 3D phenotyping of small organs (e.g., peppers, tomatoes, cucumbers, and lettuce seedlings; Nguyen et al., 2015; Syed et al., 2019). Overall, the principal advantages of structured light technology lie in its high measurement precision and low dependence on crop surface texture, rendering it highly suitable for acquisition of fine-scale 3D phenotypic information. However, deployment and calibration processes are typically complex, and equipment costs remain relatively high. Additionally, structured light methods impose stringent requirements on environmental lighting conditions and are therefore typically used in controlled indoor or laboratory environments.

Passive 3D measurement methods

Through structure-from-motion and multiview stereo algorithms, the calculation of camera poses and motion trajectories based on multiple images enables construction of crop 3D models within spatial coordinate systems. This approach has become the most widely adopted method in current 3D phenotyping (Wu et al., 2022b; Li et al., 2022c). In complex field environments, unmanned aerial vehicle remote-sensing technology has facilitated 3D phenotyping of crop populations at field scale. For example, use of Da-Jiang Innovations unmanned aerial vehicle platforms combined with structure-from-motion technology has successfully achieved precise quantification of phenotypic parameters such as crop number, height, and leaf area index in maize canopies (Zermas et al., 2020). In greenhouse single-crop research, improved structure-from-motion methods fused with accelerated-KAZE feature-matching multiview stereo vision algorithms have substantially enhanced 3D reconstruction precision for crops such as Carex, cabbage, and kale. Detection coefficients (R^2) for key traits, including crop height and canopy width, can reach 0.99 (Yang et al., 2024b). Notably, multiview stereo technology, combined with virtual design optimization methods, has further improved the extraction precision of key phenotypic parameters such as wheat (*Triticum aestivum*) single stem number, spatial distribution, and stem inclination angle; R^2 values for crop height and canopy width have reached 0.8 and 0.73, respectively (Gu et al., 2024). Structure-from-motion and multiview stereo technologies continue to advance toward high-throughput 3D phenotyping. Researchers have gradually transitioned from early limited feature extraction to comprehensive analysis systems encompassing dozens of structural traits, including basic morphological characteristics, leaf-related parameters, structural dispersion, volume, and color (Wu et al., 2024). Multiview stereo-based 3D phenotyping is well suited for capturing overall crop structure and fine details, offering strong

3D phenotyping in genomics-assisted crop breeding

flexibility and outdoor applicability. However, it requires high image quality and optimal viewing angles, warranting solutions to challenges such as insufficient view overlap and shadow interference (Zhou et al., 2024). Therefore, it is suitable for comprehensive 3D phenotyping in field environments and can be deployed on unmanned aerial vehicle or unmanned ground vehicle platforms.

Stereo vision technology estimates spatial positions within camera scenes by calculating disparities based on matched points between image pairs and subsequently applying triangulation to compute depth information (Wang et al., 2020). This technology commonly utilizes stereo cameras as information acquisition sensors and is particularly suitable for outdoor natural lighting environments, where it achieves centimeter-level detection precision. Research has shown that, using stereo matching algorithms such as semi-global block matching, wheat spike height measurement achieved 97.1% accuracy—with a leaf area root-mean-square error of only 0.37—while also providing high accuracy in estimation of key parameters such as leaf angle (Dandrifosse et al., 2020). Stereo vision technology combined with multiview dense acquisition can achieve higher-precision phenotyping, reaching millimeter-level precision when measuring parameters such as height, canopy width, and stem diameter of *Pachira glabra*; average errors are less than 2% (Peng et al., 2022). However, stereo vision exhibits strong dependence on crop texture; depth estimation precision is constrained by camera spacing and image resolution, potentially affecting performance in complex or texture-poor scenes. Thus, it is suitable for scenarios requiring real-time, low-cost 3D phenotyping, such as dynamic growth monitoring or leaf movement tracking, and can be deployed on mobile platforms for noncontact data acquisition.

Overall, time-of-flight technology offers strong real-time performance and low cost but is impacted by environmental lighting conditions and shows low resolution, making it suitable for high-throughput monitoring in controlled environments. Structured light technology achieves high-precision 3D phenotyping through projection of structured light patterns and particularly excels in capturing detailed structures. However, complex deployment processes and high costs hinder large-scale application. Structure-from-motion and multiview stereo technologies, as the most widely applied approaches, can achieve fine reconstruction of micro-crops and characterization of complex field scenes through unmanned aerial vehicle and unmanned ground vehicle platforms; dependence on dense feature matching limits real-time performance. Stereo vision systems possess real-time capability and can support dynamic crop monitoring under natural light conditions but remain constrained by camera baseline length and texture features; depth measurement precision generally reaches the centimeter level. When selecting sensors and algorithms, specific research requirements should be carefully considered to balance detection objectives for crop phenotypic traits.

Deep-learning-based 3D phenotyping

Deep-learning-based 3D phenotyping—leveraging powerful deep neural network models—can automatically extract complex features and perform end-to-end learning, thereby effectively

capturing crops' fine 3D structures and texture information. This technology demonstrates considerable advantages in handling complex backgrounds and extracting fine structures such as small leaves and curved branches. Compared with conventional methods, deep-learning-based approaches typically exhibit superior performance in precision, efficiency, and robustness of 3D reconstruction. Among current deep-learning-based methods for explicit models, approaches are primarily categorized according to model representation: voxel-based 3D models, including 3D ShapeNets (Wu et al., 2015), 3D-R2N2 (Choy et al., 2016), and VoTr (Mao et al., 2021); point-cloud-based 3D models such as PCN (Yuan et al., 2018) and PointFlow (Yang et al., 2019); and mesh-based approaches, including Pixel2Mesh (Wang et al., 2018), Pixel2Mesh++ (Wen et al., 2019), and Mesh R-CNN (Gkioxari et al., 2019).

Simultaneously, implicit-representation-based 3D reconstruction has become a prominent research direction. This technology no longer relies on mesh, point cloud, or voxel representations but instead performs 3D modeling of crops via neural networks or other implicit functions, generating continuous 3D structures. Models generated through implicit-representation-based 3D acquisition algorithms exhibit continuity and smoothness, enabling them to better describe continuous geometric shapes of crop organs. For instance, NeRF, introduced in 2020, is based on multiview images and 5D coordinates (spatial position $[x, y, z]$ and viewing direction $[\theta, \phi]$); it generates photo-realistic 3D models through differentiable volume rendering. However, NeRF has limitations, such as single-instance training without generalization capability, applicability solely to static scenes, and slow training speed. To address these limitations, numerous variant networks have emerged. Examples include Instant-NGP (Müller et al., 2022), which utilizes multiresolution hash encoding and compute unified device architecture-based acceleration to enable rapid training within minutes; NeuS (Wang et al., 2021) and Instant-NSR (Zhao et al., 2022b), which use signed distance functions and optimized volume rendering to enhance surface details and improve training efficiency. At present, most of these algorithms have been optimized on standard datasets and remain in the exploratory stage for agricultural applications. Emerging examples include Tomato-NeRF (Zheng et al., 2024) for tomato 3D reconstruction, GS-NIR (Ying et al., 2024) for pepper 3D modeling, and specialized networks for high-fidelity colored 3D mesh acquisition of walnuts (Huang et al., 2024b).

Another widely applied implicit 3D reconstruction algorithm is 3DGS, proposed by Kerbl et al. in 2023 (Kerbl et al., 2023). Although 3DGS generates results in point cloud form, its core framework utilizes Gaussian-distribution-based implicit representation. In this approach, each point in the scene is represented as a 3D Gaussian function that defines the point's volume, shape, color, and spatial uncertainty. The training process allows anisotropic splatting and fast backpropagation to achieve high-quality novel view synthesis. In crop phenotyping research, 3DGS has been successfully applied to extraction of structural features in crops such as cotton (*Gossypium hirsutum* L.) and tomato, yielding 3D phenotypic parameters that include cotton boll counting and main stem length measurement (Jiang et al., 2024), as well as tomato leaf counting and leaf area estimation (Baar et al., 2024). However, 3DGS is hindered by

multiview inconsistency, which results in suboptimal model surface quality and is disadvantageous for crops requiring high precision. The recently proposed 2D Gaussian splatting (2DGS) (Huang et al., 2024a) addresses this limitation by using 2D Gaussian discs to represent scenes, effectively improving multiview consistency. This approach can represent precise surface geometry with strong cross-view coherence. Additionally, inherent surface normals in 2DGS enable direct surface reconstruction regularization through normal constraints. Thus, compared with conventional surfel-based methods, 2DGS demonstrates superior performance in recovering surfaces from unknown geometries.

The cost of phenotyping—a pivotal consideration in breeding programs—is determined by the multifaceted interplay of technical feasibility, economic implications, and resource availability. First, regarding technical feasibility, structure-from-motion and multiview stereo techniques have been extensively adopted in high-throughput phenotyping; time-of-flight, structured light, and stereo vision technologies have also demonstrated practical viability. In contrast, emerging deep-learning-based methods exemplified by NeRF and 3DGS—despite their superior rendering performance—currently face challenges regarding limited generalizability and high computational latency in agricultural scenarios. Efforts to address such limitations are crucial for better aligning these technologies with the stringent requirements of breeding programs for 3D phenotypic accuracy and throughput. Second, economic factors play a prominent role in technology selection, given that financial feasibility greatly varies across approaches. Hardware costs exhibit a wide range: time-of-flight cameras, \$400–\$2000; structured light cameras, \$500–\$5000; stereo vision cameras, \$300–\$3000; and multiview reconstruction systems, \$800–\$30 000. In addition to hardware, hidden operational costs—such as software licensing and technical expertise—are substantial and should not be overlooked (Reynolds et al., 2019). Finally, regarding resource requirements, construction of robust deep learning models typically warrants extensive 3D data collection, annotation, and training. Although essential for model performance, this process inevitably consumes substantial human labor and time. To mitigate these resource demands, public 3D datasets can be utilized, employing strategies such as transfer learning to extract features for target objects. Prominent publicly available crop 3D datasets include Crops3D (cabbage, cotton, maize, potato, rapeseed, rice [*Oryza sativa*], tomato, and wheat) (Zhu et al., 2024b), Pheno4D (maize and tomato) (Schunck et al., 2021), Panicle-3D (rice) (Gong et al., 2021), and ACID (wheat) (Stuart et al., 2025).

3D PHENOTYPIC ANALYSIS

3D segmentation

Three-dimensional crop phenotypic analysis involves segmentation and feature extraction of acquired 3D crop models to derive multiscale 3D morphological, physiological, and growth characteristics. These span the population level (e.g., field plot vigor), individual level (single-plant morphological traits), organ level (3D structures of roots, stems, leaves, flowers, and fruits), and even the microscopic cellular level (Figure 3). To achieve such multiscale quantification, target-oriented segmentation of raw

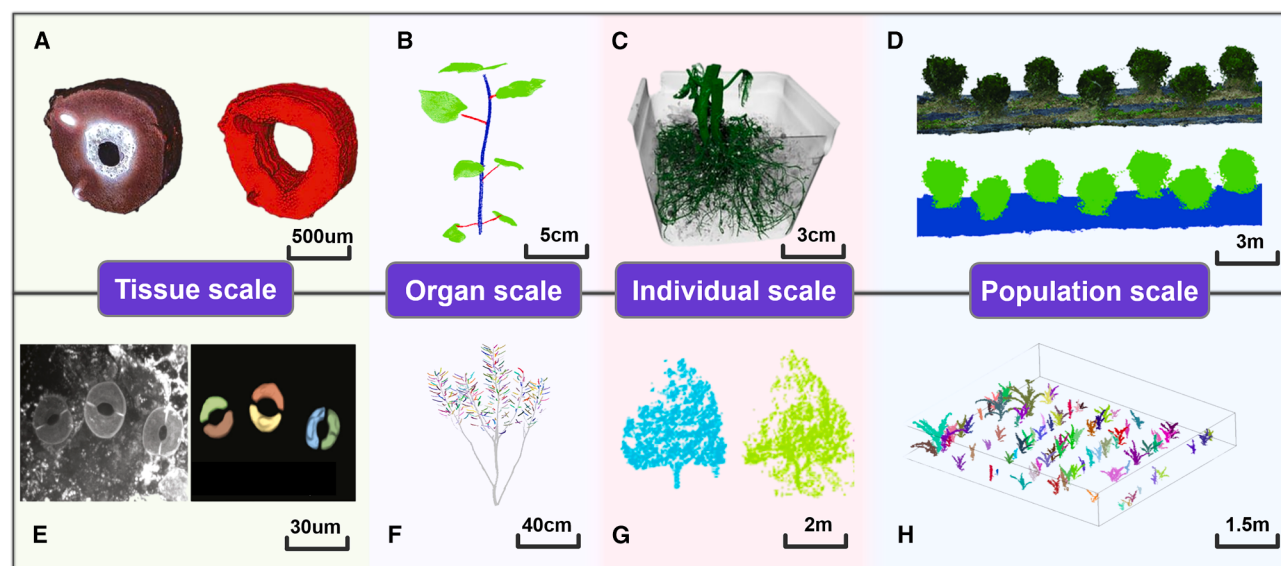


Figure 3. Multiscale 3D segmentation results for precise phenotype extraction.

This figure demonstrates the capacity of 3D segmentation to isolate targets across biological scales, serving as a prerequisite for accurate trait quantification. Examples span microscopic tissue and organ levels to individual plant and population scales.

(A) A 3D semantic segmentation of *Phaseolus vulgaris* root hypocotyl cortex (Strock et al., 2019).

(B) A 3D semantic segmentation of cotton stems, leaves, and petioles (Shen et al., 2024).

(C) A 3D semantic segmentation of tomato.

(D) A 3D semantic segmentation of mandarin orange tree populations (Qi et al., 2021).

(E) A 3D instance segmentation of guard cell stomata (Davaasuren et al., 2022).

(F) A 3D instance segmentation of rapeseed siliques (Du et al., 2023).

(G) A 3D instance segmentation of individual trees (Ning et al., 2022).

(H) A 3D instance segmentation of maize populations (Jin et al., 2018).

3D data is essential; it effectively isolates target crops or organs from complex backgrounds (such as soil, weeds, and neighboring plants) and noise. This segmentation step serves as a critical precondition for the precise measurement of phenotypic parameters in individual crops or organs, while providing the foundation for tracking organ growth dynamics across long-term time series.

Current crop 3D segmentation technologies mainly encompass 3D semantic segmentation and 3D instance segmentation. Numerous studies have successfully demonstrated crop segmentation (Li et al., 2022a, 2022b; Zarei et al., 2024). Generally, conventional 3D segmentation methods—such as clustering based on geometric features, region growing, and graph cut algorithms—do not require large-scale annotated data and impose comparatively lower demands on computational resources. Consequently, they are well suited to small-to-medium-scale scenarios characterized by data scarcity or real-time processing requirements. However, with advances in deep learning, mainstream methodologies have shifted toward deep-learning-based segmentation frameworks. These approaches greatly outperform conventional techniques in data adaptability, segmentation precision, and large-scale processing capability. Point clouds currently represent the predominant target for segmentation, primarily because (1) point cloud acquisition is convenient and supported by extensive application examples, and (2) point clouds provide advantages in computational and storage efficiency, making them particularly suitable for processing unstructured crop data.

Quantification of 3D traits

Based on segmented target populations, individual plants, or organs, researchers can achieve further quantification of 3D traits. Existing 3D trait quantification metrics can be categorized into three major classes.

Linear morphological metrics

Linear geometric parameters directly extracted from 3D point clouds or meshes constitute the first class, including plant height, canopy width, stem length and diameter, and organ-scale metrics such as leaf length and perimeter.

Shape-descriptive metrics

Shape-descriptive metrics characterize overall geometric features of organs or crops, such as projected area, volume, surface area-to-volume ratio, and leaf shape metrics.

Topological structure metrics

Topological structure metrics describe crop spatial configuration and growth patterns, including indices such as tree topology, leaf angle, and curvature. Specific representations of these metrics are described below, and their calculation methods are presented in Table 2.

Linear morphological metrics

Crop height and width are fundamental parameters describing the 3D morphology of crop organs. Plant height is typically defined as the vertical distance from the base to the tip of the plant, representing the maximum span in the vertical direction. Plant width refers to the maximum horizontal extension of the plant, encompassing spans in both the anterior–posterior and left–right directions, which collectively describe horizontal

3D trait quantification metric	Specific metric	Formulas	Notes
Linear morphological metrics	plant height	$Height = \max(Z_m - Z_n)$	Z_m and Z_n represent the values at any non-coincident point along the z axis
	plant width	$Width_x = \max(X_m - X_n)$; $Width_y = \max(Y_m - Y_n)$	X_m, X_n, Y_m , and Y_n represent the values at any non-coincident point along the x axis and y axis
	stem length	$Length_{stem} = \sum_{i=1}^n m_i - m_{i-1} $, $M = \{m_0, \dots, m_n\}$	m_i represents points on the stem
Shape-descriptive metrics	leaf surface roughness	$R_a = \frac{1}{n} \sum_{i=1}^n z_i - \bar{z} $	z_i is the height of surface points and $\bar{z}$ is the average height
	leaf circularity	$circularity = 4\pi * \frac{area}{perimeter^2}$	—
	leaf solidity	$solidity = \frac{area}{convex\ hull}$	—
	fruit shape	$R_{shape} = 1 - \frac{\sum_{i=1}^k \Delta k}{n(abc)^{\frac{1}{3}}}$	ΔK is the distance between each point in the point cloud model and the intersection of a ray passing through that point with the ellipsoid surface; a, b, c are ellipsoid parameters and n is the number of points
	fruit volume	$V = \sum_{i=1}^n v_i \cdot \delta v$	v_i represents the binary label of the i-th voxel (1 for foreground, 0 for background), and δv represents individual voxel volume
	fruit aspect ratio	$R_{aspect} = \max \frac{D_T}{D_L}$	D_T represents the transverse diameter, and D_L represents the longitudinal diameter
	leaf area	$S = \frac{\sum_{i=1}^n S_i}{2}$	S_i represents the area of a single triangular mesh in the mesh model
Topological structure metrics	curvature	$C_{(s)} = \lim_{\Delta s \rightarrow 0} \frac{A_{(s+\Delta s)} - A_{(s)}}{\Delta s} = \frac{\partial A_{(s)}}{\partial s}$	line segment length Δs approaches 0
	relative growth rate	$RGR = \frac{1}{V_t} \frac{dV}{dt} \approx \frac{\ln V_{t+\Delta t} - \ln V_t}{\Delta t}$	V_t represents volume at time t, and Δt is the time interval
	growth direction	$\vec{d_p} = \vec{p_{t+\Delta t}} - \vec{p_t}$	$\vec{p_t}$ represents the displacement vector at time t

Table 2. Formulas for key 3D trait quantification metrics.

canopy coverage (Paulus et al., 2014). Leaf length is defined as the midrib length from the stipule (where the leaf connects to the stem) to the leaf tip (the apex). However, reliance solely on Euclidean distance between these two points underestimates leaf length due to typical leaf curvature. Therefore, incorporation of additional intermediate points between the stipule and apex enables more accurate determination of leaf length (Golbach et al., 2016). Leaf perimeter refers to the length of the closed curve forming the leaf cross-sectional contour; it can be obtained by calculating and summing the Euclidean distances of boundary line segments. Stem diameter is calculated using least-squares minimization algorithms to fit a cylindrical model to the stem. The maximum coordinate difference in orientation is considered the stem diameter (Paulus et al., 2014). Stem length estimation relies on skeleton extraction results; stem top and bottom vertices are identified, and multiple intermediate skeleton points are iteratively calculated.

Shape-descriptive metrics

Shape-descriptive metrics are mainly utilized in crop classification and variety identification (Nicotra et al., 2011). The flatness

index describes the degree of flattening in leaves or fruits and is calculated as the ratio of the shortest axis to the second-longest axis. The elongation index reflects organ extension characteristics and is calculated as the ratio of the longest axis to the second-longest axis. Leaf surface roughness reflects microscopic surface irregularities. Leaf circularity is defined as $4\pi \times (\text{leaf area}/[\text{perimeter}]^2)$; it is sensitive to edge variations (e.g., serrations, lobes, and leaflets) and is also influenced by elongated shapes (Li et al., 2018). Leaf solidity represents the ratio of total area to convex hull area. Leaves with low solidity may be compound leaves with leaflets, deeply lobed leaves, or leaves with prominent petioles.

Fruit shape can be quantified using a roundness index, where a value of 1 indicates a perfect ellipsoid; lower values indicate sharper or more irregular shapes (Le Louëdec and Cielniak, 2021). Maximum longitudinal and transverse fruit diameters—analogueous to maximum plant width—are calculated as maximum coordinate differences along longitudinal and transverse directions, respectively. The ratio of longitudinal to transverse diameter constitutes the fruit aspect ratio.

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Regarding crop volume and surface area measurements, volume is an important indicator of biomass and directly reflects crop growth status. Because plants contain internal voids, calculation of convex hull volume yields inaccurate estimates of true plant volume. Consequently, researchers discretize 3D models into voxel representations and calculate total voxel counts to estimate plant volume (Underwood et al., 2016). Fruit volume is estimated in a similar manner.

Area-related leaf parameters also represent key traits of interest to breeders, particularly for organs such as leaves and roots that closely interact with the environment, thus reflecting crop photosynthetic efficiency and growth status. In 3D mesh models, leaf area can be represented as the sum of areas of all triangular mesh elements within the region. Projected leaf area refers to the 2D area formed by projecting a 3D leaf onto a specific plane. Calculation of this projected region using geometric algorithms—such as the Shoelace formula or triangulation methods—serves as an effective approach for evaluating leaf light-interception capacity.

Topological structure metrics

The first component involves quantification of topological structure. Skeleton extraction reduces complex crop 3D structures into one-dimensional skeleton lines, preserving essential topology while removing redundant information; this approach facilitates subsequent analysis and quantification. Common skeleton extraction methods include distance transform, contraction, L1-median skeletonization, and probability-based skeleton extraction. On the basis of extracted skeletons—and through optimization, node identification, and curve fitting—parameters such as crop tree topology index, topological depth, and branching ratio can be derived.

The second component comprises quantification of angles and curvatures. Organ spatial arrangement is an important characteristic for adaptation to light environments; 3D reconstruction enables accurate measurement of these geometric relationships. For example, McCormick and colleagues utilized 3D imaging technology to analyze leaf angle distribution among sorghum varieties and found that compact canopy varieties (with smaller leaf angles) performed better under high-density planting conditions, providing morphological evidence for high-yield variety selection (McCormick et al., 2016). Common angular measurements include leaf angle, defined as the angle between the leaf and main stem; leaf inclination angle, representing the tilt between the leaf and the horizontal plane (Li et al., 2023a); branch angle, defined as the angle between a branch and its parent branch; and azimuth angle, representing the angle between the leaf projection on the horizontal plane and geographic north. Within 3D models, local curvature has been defined (Hartmann et al., 2024) to quantify the degree of bending in stems or leaves. This metric is calculated by dividing the angle formed between a local organ segment and the vertical direction by the arc length of that segment. To ensure measurement precision, the organ is typically divided into small, equal-length segments for calculation. As segment length approaches zero, the curvature value at that location can be obtained with precision. Bending and twisting of crop organs constitute critical features for environmental adaptation, as well as key indicators for assessment of mechanical strength.

The third component is quantification of canopy structure. This quantification focuses on spatial structural characteristics at

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the crop population level, providing an important foundation for efforts to understand crop light interception and resource utilization. Common canopy structure metrics include leaf area index, defined as leaf area per unit ground area; canopy coverage, representing the proportion of ground covered by the canopy in vertical projection; and canopy height, defined as the average or maximum height of leaves or crowns within the canopy.

The final metric comprises time-series analysis of growth dynamics. A major advantage of 3D phenotyping techniques is the capacity to perform nondestructive time-series measurements, which capture dynamic processes of crop growth and development. By establishing sequential 3D models, various dynamic parameters can be calculated. Relative growth rate reflects current crop growth status, whereas growth direction can be derived by calculating displacement vector fields.

Figure 4 illustrates calculation schematics for plant height, plant width, stem length, stem diameter, stem inclination angle, leaf area, leaf perimeter, leaf length, leaf inclination angle, leaf circularity, leaf solidity, fruit maximum longitudinal diameter, fruit maximum transverse diameter, and fruit apex angle, using strawberry as an example.

These quantified 3D phenotypic traits provide essential quantitative data for genomics-assisted breeding analyses. However, challenging and difficult-to-quantify traits remain, such as root morphology and distribution, stem flexibility and bending resistance, and fruit glossiness. Efforts to address these gaps require that algorithm engineers develop efficient and precise quantification algorithms; breeders must establish unified evaluation standards. For example, Jin et al. (2021) innovatively utilized leaf inclination angle, leaf azimuth angle, leaf width, projected leaf area, and plant height derived from terrestrial laser scanning to comprehensively quantify crop seasonal and diurnal rhythms, yielding new insights.

APPLICATIONS OF 3D PHENOTYPING IN CROP GENETICS AND BREEDING

Three-dimensional phenotypic data display advantages over 2D data in spatial dimensionality, accuracy, and dynamic characterization. These attributes facilitate novel discoveries when integrated with genomic technologies (Supplemental Table 1). Although techniques for phenotypic acquisition and analysis have been extensively discussed, genetic research and crop breeding applications leveraging these technologies have received comparatively limited attention, and a systematic synthesis is absent. Consequently, this section systematically explores integration of 3D phenotypic data with crop genomics-assisted breeding technologies, focusing on two interconnected technical pathways and their practical implementations: QTL mapping and GWASs—crop gene function research; marker-assisted selection and genomic selection—crop genomics-assisted breeding; and practical breeding applications of 3D phenotyping, with analysis of successes, limitations, and existing challenges to provide insights for breeders.

Crop gene function research

In crop gene function research, QTL mapping and GWASs represent two pivotal tools, each with distinct advantages and

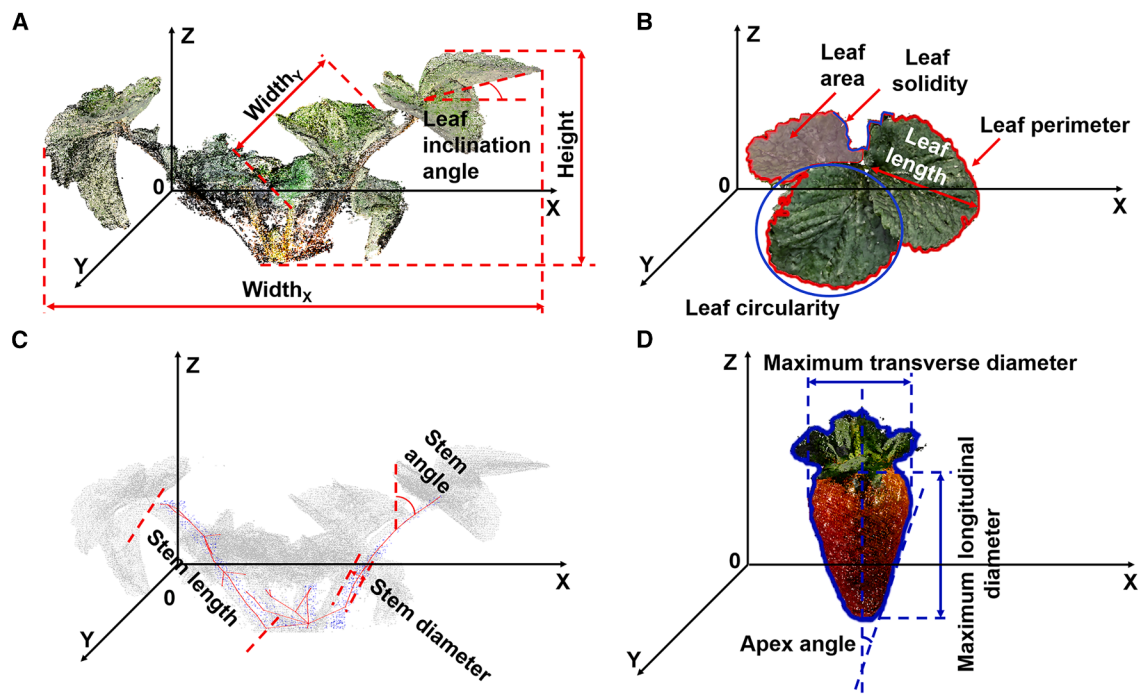


Figure 4. Schematic diagram of strawberry trait quantification based on 3D topological structure.

The figure illustrates how 3D models are transformed into quantifiable biological metrics within a spatial coordinate system.

(A) Whole-plant traits characterize global dimensions such as height, width, and canopy structure.

(B) Leaf-related traits quantify morphological parameters including leaf area, circularity, solidity, and inclination angle.

(C) Stem-related traits involve extraction of skeletal features to measure stem length, diameter, and angular orientation.

(D) Fruit-related traits quantify yield- and quality-related attributes, including maximum longitudinal diameter, transverse diameter, and apex angle.

limitations. QTL mapping is a technique used to identify genomic regions controlling quantitative traits through analysis of associations between phenotypic traits and molecular markers within specific biparental segregating populations (Collard et al., 2005). This method is effective for identifying genetic loci that strongly influence target traits, and it offers the advantage of rapid and convenient analysis. However, it generally exhibits lower mapping resolution and typically delineates larger chromosomal regions, although it requires fewer markers. Consequently, it is particularly suitable for genetic analysis of specific breeding materials. By providing more precise and multidimensional phenotypic data, 3D phenotyping techniques enable the discovery of novel trait loci while facilitating dynamic QTL mapping (Moore et al., 2013; Topp et al., 2013). Conversely, GWASs detect genetic polymorphisms across multiple individuals on a genome-wide scale, utilizing statistical analyses to identify genes associated with phenotypic variation (Korte and Farlow, 2013). The principal advantage of GWASs lies in the capacity to discern genetic variations linked to complex traits and narrow these associations to smaller genomic regions. However, the GWAS technique is susceptible to higher false-positive rates and requires precise phenotypic characterization across large populations (Wu et al., 2021). Through advances in 3D phenotyping techniques, GWASs have expanded from conventional 2D measurements to dissection of 3D spatial features. This transition provides enhanced phenotypic precision and enables identification of genetic loci that remain undetectable via 2D phenotyping. Such technological integration has demonstrated remarkable

potential in crop gene function research (Wu et al., 2024; Davis et al., 2025).

Crop genomics-assisted breeding

The translation of discovered associations between genes and 3D traits into practical applications represents a crucial step in crop genetic improvement. Marker-assisted selection enables direct screening of individuals with favorable alleles through use of molecular markers tightly linked to target genes. This approach offers operational simplicity, given that it requires only marker genotypic data for targeted selection. However, marker-assisted selection is primarily effective for major-effect QTLs and shows limited efficacy for complex traits controlled by numerous minor-effect genes (Wu et al., 2022a). Although 3D phenotyping cannot fully mitigate the limitation of marker-assisted selection to major-effect genes, it holds substantial value during marker development and validation phases, particularly for spatial architectural traits that are poorly captured by conventional 2D methods (e.g., branching angles and canopy architecture) (Boogaard et al., 2023). At present, integration of 3D phenotyping with marker-assisted selection remains largely indirect. Three-dimensional phenotyping enables more comprehensive and dynamic analysis of crop growth, facilitating discovery of novel QTLs for subsequent marker-assisted selection. Additionally, it serves as a tool for evaluating agronomic traits in lines improved via marker-assisted selection. Future opportunities lie in leveraging 3D phenotyping to develop novel markers linked to complex architectural traits and in integrating marker-assisted

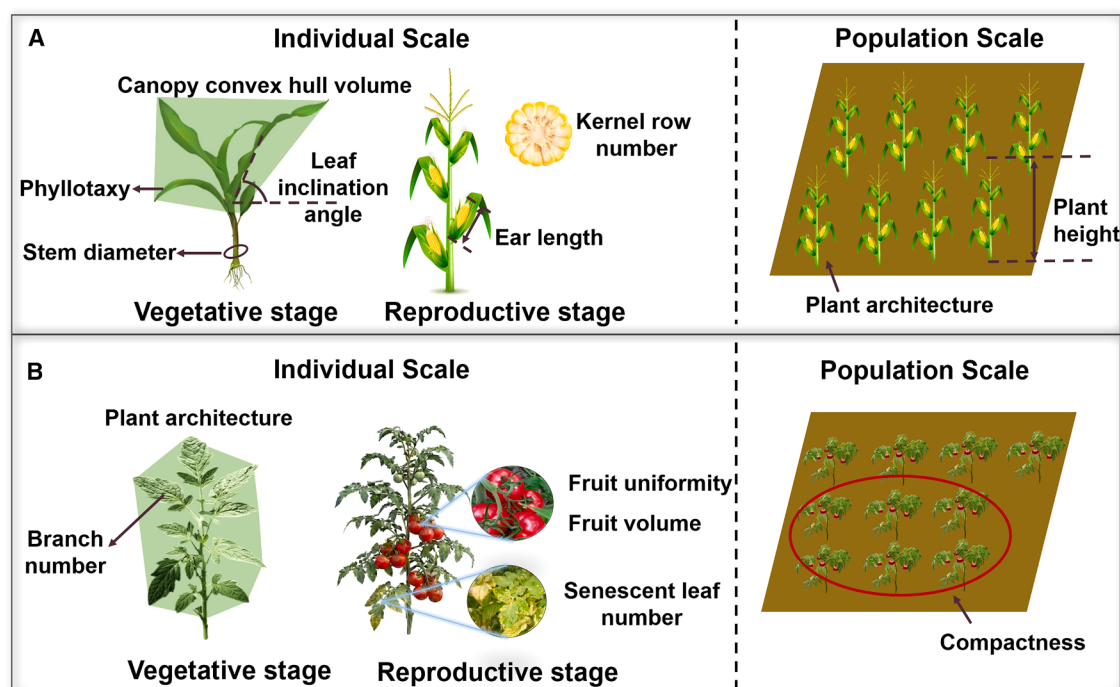


Figure 5. Key 3D traits emphasized during distinct breeding stages across representative crops.

The figure contrasts phenotypic priorities between agricultural and horticultural crops from individual to population scales.

(A) As a representative agricultural crop, maize breeding focuses on ideal plant architecture during the vegetative stage through analysis of leaf inclination and phyllotaxy to optimize light interception. During the reproductive stage, emphasis shifts to ear morphology—such as kernel row number and ear length—for yield estimation.

(B) As a representative horticultural crop, tomato breeding emphasizes canopy complexity traits, such as branch number, during the vegetative stage and fruit quality metrics—including uniformity and volume—during the reproductive stage.

(A) and **(B)** collectively illustrate how individual 3D traits translate into population-level characteristics such as canopy compactness and plant height uniformity.

selection with complementary breeding strategies, such as genomic selection.

constraints limit adoption of genomic selection in smaller breeding programs with finite resources.

Genomic selection identifies lines with optimal breeding values via genome-wide markers (Sandhu et al., 2022). By simultaneously adjusting for genome-wide marker effects, genomic selection allows concurrent selection of multiple traits, thereby enhancing selection accuracy and efficiency. Compared with marker-assisted selection, genomic selection offers superior predictive performance for quantitative traits governed by numerous minor-effect genes (Bhat et al., 2016). Because genomic selection enables selection using models trained on specific populations, it can substantially reduce reliance on phenotypic analysis across breeding generations, thus conserving time and resources. Contemporary breeders are reevaluating strategies to maximize genetic gain in genomic selection by improving phenotypic accuracy within training populations (Cobb et al., 2013). In this context, the high precision of 3D phenotyping and its ability to dissect complex traits—capabilities that surpass those of conventional 2D methods—may further accelerate genomic selection advancement. However, this approach requires extensive genomic datasets and vast computational resources, resulting in higher costs and technical barriers. Furthermore, genomic selection models must be retrained to maintain prediction accuracy when target environments or genetic backgrounds undergo pronounced shifts. These

Assessment of practical applications

High yield represents the paramount objective of crop breeding. During the vegetative stage, rational plant architecture optimizes spatial distribution of light within the canopy and increases interception of photosynthetically active radiation, thereby enhancing light energy conversion efficiency and ultimately influencing crop yield. Conversely, during the reproductive stage, the numbers of flowers and fruits, along with their spatial arrangement, serve as critical determinants of yield components. This section utilizes maize, a representative agricultural crop, and tomato, a horticultural crop, as case studies (Figure 5). Through these examples, we systematically illustrate the application of 3D trait quantification metrics at individual and population scales during two critical growth stages. Furthermore, we examine the impact of these metrics on dissection of crop gene function and advancement of genetic breeding research.

Regarding maize at the individual scale, during the vegetative stage, ideal plant architecture characteristics are primarily quantified through 3D traits such as leaf inclination angle, leaf area index, phyllotaxy, and canopy convex hull volume. These metrics effectively reflect capacity for rational light gradient distribution,

canopy compactness, and adaptation to high-density planting (Incognito et al., 2020). During the reproductive stage, analytical focus shifts to spatial posture and orientation of the ear, as well as 3D ear morphological parameters—traits that are directly linked to final yield (Li et al., 2024). In practical applications, researchers have applied multiview stereo technology to extract 3D traits from 495 maize inbred lines. Subsequent GWASs combined with genotypic data revealed that 3D spatial features, such as convex hull volume, were significantly associated with the density-tolerant gene *GRMZM2G072274*, providing critical technical support for breeding under high-density cultivation conditions (Wu et al., 2024). Additionally, researchers reconstructed maize at the heading stage via the 3DGS algorithm and extracted key 3D phenotypic traits—including leaf angle. These traits were subsequently incorporated into genomic selection models, demonstrating that refined individual-scale 3D traits can greatly accelerate screening of ideal plant architectures (Wu et al., 2025). Further studies have established that leaf angle is closely associated with crop compactness; 3D traits involving leaf angle and leaf length (constructed via depth cameras) were linked to loci identified through QTL mapping, then confirmed to show correlations with photosynthetic capacity utilization (McCormick et al., 2016).

At the maize population scale, 3D phenotyping mainly targets traits such as plant height, vertical canopy structural parameters, and density characteristics. These traits are typically quantified using unmanned aerial vehicle remote sensing combined with multiview stereo algorithms—a methodological framework also applied to wheat populations under field conditions. For instance, to address limited precision in population height measurements caused by lodging and canopy heterogeneity, researchers acquired high-resolution RGB images of wheat across the growth cycle using unmanned aerial vehicles. By applying structure-from-motion algorithms to generate high-precision 3D point clouds, they successfully quantified population-level canopy height. Furthermore, on the basis of canopy height, they analyzed rapid growth periods and growth efficiency. GWASs then mapped loci near the *TaDWF4-3A* and *WPCL1-3A* genes, which are known regulators of yield and nitrogen use efficiency in wheat (Chen et al., 2024).

For tomato, during the vegetative stage, yield formation analysis focuses on phenotypic metrics such as plant height, internode length, stem diameter, and branch number. During the reproductive stage, emphasis is placed on inflorescence node position, fruit set per plant, and individual fruit morphology, while also considering functional leaf traits (Rossi et al., 2022; Wang et al., 2022). These traits can be acquired through multiview 3D reconstruction approaches, such as trait calculation based on tomato canopy 3D reconstruction (Zhu et al., 2023) or extraction of fine-scale parameters—including internode length and diameter, leaf branching angle, and phyllotaxy—via quantitative structure modeling algorithms (Xin et al., 2024). Alternatively, dynamic growth modeling of tomato inflorescences has been achieved using elastic mechanics data (Liu et al., 2025). At present, application of tomato 3D phenotyping in genetic breeding remains at an exploratory stage. However, analogous research has made substantial progress in grapevine. Bunch compactness, a critical 3D trait, is closely associated with

susceptibility to gray mold (*Botrytis cinerea*), such that compact bunches exhibit higher infection risk. By utilizing high-throughput 3D phenotyping platforms to precisely estimate the heritability of traits such as berry size and bunch width, researchers have identified more than 20 stable resistance-related QTLs across multiple mapping populations, providing molecular marker support for breeding loose-bunch varieties (Rist et al., 2022).

In tomato population cultivation, precise regulation of plant height, branching patterns, and canopy structure enables breeding of high-yielding varieties appropriate for intensive production systems (e.g., vertical farming). These varieties typically require compact plant architecture, optimized light interception, and high resource-use efficiency to adapt to limited spaces and multilayered layouts. However, severe interplant occlusion, complex canopy overlap, and light heterogeneity in semi-structured greenhouse environments represent key challenges to large-scale population-level 3D data acquisition; dedicated sensors and equipment designed specifically for greenhouse applications remain relatively scarce. Published studies have predominantly employed unmanned ground vehicle phenotyping platforms to perform multiview adaptive acquisition of RGB-D and multispectral imagery. Through integration of 3D spatial-spectral data fusion, high-quality 3D multispectral point clouds can be generated to dissect spatial heterogeneity (e.g., morphological and physiological variation) at individual-plant or small-population scales (Xie et al., 2024). Nevertheless, examples of 3D genetic dissection at large-population scales remain rare, constraining elucidation of genetic mechanisms that translate superior individual traits into population-level yield advantages. Going forward, horticultural crop breeding should prioritize development of group-level 3D compactness indices tailored to intensive cultivation systems. This tailoring includes proposed metrics such as point-cloud-based canopy filling degree, spatial occupation volume, and light distribution optimization; these metrics can establish a quantitative evaluation framework spanning individual and population levels. Such advances will facilitate screening of compact, high-efficiency plant architectures and promote synergistic optimization of yield, resource utilization rate, and agricultural energy costs.

In summary, given that single-view imaging is susceptible to leaf occlusion and overlap—factors that hinder accurate quantification of 3D spatial features of plant architecture—3D phenotyping technology demonstrates clear advantages in evaluation of ideal plant architecture. It provides more precise and comprehensive canopy structural parameters, facilitating more effective dissection of the genetic basis underlying architecture-related traits and enabling discovery of genetic loci that remain undetectable via conventional 2D phenotyping.

FUTURE PERSPECTIVES

Current research extensively demonstrates the remarkable potential of integrating phenomics with genomics (Marsh et al., 2021; Mansoor et al., 2024). Although the synergy between precise 3D phenotyping and breeding technologies offers considerable opportunities for crop genetic improvement, it is also accompanied by notable challenges. In the future, application and optimization of these approaches within breeding programs can be advanced through the following key directions.

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First, realistic barriers to implementation of 3D phenotyping systems must be addressed. Most current 3D models have mainly been developed for major crops such as maize, wheat, and soybean; customized algorithmic optimization is needed to accommodate the specific structural characteristics of other crop species. Furthermore, continuous operational expenditures—including initial equipment costs (ranging from thousands to hundreds of thousands of dollars), data storage, computational infrastructure, labor input, and facility maintenance—remain high (Reynolds et al., 2019). Although costs associated with 3D data acquisition constitute only a minor fraction of total expenses in genomics-assisted breeding, overall economic viability depends on whether the incremental effective information gained greatly outweighs marginal costs, particularly considering the commercial value of new varieties. As evaluated population size increases, per-plant costs of high-throughput 3D analysis noticeably decrease, conferring a distinct advantage in large-scale breeding programs.

Second, phenotyping strategies should be selected using a target-oriented approach. Conventional 2D phenotyping primarily captures planar, static metrics such as vegetation indices and canopy coverage, making it difficult to reflect spatially dynamic changes and occlusion effects. Critical evaluation of limitations inherent to 2D phenotyping in specific breeding scenarios provides valuable guidance for technology selection. In a study of salt stress in barley, conventional 2D static imaging failed to capture continuous micro-scale temporal changes, resulting in omission of key genetic signals. Conversely, researchers utilizing 3D reconstruction technology precisely quantified dynamic leaf elongation rates and successfully mapped an early salt-response-specific QTL on chromosome 3H (Ward et al., 2019). This case indicates that, in genomics-assisted breeding, 3D phenotyping should not represent a simple accumulation of technologies but must be prioritized for specific breeding bottlenecks in which high-precision 3D methods are essential, including early dynamic growth rate assessment, spatial topological optimization, and dissection of cryptic traits. For general biomass estimation or routine growth monitoring, low-cost 2D approaches remain efficient and practical.

Third, expansion of high-throughput field applications must be promoted. Existing 3D phenotyping technologies—predominantly laboratory-based—are increasingly transitioning to field and greenhouse environments. Unmanned phenotyping platforms (e.g., unmanned aerial vehicles and unmanned ground vehicles) equipped with LiDAR, point cloud processing systems, and multi-spectral sensors enable automated, high-throughput acquisition of 3D traits across large-scale populations. These platforms effectively address challenges such as plant occlusion in field settings, light heterogeneity, and dynamic environmental variability. They support real-time, continuous monitoring throughout the crop growth cycle, providing more representative and reliable phenotypic datasets for genetic breeding research.

Fourth, innovations in artificial intelligence (AI)-assisted breeding are transformative. Currently, the rapid evolution of AI is reshaping every aspect of modern life. AI systems such as AlphaFold and RoseTTAFold have achieved breakthroughs in protein structure prediction, successfully predicting hundreds of millions of structures—a figure that far exceeds the cumulative total from historical experimental determinations (Jumper et al., 2021).

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Zhu et al. proposed CropGPT (Zhu et al., 2024a), advocating resource sharing and the use of big-data-driven AI to advance breeding. AI can support crop breeding across multiple dimensions, such as development of self-supervised and semi-supervised learning approaches to reduce the substantial human resource burden associated with data annotation; construction of interpretable AI models to render algorithmic decision-making transparent and provide biologically meaningful explanations; and facilitation of AI-driven reverse breeding design. The latter, which predicts optimal gene combinations for target traits through large-scale simulation and optimization, represents one of the most disruptive recent innovations.

Finally, efforts to strengthen interdisciplinary talent cultivation and collaborative innovation mechanisms are essential. Three-dimensional phenotyping-driven genomics-assisted crop breeding constitutes a complex interdisciplinary engineering project requiring deep integration of expertise across computer vision, data science, quantitative genetics, and plant biology. Conventional breeding experts often lack systematic training in computational technologies such as 3D reconstruction and deep learning, whereas professionals in computer vision and data science frequently lack comprehensive understanding of crop developmental biology and breeding objectives. Therefore, establishment of robust collaborative frameworks among breeding institutions, research institutes, and technology enterprises is urgently needed. Through initiatives such as joint training programs and interdisciplinary workstations, composite expertise spanning phenotypic analysis algorithms and genetic breeding theories can be systematically cultivated. Furthermore, substantive field collaboration between algorithm engineers and breeders should be encouraged to jointly address technical implementation challenges, thereby facilitating efficient translation of algorithmic innovations into practical breeding applications.

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AUTHOR CONTRIBUTIONS

N.Y. and X.F. designed the study. N.Y. wrote the manuscript. Z. Huang, Y.S., R.C., Y.C., and Y.T. contributed to literature analysis and investigation. N.Y., M.G., Y.Y., Z. Hu, C.P., and X.F. revised the manuscript. Y.H. and X.F. supervised the project and acquired funding. All authors read and approved the final version.

SUPPLEMENTAL INFORMATION

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