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Integrating 3D phenotyping and functional-structural plant models for crop ideotype breeding

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Crop ideotype breeding aims to design plant architectures that enhance yield and resource use efficiency. Accelerating this process demands a framework for assembling accurate three-dimensional (3D) architecture. This Perspective synthesizes advances in technologies and methodologies in 3D architectural phenotyping. Rapid progress has enabled translating these advances into tangible gains in breeding efficiency. To this end, we propose integrating functional-structural plant models as an overarching framework that optimizes plant architecture combinations, shifting breeding from experience-driven to predictive ideotype design. Convergence of 3D phenotyping, plant modeling and artificial intelligence holds transformative potential to accelerate breeding cycles, enhancing productivity, sustainability, and food security.

Ensuring global food security under accelerating population growth and climate change remains a critical challenge[1,2]. While sustained genetic improvements have significantly boosted crop yields over the past decades, further gains through conventional breeding strategies alone are becoming increasingly difficult to achieve[3]. Conventional breeding approaches, which depend heavily on manual phenotypic assessment and experience-based selection, are constrained by low throughput, evaluator subjectivity, and limited capacity to characterize complex plant architectures. These limitations prevent them from efficiently supporting the rapid development of high-yielding, high-quality, and stress-resilient cultivars[4]. For major crops such as rice and maize, the breeding cycle from hybridization to varietal stabilization typically spans 8–10 years, underscoring the urgent need for more efficient and predictive breeding frameworks[4,5].

Crop ideotype breeding, first proposed by Donald in 1968, offers a conceptual pathway towards rational crop improvement by optimizing plant architecture to enhance light interception, resource-use efficiency, stress tolerance, and yield potential[6]. Central to this concept is the spatial organization of plant organs, particularly canopy and root system architecture. Canopy architecture refers to the spatial arrangement and orientation of leaves, stems, and branches within a plant community, which directly governs photosynthetic efficiency and competitive interactions[7]. Root system architecture, defined by the spatial configuration and branching patterns of roots within the soil matrix, plays a complementary role in regulating water and nutrient acquisition, anchorage, and stress adaptation[8]. Together, these coordinated shoot-root architectures determine whole-plant performance and resource-use efficiency. A representative research example is the “smart canopy” ideotype in maize, in which a vertical gradient of leaf inclination angles enables efficient light distribution across canopy layers, while root architectural optimization further enhances resource capture under high-density planting conditions[9]. These coordinated traits provide important targets and acceleration strategies for the development of high-density-tolerant varieties.

Despite its conceptual appeal, the translation of ideotype theory into breeding practice has been fundamentally constrained by an

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inability to accurately quantify and manipulate plant architecture in three-dimensional (3D) space, including spatial representation, arrangement, and interactions among organs. Most current phenotyping efforts still rely on two-dimensional (2D) measurements, such as single-view RGB images, which are inherently limited in their ability to capture 3D structural information[10]. Consequently, they fail to accurately represent 3D geometry, organ orientation, spatial relationships among organs, and the within canopy 3D architectural organization. As a result, critical architectural traits such as leaf angle distribution, internode curvature, branching topology, and within-canopy light gradients are either underrepresented or entirely overlooked, leading to incomplete and potentially biased phenotypic characterization[11,12]. These limitations result in substantial information loss when representing inherently 3D structures, leading to imprecise characterization of key architectural traits and ultimately constraining the accuracy and power of genotype to phenotype (G2P) association analyses. The existing G2P gap highlights that advances in genomics have far outpaced our capacity to phenotype complex plant traits, particularly those related to spatial architecture[13].

With the rapid development of computer vision technologies and phenomics, recent advances in 3D plant phenotyping have begun to address this gap by enabling explicit quantification and reconstruction of organs, plants, and population scales[14]. In particular, deep learning-driven approaches, including point cloud-based networks, organ-level semantic and instance segmentation, and attention mechanisms for feature representation, have markedly improved the resolution and scalability of extracting complex structural traits from high-dimensional data[15]. These approaches provide direct access to spatially explicit architectural traits, capturing organ topology, geometry, orientation, and their hierarchical organization within the canopy, thereby preserving information that is inherently lost in 2D representations[16]. However, most current 3D phenotyping pipelines remain largely descriptive and static, focusing on geometric reconstruction rather than functional integration, and often treat architectural components as independent measurements. Consequently, while structural complexity can be measured with increased precision, the emergent, coordinated nature of crop ideotypes across space and time remains difficult to interpret and exploit for ideotype-driven breeding.

Functional-structural plant models (FSPMs), referred to here as plant models, represent a mechanistic modeling framework that explicitly weaves plant 3D architecture with physiological processes, enabling the simulation of growth, development, and environment-plant interactions across scales[17]. The integration of 3D phenotyping and functional-structural plant models is urgently needed at this juncture due to a convergence of technological advancements and escalating challenges in agriculture. This integrative ambition echoes longstanding calls in organismal plant biology to bridge organ- and whole-plant perspectives[18]. Over the past decade, we have reached critical tipping points in both computational capacity and imaging technologies. The emergence of high-throughput 3D imaging platforms, coupled with machine learning algorithms, has made it possible to capture plant architecture in unprecedented detail and scale. This integration was not feasible a decade ago, as the necessary imaging technologies, such as LiDAR and RGB-D sensors, lacked the resolution and field deployment capabilities required for real-world applications. Additionally, advancements in plant modeling now allow for the dynamic simulation of plant growth, enabling predictive ideotype breeding across a range of environmental conditions. These breakthroughs provide a timely opportunity to accelerate crop improvement, reducing traditionally long breeding cycles and enhancing crop resilience to climate change.

Collectively, by elucidating organ-level 3D phenotyping and their breeding practice across shoot and root systems, we highlight that integrating 3D traits, phenotyping, and plant models can transform static architectural traits into predictive and iterative ideotype designs. To construct this perspective, we conducted a comprehensive yet non-systematic literature survey using web of science and Google Scholar with keywords including “3D phenotyping”, “functional-structural plant model”, “crop ideotype”, “organ-level phenotyping”, and “predictive breeding”, with study selection guided by conceptual relevance and the authors’ interdisciplinary expertise in plant phenomics, crop modeling, and quantitative genetics. Distinct from previous work that largely focus on technological advancements or process-based growth models, we argue that these existing works, despite their contributions, lack a framework-level synthesis that explicitly couples plant architecture, function, and development. In contrast, this study focuses on the framework-level approach to understanding how plant form, function, and development emerge across hierarchical scales, thereby accelerating ideotype breeding cycle[19–21]. To facilitate readability and avoid repetitive definitions, a list of abbreviations used throughout this manuscript is provided in Supplementary Data 1.

3D complexity in crop ideotypes

The 3D architecture of plants serves as the structural foundation for aboveground functions such as light interception, air circulation, and mechanical support, while also underpinning belowground resource acquisition and anchorage. In crop ideotype research, this complexity emerges from the spatially intricate and dynamically evolving arrangement of organs, including leaves, stems, reproductive structures, and roots, as well as their interactions with light, airflow, soil resources, and neighboring organisms[9]. At the organ scale, this structural foundation manifests as geometric and structural diversity; individual organs vary not only in morphological dimensions but also in spatial configuration, specifically in traits such as torsion, curvature, planarity, and orientation. Importantly, these organs are not randomly arranged but organized into coordinated 3D structures governed by phyllotactic patterns, internode elongation, radial expansion, and vertical stratification, while root systems exhibit their own hierarchical branching architectures shaped by gravitropism, hydrotropism, and soil resource gradients[22]. Such directional and multi-domain organization shapes branching patterns, topology, and canopy stratification aboveground, and root foraging patterns and soil exploration belowground, thereby jointly regulating resource capture efficiency and system-level performance[23]. Through multi-scale coupling, subtle variations in individual leaves or branches can propagate upward to influence overall canopy morphology and function, highlighting the tightly integrated regulation of plant performance across scales[15]. Capturing this 3D structural complexity is therefore essential for defining ideotype architectures, yet remains challenging due to the nonlinear, highly variable, and developmentally plastic nature of plant form[24].

Compared to the geometric and topological attributes of individual plants, the ideotype for population level exhibits higher-order emergent 3D characteristics. The complexity of population level arises not only from the sum of individual plant architectures but also from their spatial interactions, including inter-plant shading, competition for light and space, root zone overlap, and belowground competition for water and nutrients, as well as airflow modulation within the canopy[25]. Key features of population-level 3D complexity include row and plant spacing, planting density, and sowing pattern, which collectively shape canopy porosity, vertical stratification, and light penetration profiles, while also influencing soil resource depletion patterns and root system spatial segregation[26]. Moreover, population architecture is dynamically modulated by plant plasticity above and below ground. As individual plants adjust leaf angles, elongate stems, or reconfigure root growth in response to neighboring competition, the overall canopy-root system architecture continuously reorganizes, producing emergent properties that cannot be predicted from individual plants alone[27]. Thus, 3D complexity at the population level is not

merely the cumulative sum of individual structures but a macroscopic system- level trait shaped by coordinated shoot/root interactions, spatial competition, and resource redistribution.

Collectively, the 3D complexity of a crop ideotype is an emergent, cross-scale property that can't be reduced to individual architectural traits. It arises from the coupling between developmental programs, structural organization, and environment-driven plasticity, operating across organ, plant, and population levels. This inherently dynamic nature demands a shift from static trait descriptions to integrated representations of structure-function relationships across scales. Such a framework is essential for linking 3D architecture to core agronomic functions, including resource capture, mechanical stability, and yield formation.

3D crop phenotyping

The rapid development of sensing technologies and computational methods has enabled high-resolution reconstruction of crop architecture in 3D space. Importantly, contemporary 3D phenotyping is no longer defined by single sensing modalities, but by integrated pipelines that combine data acquisition, reconstruction, and trait extraction across multiple scales[28,29].

As summarized in Supplementary Data 2, existing sensing technologies for plant 3D phenotyping involve inherent trade-offs among resolution, throughput, cost, and operational constraints. LiDAR-based approaches generate high-density point clouds that enable precise quantification of canopy geometry and structural heterogeneity, particularly under dense field conditions[30,31]. However, their deployment is often constrained by high equipment costs, sensitivity to scanning angle and occlusion, and substantial computational requirements for point cloud processing[32]. In contrast, RGB-D imaging provides a portable and cost-effective solution for depth-aware reconstruction, supporting high-throughput field phenotyping, yet its performance is limited by restricted sensing range, susceptibility to ambient lighting conditions, and reduced accuracy in complex outdoor environments[33]. Multi-view stereo (MVS) methods reconstruct 3D structure from overlapping RGB images, offering flexible and scalable alternatives for organ-level and plot-level analysis[34]. Nevertheless, MVS reconstruction depends heavily on image quality and viewpoint coverage, and often struggles with textureless surfaces, dense canopies, and wind-induced motion, which can introduce reconstruction artifacts[35]. UAV-based platforms further extend spatial coverage and throughput, particularly at the canopy scale, but typically sacrifice fine structural resolution and introduce additional challenges in data processing and environmental sensitivity.

Belowground sensing technologies also involve a distinct set of trade-offs. High-fidelity, lab-based methods such as X-ray computed tomography, MRI, and neutron tomography achieve superior resolution and structural detail, as indicated by their high ratings in resolution and data complexity, but are limited by low throughput, high cost, and restricted spatial scale[36–39]. In contrast, field-deployable approaches such as minirhizotron imaging, electrical methods, and ground-penetrating radar (GPR) offer improved scalability and moderate throughput, albeit with reduced resolution and varying data processing demands.

Beyond sensors, imaging platforms such as MVS-Pheno leverage these advantages to generate high-fidelity textured models from commodity RGB cameras, although their performance can degrade under field conditions where illumination variability and occlusion are difficult to control[40]. Moreover, data processing approaches such as attention mechanism-driven organ segmentation, have substantially improved the extraction of structural traits from complex 3D data[41–43]. As a result, 3D phenotyping can now capture detailed architectural descriptors, including organ geometry, spatial orientation, hierarchical organization, and population-level structural patterns.

Shoot systems. 3D leaf phenotyping has evolved from simple planar measurements of leaf length, width, and area toward an integrated characterization of the full spatial deployment of foliage, in which leaf orientation, self-twist, and curling are jointly resolved in 3D space[44]. This progression can be understood as a shift from size-centric traits to surface morphological and orientation-based descriptors, each enabled by distinct sensor technologies (Supplementary Data 3). Early RGB and LiDAR systems reliably capture organ-level dimensions such as leaf length, width, and area, which determine light interception potential, vertical canopy coverage, and internal shading[45]. However, leaves are intrinsically non-planar, with 3D traits such as leaf planeness, self-twist, and margin amplitude jointly quantifying curvature and edge complexity, thereby modulating light scattering, absorption uniformity, and boundary-layer airflow[16]. These traits became measurable with the integration of RGB-D, terrestrial laser scanning (TLS), and multi-view stereo (MVS) across sorghum and maize[16]. In parallel, orientation-related traits such as inclination angle, azimuth, included angles between adjacent leaves, and petiole inclination, govern the vertical and radial deployment of foliage, shaping canopy openness, light penetration, and mutual shading[46]. Moreover, LiDAR and 3D scanning now enable high-throughput quantification of these traits under field conditions across maize, rice, tomato, beet, peanut, and other crops. Enabled by advances in RGB-D, LiDAR, multi-view reconstruction, and spectral sensing, the full set of size, surface, and orientation traits can be systematically phenotyped in diverse species, including maize, sorghum, rice, wheat, and tomato[47,48], transforming leaf architecture from a list of static measurements into a dynamic, functionally interpretable 3D trait space.

Stem 3D phenotyping practice is also gradually moving beyond traditional measurements of length or diameter toward a systematic characterization of stem spatial architecture, mechanical support, and coordination at the population level[49]. Current studies focus on key 3D traits such as internode distance, branch/tiller number and angle. Such traits collectively determine plant height, canopy stratification, spatial occupancy, and lodging resistance, while also playing a key role in regulating light interception, ventilation, and competitive interactions[50]. With the aid of multi-sensor acquisition and reconstruction technologies, stem architecture can now be captured non-destructively and at high-throughput under field conditions, enabling continuous quantification from individual plants to entire canopies[51–54]. Technically, this progression is exemplified by LiDAR-based approaches such as the Stratified, Clustered, And Growing-based (SCAG) algorithm, which segments high-density point clouds to isolate individual plants, hierarchically identifies stems and branches, and derives 3D branch angles from growth vectors, thereby enabling comparative analysis across 152 soybean cultivars[55]. Such datasets further enable the derivation of emergent, heritable traits such as ratios of branch angle to plant height or stem length, thereby linking stem architectural features to density tolerance and agronomic performance[34]. Complementing LiDAR, RGB-D imaging has emerged as a cost-effective and portable alternative, extending 3D phenotyping to more accessible field applications. Synchronized RGB-D data can be registered and skeletonized to reconstruct stem geometry with high accuracy, as demonstrated in maize, where stem diameter estimation achieved a MAPE of 3.01% ($R^2 = 0.96$)[56]. In parallel, consumer-grade RGB-D sensors mounted on mobile platforms enable dynamic, in situ acquisition across diverse crops, including maize, tobacco, and cotton, showing strong agreement with manual measurements[57]. This practice-oriented approach to stem 3D phenotyping provides refined structural variables for dissecting structure-function relationships and offers a quantitative foundation for ideotype design, lodging-resistant breeding, and architectural optimization.

Reproductive organ 3D phenotyping has likewise advanced from simple measurements of length or count toward a structural understanding of how ears, panicles, and other inflorescences occupy space,

intercept light, and contribute to sink capacity[58,59]. Enabled by diverse imaging modalities such as RGB, RGB-D, TLS, LiDAR, multi-view stereo, and X-ray CT, these traits can now be captured non-destructively across major cereals, including sorghum, maize, and rice[21,36]. Key 3D traits, including ear number, ear height, ear volume, panicle depth, and panicle length, encode essential information on reproductive structure size, spatial exposure, and potential yield formation[33]. Ear number and ear volume directly reflect yield component count and sink strength, while ear height determines agronomic adaptability and lodging risk by influencing the vertical position of reproductive organs within the canopy[60,61]. In parallel, panicle depth and panicle length describe the internal compactness, branching display, and grain exposure of inflorescences, which together shape micro-light environments, pollination effectiveness, and ultimate yield potential[62].

Root systems. Root 3D phenotyping has long been constrained by the physical inaccessibility of underground structures, limiting trait analysis to rudimentary measurements of length or biomass after destructive washing[63,64]. Recent advances have witnessed a methodological shift with integrated advances in X-ray computed tomography (CT), terahertz imaging, electrical capacitance, structure from motion (SfM), and fringe projection profilometry (FPP) now enabling non-destructive, high-throughput quantification of multiple root architectural traits (Supplementary Data 3). Early techniques, such as grayscale imaging combined with SfM, reliably captured root length and surface area in transparent media, but could not resolve angular deployment or volumetric allocation[65]. The addition of X-ray CT and terahertz imaging overcame this by penetrating opaque soils, delivering precise measurements of root diameter, growth angle, volume, and surface area across species including maize, rice, wheat, sugar beet, and Arabidopsis[66–70]. Recent integration of automated reconstruction pipelines with machine-learning segmentation has made spatially explicit 3D root phenotyping scalable, allowing systematic mapping of depth allocation, angular distribution and root-soil interactions[71,72]. Consequently, root systems are no longer treated as a black box but as a quantifiable functional module of whole-plant architecture, directly supporting breeding for water- and nutrient-use efficiency, stress resilience, and yield optimization.

3D crop breeding practices

Despite the successful development of ideotype cultivars with convergent 3D architectures in crops such as wheat and rice, these gains have historically relied on experience-driven, multigenerational selection that is inherently slow and low-throughput[73,74]. More recently, 3D phenotyping has begun to be incorporated into breeding programs to support ideotype-oriented selection and genetic analysis[75]. The studies summarized in Supplementary Data 4 illustrate not only the diversity of 3D phenotypes now accessible to genetic analysis, but also the tangible progress toward identifying candidate genes and QTLs that underpin ideotype variation.

In modern crop breeding, 3D leaf phenotyping has become a core technology for constructing ideotype architectures, enabling in-depth quantitative evaluation of leaf geometry and spatial configuration. For example, McCormick et al.[76]. used depth images to reconstruct 3D sorghum plants and identified QTLs on Chr3 and Chr6 that control leaf inclination angle, directly demonstrating how 3D reconstruction can uncover genetic determinants of leaf orientation. Additionally, Liu et al.[77]. Performed GWAS on 495 maize inbred lines using 3D-derived leaf angle and leaf area index, pinpointing several novel SNPs associated with leaf inclination, thereby enabling marker-assisted selection for more erect canopies. Moreover, 3D phenotyping of rice leaf angle and tiller angle has provided key support for the high-precision localization of related genetic loci and candidate genes[78].

The stem serves as the primary structural axis that supports plant architecture and facilitates the transport of water, nutrients, and assimilates, thereby playing a central role in crop growth and development. High-precision 3D phenotyping of stem architecture holds substantial genetic and breeding value, as it enables a deeper understanding of plant height dynamics and provides critical insights for enhancing lodging resistance. In sorghum research, voxel carving technology, combined with GWAS and QTL analysis, has successfully identified core genetic loci regulating plant height, such as *Dwarf 3*, *Dwarf 2*[76]. Fei et al.[79] combined UAV-based 3D canopy models with GWAS in wheat, detecting stable QTLs for plant height components (e.g., internode length and peduncle length) that were previously obscured by conventional 2D measurements. These research findings not only enhance the genetic understanding of stem spatial development mechanisms but also provide scientific digital tools for constructing ideal plant architectures with improved lodging resistance and stable yields.

In the reproductive stage, the focus subsequently shifts to the spatial posture and orientation of the ear/panicle/spike, traits that are tightly associated with final yield[80]. Using a high-throughput phenotyping system based on panoramic surface imaging, Wang et al.[81] quantified 20 ear-related traits, including 3D shape plus color traits, for 407 inbred lines of maize and identified 58 candidate genes, such as *Zm00001d051328* controlling ear circumference and *zma-MIR159f* regulating ear shape. Importantly, this study integrated 3D ear volume and width-length ratio into GWAS, revealing that ear volume QTLs colocalized with known yield-related genes, demonstrating how 3D traits can refine genetic mapping of sink strength. Additionally, Shen et al.[82]. performed QTL mapping for spike compactness and awn length using 3D-derived traits, identifying TaSPI-A1 as a key regulator of spike morphology, an example of how 3D phenotyping directly enables gene discovery for inflorescence architecture. A GWAS analysis revealed the genetic architecture underlying wheat spike morphology, providing a valuable resource for the molecular design of spike traits to support future wheat breeding.

The evolution of 3D root phenotyping is bringing belowground traits from invisibility into the realm of quantification and genetic improvement, allowing these structures to be integrated into breeding pipelines with explicit spatial and architectural resolution. For example, by quantifying root system topology and convex hull volume in rice using 3D in situ imaging platforms, Topp et al.[64] extracted root angle, depth, and branching intensity, and found that QTLs for root convex hull volume co-localized with regions influencing drought tolerance, providing a direct link between 3D root architecture and stress adaptation. Li et al.[83] deployed DIRT/3D, the first field-ready 3D root phenotyping system, to quantify large-scale maize root architecture, integrating traits such as root depth and surface area to resolve genetic variation and identify key regulatory genes, such as *ZmETR3* (*GRMZM2G075368*). In wheat, root length, one of the core linear structural traits, has been successfully associated with *TraesCS2A01G516200* through 3D reconstruction coupled with GWAS[84]. Moreover, complex spatial traits such as root angle and root volume, which reflect directional distribution and resource-acquisition capacity, have enabled the discovery of 23 *SNPs* and 29 candidate genes in cassava, providing molecular targets for optimizing root system architecture[85].

At the whole-plant level, Wu et al.[34] used the MVS-Pheno platform to perform multi-view 3D reconstruction on 495 maize inbred lines and defined 44 structural traits, encompassing basic morphology, projected-area traits, leaf-related traits, plant-structure dispersion traits, and volume-related traits. A GWAS of 17 traits identified 40 SNP/QTLs in total, and notably revealed that convex-hull volume is significantly associated with the density-tolerance gene *GRMZM2G072274*, offering valuable insights for improving high-density-tolerant maize breeding and production[34,86]. This whole-plant 3D approach also detected QTLs for plant shape descriptors (e.g., eigen-values of the 3D point cloud covariance matrix), which were not

accessible through conventional trait lists, illustrating the power of comprehensive 3D phenotyping for discovering novel genetic determinants of overall plant architecture[34]. This shift from organ-level to whole-plant 3D genetics improves selection precision and supports development of varieties suited to high-density planting and stress environments.

Collectively, despite rapid advances in 3D crop phenotyping, most studies still concentrate on extracting and validating 3D structural traits; only a few have been translated into routine selection decisions/deployment in breeding pipelines. Nevertheless, the examples above demonstrate that when 3D traits are integrated with GWAS, QTL mapping, or genomic selection, they can uncover genetic regions that remain invisible to 2D methods, thereby accelerating the discovery of alleles controlling organ geometry, orientation, and canopy-level organization. 3D traits can now be measured and genetically dissected, and they are increasingly applicable in GWAS, QTL mapping, and marker-assisted selection, paving the way for spatial-architecture-informed breeding.

Ideotype design guided by plant models

Despite 3D phenotyping has substantially expanded the portfolio of measurable architectural traits, a fundamental gap persists between the description of plant structure and the prediction of its functional consequences in target environments. This gap, extensively discussed by Martre et al.[87], arises from several intrinsic limitations of purely observational phenotyping. Even the most comprehensive 3D phenotypic datasets remain inherently correlative, documenting the state of a plant under a specific set of environmental and management conditions, but they lack the mechanistic basis to forecast how that architecture will perform in a different G×E×M context. Additionally, 3D phenotyping heavily relies on AI techniques, such as deep learning-based organ segmentation, whose segmentation accuracy may drop dramatically when applied to novel cultivars[41]. For example, in cultivars with high tillering capacity and dense leaf distributions, the PointNet model maintained high classification accuracies of 89.06% and 91.16%, but when transferred to a cultivar with an extreme leaf-to-panicle ratio, accuracy dropped nearly 40% because of severe class imbalance[88]. Collectively, traits measured in isolation do not act independently; without a process-based framework to integrate these interactions, their emergent contributions to whole-plant function and agronomic performance remain largely unrealized.

Plant models offer a principled solution by explicitly coupling structure to function through process-based representations of plant growth[19,20]. By coupling 3D architecture with modules that describe light distribution, photosynthesis, transpiration, carbon and nitrogen allocation, and developmental dynamics, plant models integrate discrete structural variables into meaningful input parameters within process-based models, effectively compensating for several limitations of 3D phenotyping[20,89]. For example, simulations in wheat have demonstrated how coordinated variation in leaf angle distribution, internode length, and tillering pattern reshapes canopy light interception and photosynthetic efficiency under contrasting nitrogen regimes and planting densities, thereby identifying ideotypes optimized for specific production scenarios[90]. More broadly, by embedding physiological constraints and enabling "what-if" experimentation, plant models transform high-dimensional phenotypic descriptions into predictive, testable hypotheses, providing a mechanistic foundation for ideotype-oriented breeding. Nevertheless, plant models are not infallible. Their main limitations lie in that accurate simulations require large numbers of measurable physiological and structural parameters, yet their acquisition is often time-consuming and constrained by experimental conditions[20]. Consequently, in practical breeding pipelines, neither plant models nor 3D phenotyping alone can independently bridge the gap from genotype to field performance.

Thus, the most effective strategy is to integrate them into a synergistic analytical framework, thereby establishing a complementary toolchain for ideotype-oriented breeding (Fig. 1). High-

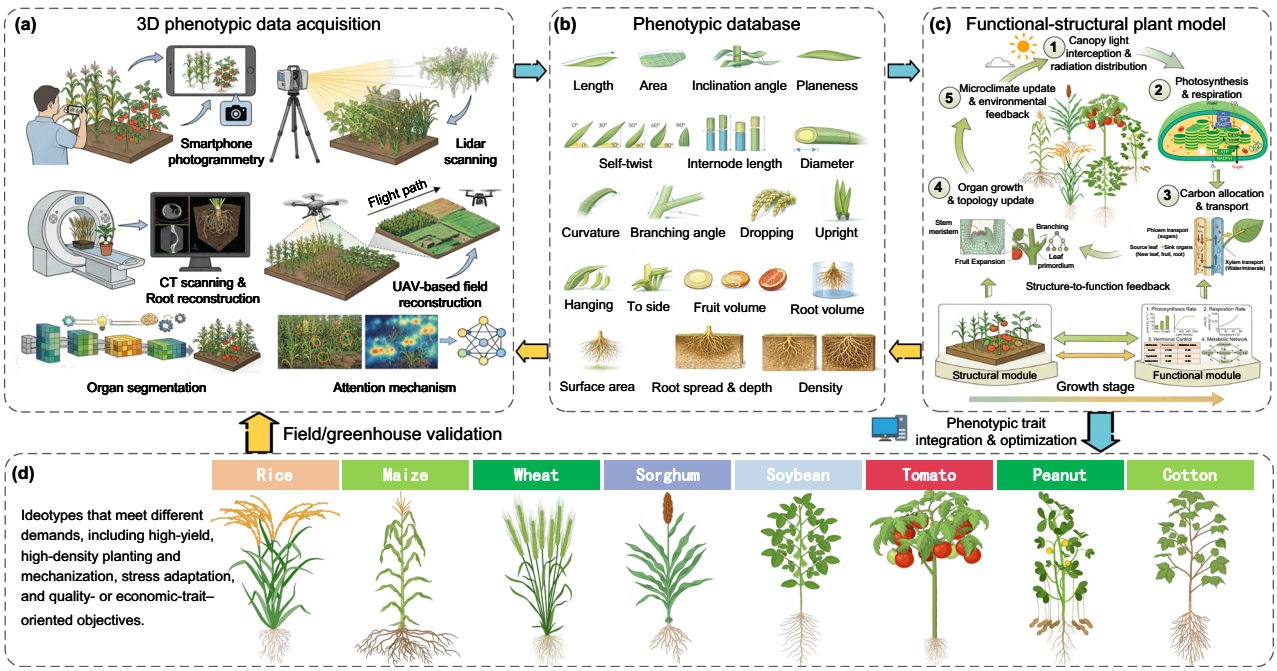

Fig. 1 | A framework demonstrates how integrating 3D crop phenotyping with plant models enables ideotype-design breeding. a Multi-source 3D phenotyping technologies across shoot and root system, including imagery acquisition, 3D reconstruction, attention mechanism-based organ segmentation; **b** standardized architectural trait extraction and database construction; **c** integration of architectural traits into plant models for optimizing the simulation of light interception, photosynthesis, and biomass allocation, etc.; **d** iterative validation and breeding applications. Figure created in BioRender. Quan, Wei. (2026) https://BioRender.com/g5b4cp8.

throughput 3D phenotyping, which encompasses smartphone photography, LiDAR, CT scanning with root reconstruction, organ segmentation, and field or greenhouse validation, first generates standardized architectural trait databases that capture a rich spectrum of traits such as inclination angle, planeness, self-twist, branching angle, root volume, etc. These databases provide population-level variation maps and empirical foundations for model parameterization and uncertainty estimation. Plant models then translate these architectural parameters into dynamic functional outputs by simulating light distribution, leaf area index, and canopy porosity, photosynthesis and respiration, carbon allocation and transport, while also simulating organ growth and topology update, and the iterative structure-to-function feedback loops during crop growth and development. Finally, key structure-function bridging indicators predicted by the models are fed back into phenotyping platforms to guide subsequent temporal measurements and field validation, forming an iterative loop of parameterization, prediction, and validation. Within this complementary framework, the process-based simulation capacity of plant models, combined with the scalability of high-throughput structural measurements, transforms ideotype design from a descriptive concept into testable and verifiable breeding targets, tailored to meet diverse demands such as high yield, high-density planting and mechanization, stress adaptation, and quality- or economic-trait-oriented objectives across major crops, including rice, maize, wheat, sorghum, soybean, tomato, peanut, and cotton.

Recent work has demonstrated the practical integration of high-throughput 3D phenotyping with plant models in many crops (Supplementary Data 5). Zhang et al.[91] built a morphology-based 3D rice model that assimilates architectural traits from indoor and field phenotyping, achieving $R^2 = 0.86$ for leaf area index simulation while visualizing growth-stage dynamics and directly linking structural databases to functional outputs. Moving from reconstruction to automated pipeline generation, Hadadi et al.[92] developed a LiDAR-based procedural pipeline that automatically generates organ-level maize architectures as explicit inputs to FSPMs; coupled with evolutionary optimization, it identified canopy designs that boost light interception and biomass under high-density planting. Advancing to full functional-structural integration, Blanc et al.[93] created WALTer, a plant model coupling 3D wheat architecture with light and carbon-nitrogen metabolism. Simulating binary mixtures of wheat cultivars differing in leaf dimensions, insertion angle, tillering, and height, they found that mixing contrasting leaf dimensions and tillering capability significantly enhanced stand productivity, whereas varying insertion angle alone had marginal effects, demonstrating that embedding detailed 3D architectural data into plant models enable quantitative prediction of mixture performance and provides simulation-based assembly rules for designing productive wheat cultivar mixtures without exhaustive field trials. These examples demonstrate that the iterative feedback between 3D structural trait databases and plant models transforms ideotype design from a descriptive concept into a testable, data-driven breeding strategy.

Current challenges and future prospects

Despite their conceptual appeal, integrative 3D trait-modeling frameworks remain challenges to deploy in operational breeding. For AI-driven 3D phenotyping, deep learning is limited by costly, expertise-intensive annotation, weak cross-domain generalization, and substantial computational demands for high-resolution data[41]. For plant models, mechanistic fidelity incurs practical costs that parameter-rich models are difficult to estimate and often rely on controlled conditions and root systems are frequently simplified or omitted, limiting relevance in resource-limited environments[17]. Additionally, at the breeding scale, throughput, resolution, and economics remain misaligned, with field-based 3D acquisition slow relative to trial size, occlusion in dense canopies biasing reconstruction and trait estimation, and cost-benefit gains over conventional selection rarely quantified[94].

Achieving this integration requires a key transition from exhaustive observation to predictive reconstruction of plant architecture through hybrid sensing-modeling frameworks[18,95]. Generative AI may bridge data gaps by synthesizing biologically plausible 3D plant architectures and inferring missing structural and developmental information, enabling a shift from measurement-driven to model-assisted phenotyping[10,96]. For example, diffusion-guided 3D generation frameworks have successfully reconstructed complete 3D plant geometries from limited partial observations, recovering hidden internal structures that are not directly visible[97]. Moreover, translating such sparse but informative trait panels into actionable predictions of whole-plant performance will require plant models that can operate reliably on incomplete or inferred structural data. Currently, most plant models rely on detailed, organ-level parameterization and high-resolution environmental inputs, making them ill-suited for the high-throughput, population-scale prediction demanded by breeding[17]. Consequently, development of lightweight, data-assimilating and iterative plant models will be essential to bridge the gap between 3D phenotyping and operational breeding decisions. Additionally, high-resolution architectural traits that resolve novel QTLs in research settings can't be deployed as routine selection indices across entire breeding populations, confining 3D ideotype breeding largely to proof-of-concept studies[9]. Overcoming this limitation will require not only faster acquisition and reconstruction algorithms, but also a strategic rethinking of 3D architectural sampling, such as shifting from exhaustive organ-level reconstruction per individual to sparse yet informative trait panels.

Concluding remarks

The pursuit of superior crop ideotypes rests on understanding how architectural traits integrate across scales to determine whole-plant performance as a dynamic, three-dimensional system. This Perspective proposes that the integration of 3D phenotyping with plant models enables a system-level analysis of crop ideotypes. In this synergistic framework, precise 3D phenotypic data parameterize mechanistic models that simulate how plant architecture dynamically interacts with light, water, and nutrient resources. Such models, in turn, support the prediction, evaluation, and optimization for ideotypes of crops tailored to specific environments, generating targeted breeding strategies that are subsequently validated and iteratively refined through further phenotyping. This convergence is reshaping crop breeding, shifting the paradigm from empirical, trial-and-error selection to predictive ideotype design. It enables the in silico exploration of a wide range of genetic and environmental scenarios, accelerating the development of varieties for enhancing yield, resource use efficiency, and stress resilience.

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Author contributions

Y.S. conceived and supervised the study. Q.W. collected literature, performed data analysis, and drafted the manuscript. X.Z. collected literature and contributed to the draft. J.Y. and S.L. contributed to the literature collection and making tables. H.Y. and X.L. contributed to the draft. A.J. and M.H. improved the manuscript. Q.W., Y.S., and H.H. finalized the manuscript. All authors read and approved of the final manuscript.

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Competing interests

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Additional information

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