

Review

Genomics, phenomics, and machine learning in transforming plant research: Advancements and challenges

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Received 7 July 2023; Accepted 12 September 2023; Available online 13 February 2024

ABSTRACT

Advances in gene editing and natural genetic variability present significant opportunities to generate novel alleles and select natural sources of genetic variation for horticulture crop improvement. The genetic improvement of crops to enhance their resilience to abiotic stresses and new pests due to climate change is essential for future food security. The field of genomics has made significant strides over the past few decades, enabling us to sequence and analyze entire genomes. However, understanding the complex relationship between genes and their expression in phenotypes - the observable characteristics of an organism - requires a deeper understanding of phenomics. Phenomics seeks to link genetic information with biological processes and environmental factors to better understand complex traits and diseases. Recent breakthroughs in this field include the development of advanced imaging technologies, artificial intelligence algorithms, and large-scale data analysis techniques. These tools have enabled us to explore the relationships between genotype, phenotype, and environment in unprecedented detail. This review explores the importance of understanding the complex relationship between genes and their expression in phenotypes. Integration of genomics with efficient high throughput plant phenotyping as well as the potential of machine learning approaches for genomic and phenomics trait discovery.

Keywords: Plant; Phenomics; Traits; Horticulture; Breeding; Crop improvement; Machine learning

1. Introduction

Meeting the burgeoning demands of a global population, projected to reach 8.3 billion by 2030 and 10 billion by 2050, poses significant challenges in ensuring adequate food, energy, and water resources. Vital agricultural efforts append on augmenting crop yields by 2.4% annually, a pace that currently lags at 1.3% growth. Up to 40% of the world's grain cultivation area has stagnant yields (Rose and Chilvers, 2018; Watson et al., 2018). The task of providing adequate nutrition for a rapidly expanding global population underscores the urgency to enhance crop yields and ensure food security. On the other hand, as the global population

burgeons resources become scarcer and weather patterns turn more unpredictable, agriculture faces a tough task in this century. The challenge is to develop crops that can produce a lot of food and handle stress, ensuring that we have enough to eat (Zia et al., 2023). Advances in genome science, speed breeding, and omics technologies, despite challenges, hold the key to addressing these pressing concerns and fostering sustainable agricultural practices (Altaf et al., 2023).

Traditional breeding methods have yielded crops with improved nutrition and output, yet the incremental growth of major crop yields, including rice, wheat, and maize, falls short of future needs (Park et al., 2019; Hinterberger et al., 2022; Mahmood

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Peer review under responsibility of Chinese Society of Horticultural Science (CSHS) and Institute of Vegetables and Flowers (IVF), Chinese Academy of Agricultural Sciences (CAAS)

<https://doi.org/10.1016/j.hpj.2023.09.005>

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et al., 2023). Overcoming the constraint of protracted crop production cycles, a breakthrough known as “speed breeding” has hastened research by shortening breeding cycles (SB). Genome science has revolutionized the precise examination of desirable traits, expanding beyond model organisms. Employing next-generation resequencing techniques has expedited genome reading for numerous crop plants at a reduced cost (Hussain et al., 2023). While genome editing holds promise for quicker crop development with minimal off-target effects, it still necessitates time-consuming tissue culture and specialized containment facilities for CRISPR-mediated genetic manipulation (Chen et al., 2019; Wang et al. 2023; Yu et al., 2024). The comprehensive realm of omics encompasses the analysis of biological data derived from genomes, transcriptomes, proteomes, and metabolomes, among other facets. Various omic technologies, such as gene sequencing, transcription profiling, metabolite and protein analysis, offer insights into the intricate mechanisms underlying seed germination, abiotic and biotic stressors, and systemic gene and metabolite activity. The integration of these approaches is instrumental in unraveling the intricacies of food insecurity and aiding its mitigation (Barah et al., 2021; Altaf et al., 2023; Zhang et al., 2023). Plants are frequently subjected to high-density single nucleotide polymorphism (SNP) genotyping in order to study genetic variation and help trait-driven efforts to clone and comprehend certain genes (Sedeek et al., 2019). Genomic techniques allowed for the prediction of genes' type, location, function, and interactions. However, next-generation phenotyping technologies must be used to validate gene predictions for them to be accurate. The accuracy with which the relevant Quantitative Trait Loci (QTLs) or chromosomal areas are located, and their effects are reliably assessed to establish the phenotype–genotype relationship depends on the precision with which the phenotyping data are recorded (Tuberosa, 2012; Großkinsky et al., 2015).

The knowledge gap between the genotype-to-phenotype is one of the most significant issues in contemporary plant breeding (Großkinsky et al., 2015). While genomics research has provided a wealth of knowledge on the genetic makeup of different plant species, plant phenotyping is now limited by sequencing techniques and the data they provide (Yang et al., 2013; Diaz-Garcia et al., 2016). Conventional plant phenotyping methods have a relatively low throughput, which precludes thorough study of features within a single plant and across cultivars. These methods rely on manual measurement of chosen attributes from a small sample of plants (Furbank and Tester, 2011). In recent years, the advancement of available genomic databases and phenotyping databases has not only facilitated the identification of gene function, new genes/QTL, and the analysis of genetic architecture for complex traits, but it has also led to an increase in the genetic gain for traits with low heritability (Pratap et al., 2019). Furthermore, there has been significant progress in the potential scope and throughput of plant phenotyping studies through the adoption of image-based approaches. Over the past five years, various factors such as the introduction of new imaging technologies, implementation of robotic and conveyor belt systems in greenhouses, and the utilization of ground-based and aerial imaging platforms in fields have collectively contributed to enhanced monitoring of plants and crops (Fahlgren et al., 2015).

However, a critical prerequisite for the successful utilization of image-based phenotyping technologies is the accurate and reliable conversion of these images into precise phenotypic measures. For these instruments to be versatile and applicable across diverse scientific domains, they must possess the capability to measure a wide array of phenotypes. Addressing the challenge of predicting phenotypes using both genomic and environmental information is of utmost importance. In this context, machine learning methods have emerged as potent tools capable of making precise predictions from the extensive and intricate biological data. In essence, this review stands as a bridge connecting the realms of research and education. We can access novel approaches to enhance their trait detection endeavors and can gain insights into the burgeoning landscape of machine learning's impact on trait discovery. The convergence of machine learning, genomics, and phenotyping underscores a field that is rapidly maturing and offering exciting avenues for unraveling the intricacies of genetic traits.

2. Plant genomics and phenomics

Plant phenomics occupies a crucial position at the intersection of genetics, phenotypic traits, and machine learning, as highlighted in this paper. This dynamic field involves the systematic measurement and analysis of plant and animal traits to unravel the intricate interplay between genetic makeup and environmental influences. Employing cutting-edge technologies such as high-throughput imaging, sensor networks, and data analytics, plant phenomics enables the holistic characterization of diverse phenotypic attributes (Li et al., 2021; Interdisciplinary Plant Science Consortium, 2023). This comprehensive approach offers valuable insights into plant growth, development, and responses to varying conditions. By integrating genetics, phenomics, and machine learning, we can decipher complex genotype–phenotype relationships, facilitating the optimization of desired traits (Yang et al., 2013, 2020; Singh et al., 2023). This synthesis of disciplines paves the way for advancements in crop breeding, ensuring the creation of resilient plant varieties with improved yields, stress tolerance, and sustainability in the face of evolving agricultural challenges (Watson et al., 2018; Park et al., 2019).

Genomics has revolutionized agriculture and horticulture fields by providing new insights into the genetic basis of important crop traits, helping to address some of the key challenges facing agriculture and horticulture sectors in the 21st century. Genomics has played a pivotal role in advancing the development of novel plant selections, leading to improved yield, disease resistance, drought tolerance, and nutritional quality in crops (Li et al., 2021; Ferrão et al., 2023). These findings serve as a foundation for creating new crop varieties using traditional breeding methods, as well as modern techniques like genetic engineering and gene editing. As a result, the application of genomics in agriculture holds great promise for enhancing food security and sustainability in the face of evolving challenges (Sedeek et al., 2019; Aguilar et al., 2020; Ali et al., 2020; Gao, 2021). Genomics can assist to develop more sustainable agricultural practices, by enabling the breeding of crops that require less water, fertilizer, or pesticides, and by identifying plant–microbe interactions that can enhance soil health and nutrient cycling (Watson et al., 2018;

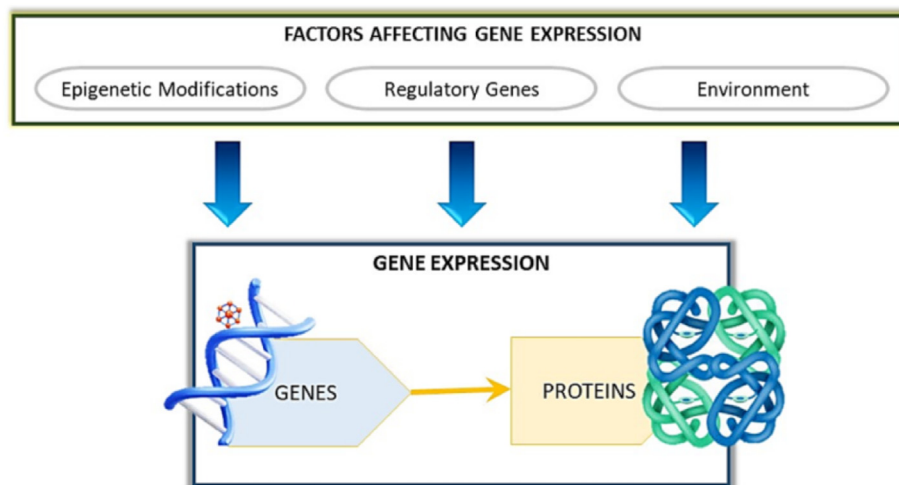


Fig. 1 Major factors affecting the gene expression

Bailey-Serres et al., 2019; Sedeek et al., 2019; He and Zhao, 2020; Gao, 2021; Mahmood et al., 2023). The increasing adoption of gene editing techniques and continued exploration of natural genetic diversity offer exciting opportunities to create new alleles and select favorable genetic variations for crop improvement (Huang and Han, 2014; Barrangou and Doudna, 2016; Nunes-Nesi et al., 2016; Schiml and Puchta, 2016).

The combination of genomics and phenomics has the potential to enhance breeding practices and create crop varieties that are resilient to changing climates and adaptable to modern breeding requirements. The relationship between genes and their expression in plant phenotypes is complex and multifaceted (Interdisciplinary Plant Science Consortium, 2023). Genes contain the instructions for building proteins, which in turn determine the traits or characteristics that are expressed in plants (Ferrão et al., 2023). However, the expression of genes is not always straightforward or predictable and can be influenced by a variety of factors (Fig. 1).

The environment plays a crucial role in influencing gene expression in plants. With exposure to various environmental conditions like temperature, light, water availability, soil nutrients, pests, and pathogens, the plant's genetics interact dynamically. These interactions determine the activation or suppression of specific genes and regulate the extent of their expression. The intricate interplay between the plant's genetic makeup and the surrounding environment significantly impacts its growth, development, and responses to external stimuli. (Bochner, 2003; Nordborg and Weigel, 2008; Ghanem et al., 2015; Singh et al., 2022). Another important factor that can influence gene expression is epigenetic modifications. Epigenetic modifications are changes to the structure of DNA or the proteins that interact with it, which can affect how genes are expressed. For example, DNA methylation and histone modifications can silence or activate certain genes, depending on the specific modifications that occur. Also, gene expression in plants is influenced by interactions between different genes. Some genes act as regulators, turning others on or off based on the plant's development or environmental conditions. These interactions

lead to complex traits controlled by multiple genes. Then the relationship between genes and their expression is dynamic and influenced by genetics, environment, and epigenetics. Understanding these factors is key to improving crop yields and sustainability in agriculture (Pfluger and Wagner, 2007; He et al., 2011; Morrell et al., 2011; Yin et al., 2017; Chen et al., 2019; Pieruschka and Schurr, 2022; Xiao et al., 2022).

3. Plant phenotyping technology

3.1. The key technology to unlock the potential of plant system

The integration of agronomy, plant ecology, and genetics through plant phenotyping has emerged as a powerful tool for advancing agricultural research. However, traditional field-based evaluation of plant phenotypes can be time-consuming and inefficient (Li et al., 2021). To address this challenge, High-throughput field phenotyping (HTP) has been developed integrating advanced sensing technologies and data processing techniques to enhance efficiency, while also demonstrating non-destructive characteristics and high reproducibility (Neumann et al., 2015).

HTP systems utilize mobile platforms and advanced sensors to autonomously gather data in the field, reducing the need for human intervention (Neumann et al., 2015; Kirci et al., 2022). Recent advancements in image processing have propelled sensor-based crop monitoring into widespread use, overcoming previous limitations in phenotyping research. Despite these improvements, field phenotyping remains a critical bottleneck for agricultural genetic advancements (Roth et al., 2020). Ground and Aerial HTP Systems have been developed, each with distinct advantages. Ground systems offer higher payload capacity for heavier sensors and equipment, ensuring superior data quality by controlling environmental variables and minimizing susceptibility to wind. Aerial systems, on the other hand, offer enhanced efficiency and coverage, allowing for broader data collection. Current trends emphasize the shift towards autonomous phenotyping robots for data collection, replacing earlier human-

operated tractors and pushcarts (Araus and Cairns, 2014; Li et al., 2021). Sensors for Phenotypic Measurement offer diverse capabilities. Conventional phenotyping robots are also consisting of mobile platforms equipped with a range of sensors, including phenotyping sensors for measuring phenotypic features and perception sensors for navigation. Phenotyping sensors can be non-contact (e.g., LiDAR, RGB-D cameras, multispectral, hyperspectral, thermal, stereo sensors) or contact-based. RGB cameras, widely used for their ability to count organs and assess plant shape, remain popular. For detailed spectrum information, multispectral, hyperspectral, and thermal cameras prove more beneficial than RGB counterparts. Multispectral and hyperspectral cameras facilitate the evaluation of vegetation indices, aiding in identifying factors like fruit ripeness, stressors, and diseases. Thermal cameras, sensitive to plant temperature and water supply health, require careful environmental monitoring for accurate calibration. Perception sensors, especially in Phenotyping Robots aid in localization and path planning, with penetrometers being a common example (Colaço et al., 2018; Ku et al., 2023; Zhang et al., 2023).

HTP's comprehensive approach enables the simultaneous assessment of chlorophyll distribution, photosynthetic gene expression, fruit quality parameters, and potentially flavor compounds, offering a holistic view of the intricate interactions at play. This aligns with the pursuit of fundamental biological insights. Simultaneously, HTP's capacity to generate extensive datasets encompassing diverse genotypes and environmental conditions provides actionable insights for applied plant science. By integrating genetic analyses, like QTL mapping, with HTP data, we can identify genomic regions associated with fruit quality traits, guiding breeding efforts to develop varieties that balance production traits with flavor and quality, aligning with the goals of crop improvement and sustainable agriculture. The contrasting perspectives of (Powell et al., 2012) and Mattia and Scott (2017) on tomato fruit traits present a valuable opportunity to leverage high-throughput phenotyping (HTP) methodologies, contributing to ongoing debates with implications for research questions in both pure biological and applied plant science programs. In bridging the gap between biological understanding and practical crop improvement, HTP emerges as an interdisciplinary tool capable of addressing complex debates and informing research questions across diverse contexts. The study by (Bhandari et al., 2023) also highlights the significant scope for high-throughput phenotyping (HTP) and the value of quality manually curated data in advancing our understanding of complex traits, particularly in fresh-market tomato breeding programs. Their emphasis on objective yield assessment, the limitations of manual harvesting practices, and the challenges associated with environmental influences on yield traits underscores the potential of HTP to provide standardized and reproducible phenotypic data. HTP, when integrated with genetic analyses such as GWAS and genomic selection (GS), offers an opportunity to improve the accuracy of identifying genetic associations with yield-related traits. Moreover, the study's insights into positive/negative allele effects for various traits emphasize the need for a comprehensive understanding of the genetic basis of complex traits beyond yield, a task where HTP's ability to capture diverse traits makes it a promising tool (Fig. 2). HTP, combined with quality curated data, can enhance our ability to dissect trait

genetics, address environmental interactions, and support informed breeding decisions, ultimately leading to improved varieties with enhanced yield and quality characteristics (Bhandari et al., 2023). The integration of phenotype technology, encompassing advanced sensors and autonomous robotics, holds immense promise for unlocking the potential of plant systems (Arakeri et al., 2017; Eraslan et al., 2019). These technologies bridge the gap between genetics and phenotypic traits, offering unprecedented insights into plant behavior and interactions with the environment. As the field of plant phenotyping continues to evolve, the synergy between genetics, phenomics, and machine learning will drive innovations in agriculture, enabling the development of more resilient and productive crop varieties.

These techniques identify candidate genes that can be introduced into crops through genetic engineering or genome editing. In contrast, molecular breeding employs molecular markers to find genomic areas connected to desirable traits when breeding. As a result, these techniques support the development of crops with enhanced agronomic traits and phenotypes.

3.2. Advanced imagery technologies in high-throughput phenotyping

In recent years, significant strides have been made in the development of ground-based and aerial high-throughput phenotyping platforms, encompassing diverse configurations such as fixed, vehicle-based, self-propelled, and portable systems (Busemeyer et al., 2013; Zhou and Nguyen, 2021). Portable platforms rely on human operators or wheeled carts for mobility, while fully automated facilities integrate robotic mechanisms, precise environmental control, and sophisticated sensing equipment. Aerial phenotyping platforms, including satellites, low-flying aircraft, and unmanned aerial vehicles, represent another dimension of phenotypic assessment. Both ground-based and aerial platforms offer valuable means to accurately evaluate plant growth and development, although each approach has inherent limitations. The cost-intensive nature and safety concerns associated with robotic platforms pose challenges, while vehicle-based platforms hinge on skilled operators (Fig. 3). Stationary systems face limitations in coverage, and portable solutions might compromise effectiveness. Aerial platforms, on the other hand, grapple with issues of limited resolution and payload capacity. A diverse array of imaging technologies plays a pivotal role in facilitating plant phenotyping. Two- or three-dimensional imaging systems enable direct measurement of plant morphological attributes, encompassing characteristics like color, size, shape, texture, and architectural features of various plant parts (Ruixiu et al., 1989; Montes et al., 2007; Neumann et al., 2015). Furthermore, physiological traits and pathological indications stemming from pests and diseases can be either directly or indirectly detected using imaging methods based on visible light, thermal, fluorescence, spectral, and three-dimensional techniques (Abebe et al., 2023). Notable examples of imagery captured through various methods for crop monitoring are documented (Araus and Cairns, 2014). As technology advances, these innovative imaging approaches continue to redefine the landscape of high-throughput phenotyping, offering unprecedented insights into plant traits and health.

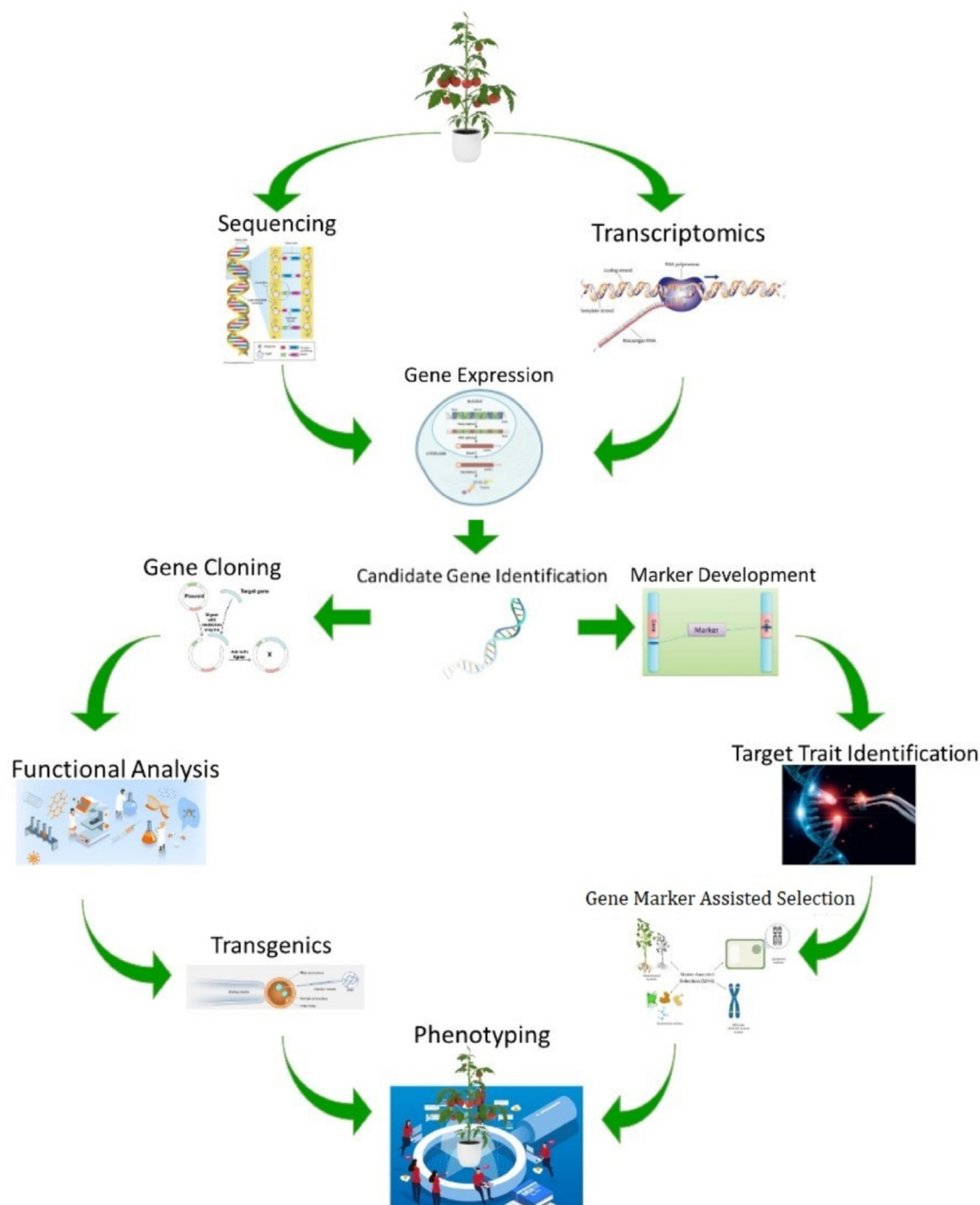


Fig. 2 Comparative genomics, transcriptomics and functional genomics are useful tools in marker-assisted breeding for improving crops

3.2.1. Visible light imaging

The primary instruments for evaluating the morphological characteristics (color, shape, size, and texture) of plants are visible-band imaging devices. Digital red-green-blue (RGB) cameras are now reasonably priced and appropriate for both ground and aerial applications thanks to advancements in technology. Digital single lens reflex (SLR) cameras are the go-to option for

many phenotyping applications due to their quickness and good quality in low light. This imaging technology can use 2D pictures that operate within the same wavelength range as the human eye (between 400 and 700 nm) to analyze various physical features and document changes in plant growth. However, 3D imaging techniques have also been developed to provide more accurate measurements of morphological characteristics by displaying

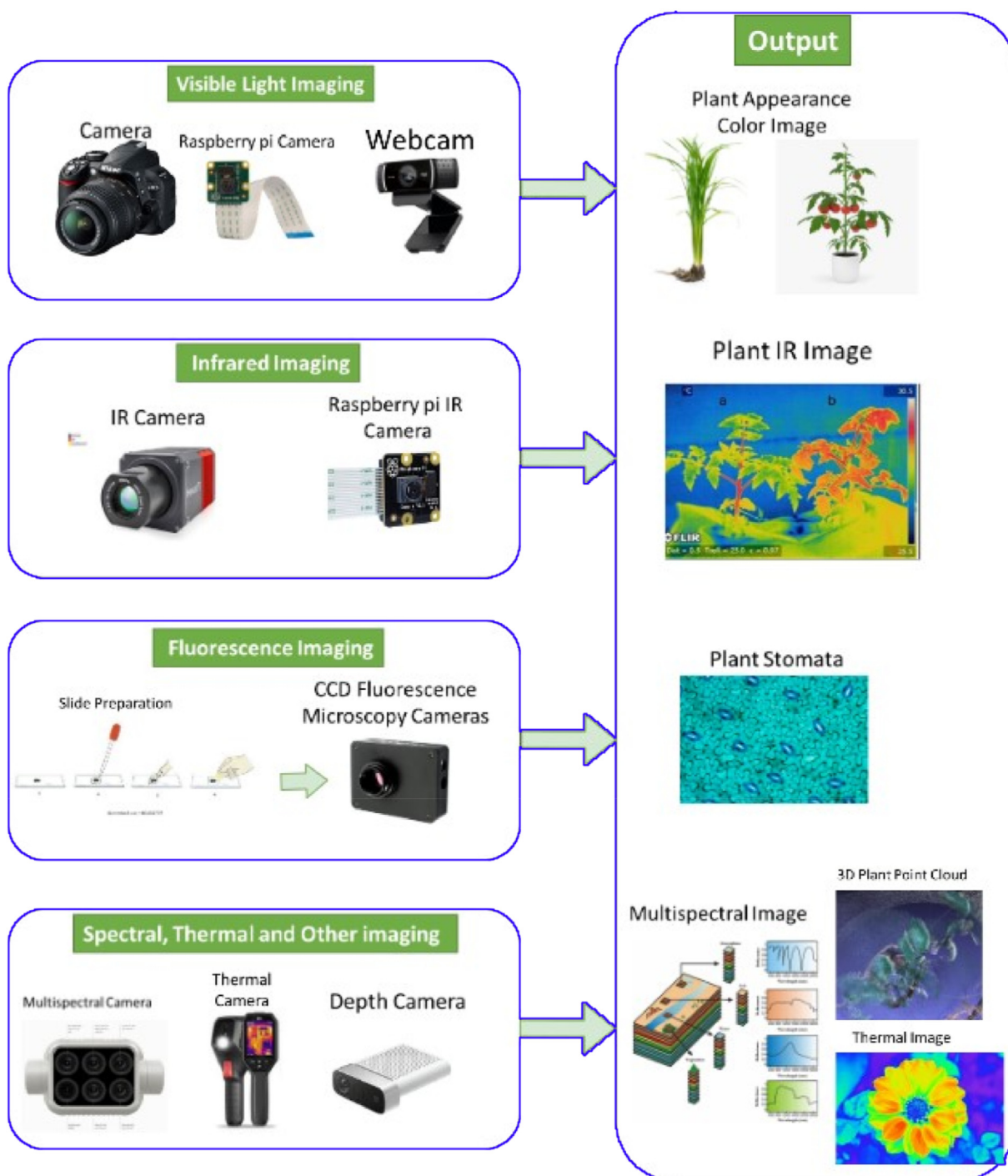


Fig. 3 The image depicts various types of equipment used for capturing visual data, and the corresponding data obtained from using each device

spatial and volumetric information of phenotypic images. Although being the most straightforward approach for plant phenotyping, its disadvantage is that visible pictures only convey physiological information, and the most frequent issue is the overlap of neighboring leaves and background soil during segmentation (Duan et al., 2011; Borisjuk et al., 2012; Li et al., 2014; Colaço et al., 2018).

3.2.2. Infrared imaging

Infrared imaging is a powerful tool in phenotyping as it allows for non-destructive and non-invasive monitoring of plant physiological processes. Infrared imaging operates by detecting thermal radiation, which is the heat emitted by objects. The warmer an object is, the more thermal radiation it emits. Radiation pictures can be screened using either a near-infrared (NIR) or a far-

infrared (Far-IR, also known as IR thermal) imaging technology. Due to the fact that healthy plants reflect a significant amount of NIR light, several studies have combined visual and NIR imaging to identify vegetative indices (800–1 400 nm). Moreover, soil and unhealthy plants reflect considerably more red light as compared with healthy plants (Yang et al., 2013). The main benefit of using visible light and NIR imaging is being able to gauge how plants are responding to various stresses. When nitrogen status is stressed, multi-trait screening and NIR digital imaging approaches are more appropriate (Rajendran et al., 2009). Infrared thermal imaging can be used to see temperature changes for drought resistance. A thermal infrared imaging approach has been developed that can analyze mutant screens, tissue tolerance, osmotic tolerance, drought tolerance, salinity tolerance, and Na⁺ exclusion in both labs and fields. Comparisons of chlorophyll pigments, leaf color, and canopy temperature may be made using it (Merlot et al., 2002; Munns et al., 2010). Infrared imaging can be used to detect changes in photosynthesis activity, which can provide insights into a plant's growth and development and is useful for plant breeding programs, where the goal is to select plants with desirable traits, such as drought tolerance or disease resistance.

3.2.3. Fluorescence imaging

Fluorescence imaging is a valuable tool applicable in both controlled laboratory environments and field settings for assessing the metabolic health and photosynthetic capacity of plants. This technique involves stimulating a plant's photosystems and measuring the resulting fluorescence emitted by the chlorophyll complex as it absorbs light with a shorter wavelength. The intensity of fluorescence directly reflects the plant's efficiency in utilizing absorbed light, making it a reliable indicator of its ability to absorb actinic light (Li et al., 2014). Multi-color fluorescence imaging, extending across the red to far-red and blue to green regions, enables the simultaneous collection of fluorescence emissions, providing an efficient approach for investigating the *in vivo* photosystem II status (Maxwell and Johnson, 2000). While the power requirements have historically confined fluorescence imaging mostly to controlled settings (Baker and Rosenqvist, 2020), its key advantage lies in its ability to illuminate the photosynthetic capacity of plants. Through measuring chlorophyll fluorescence, we can evaluate photosynthetic efficiency, gauge plant stress levels, and explore responses to environmental challenges like drought, heat, and nutrient deficiencies. Such insights not only aid in understanding adaptive mechanisms but also foster the development of more resilient crop varieties (Giovannoni, 2001; Jansen et al., 2009; Li et al., 2021). In essence, fluorescence imaging stands as a potent tool for unraveling the intricate dynamics of plant health, growth, and productivity, with broad implications for both research and agricultural advancements.

3.2.4. Spectral, thermal and other imaging

Spectral imaging has emerged as a promising tool for high-throughput phenotypic analysis of plants, benefiting from ongoing technological advancements that enhance spectral and spatial resolutions, as well as stability in various environmental contexts. While frequently applied in controlled settings, this technology has proven successful even on large-scale field

phenotyping platforms like aerial vehicles (helicopters, balloons, drones, and cranes). Thermal imaging offers a wide measurement range, high accuracy, and sensitivity, making it valuable for non-contact and automated in-situ measurements. Unlike conventional temperature monitoring methods, thermal cameras enable high-resolution temperature measurement across an area. However, accurate calibration is challenging due to environmental influences such as soil background and meteorological factors, necessitating adjustments (Prashar and Jones, 2016). Advancements in optical 3D tomography, functional imaging, and techniques like positron emission tomography (PET), magnetic resonance imaging (MRI), and Förster resonance energy transfer (FRET) sensors have enabled improved visualization of plant physiological changes, stress, and photosynthetic performance (Jones and Sirault, 2014; Deery and Jones, 2021).

Various imaging sensor technologies, including LIDAR sensors, stereo vision, photon mixer devices (PMD), and time-of-flight cameras, contribute to 3D mapping of plants. LIDAR, in particular, is widely used for 3D canopy reconstruction due to its accuracy, resilience, and high-resolution capabilities (Colaço et al., 2018). Tomographic methods have demonstrated advantages in root system identification, water transportation measurement, and quantitative analysis of photosynthesis, vital for root phenotyping (Lin et al., 2019; Lynch et al., 2021). The adoption of 3D imaging technologies has been hindered by cost and complex data processing challenges, which the evolving landscape of technology and big data research might help overcome. Despite the potential, issues such as the cost and scanning times of CT imaging need to be addressed (Downie et al., 2015). Notably, the acquired images from various methods necessitate thorough analysis and processing before the examination of plant phenotypic traits can take place. The ongoing convergence of advanced imaging techniques and data analytics holds the promise of revolutionizing plant phenotyping and advancing our understanding of plant traits in unprecedented ways. Image processing requires some basic techniques, and the most crucial pre-processing step is often featuring extraction, followed by picture segmentation (Fig. 4). The intended plant attributes are subsequently deduced through data analysis from these features (Li et al., 2014). HTP in plants and the broader domains of computer vision and robotics share intriguing similarities and distinct differences, illuminating the interdisciplinary nature of modern scientific exploration. These fields converge at the intersection of cutting-edge technology and biological understanding, albeit with unique nuances that underscore their respective focuses. Similarities arise in the core principles that underpin HTP, computer vision, and robotics. All three areas emphasize the extraction and interpretation of visual information. Computer vision, often driven by artificial intelligence, seeks to enable machines to comprehend visual data like images and videos, akin to the way humans do. Similarly, HTP harnesses imaging technologies to capture intricate plant traits and physiological responses, unraveling hidden patterns through data-driven analyses. Robotics, on the other hand, aims to imbue machines with autonomy and intelligence to interact with the physical world, bearing semblance to how plants interact with their environment to adapt and grow. Yet, dissimilarities arise from the domains' primary objectives. Computer vision and robotics frequently center on navigation, manipulation, and decision-making in real-time

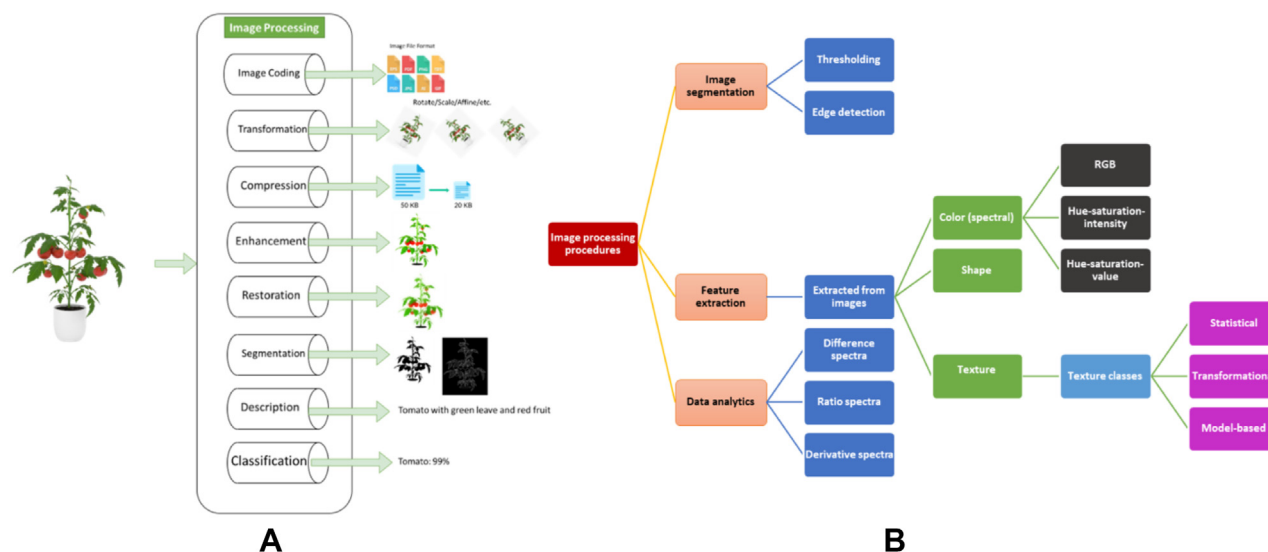


Fig. 4 Image processing (A) and Segmentation and data Analytics (B)

(A) In image processing, coding, compression, description and classification are important preprocessing techniques. (B) Segmentation and data Analytics. Segmentation is the process of dividing the image into meaningful regions or objects, such as leaves or stems. This can be done using techniques such as thresholding, edge detection, or region growing. Feature extraction is a crucial step that helps to identify and extract relevant features from an image. Feature extraction involves identifying and extracting relevant features from the segmented images, such as color, texture, or shape.

scenarios, often in uncontrolled and dynamic environments. Contrastingly, HTP in plants is primarily concerned with quantifying and understanding biological phenomena, ranging from growth patterns to stress responses. The controlled settings of greenhouses and laboratories lend themselves to detailed observations, in contrast to the unpredictable outdoor environments common in robotics and computer vision applications (Haug and Ostermann, 2015; Arakeri et al., 2017; Rose and Chilvers, 2018; Zhao et al., 2020; Abbasi et al., 2022).

Furthermore, the dimensions of time and scale in these domains diverge. Computer vision and robotics often operate in rapid, dynamic time frames, requiring real-time decision-making (Arakeri et al., 2017). HTP, conversely, spans various temporal scales, from tracking minute physiological changes over weeks to studying plant evolution across generations. This temporal variance reflects the distinct biological rhythms inherent to plant life. The confluence of HTP in plants, computer vision, and robotics showcases the transformative potential of interdisciplinary collaboration. While the objectives of each domain may differ, the shared pursuit of unlocking patterns and insights from visual data underscores their interconnectedness (Rose and Chilvers, 2018; Yang et al., 2020; Abbasi et al., 2022). Bridging these domains enriches our understanding of both the biological world and the technologies that empower us to explore it.

4. Omics to phenotyping

The study of omics, encompassing fields like genomics, proteomics, metabolomics, and more, plays a pivotal role in unraveling the genetic and molecular basis of traits in plants, particularly in the context of their responses to the environment and efforts to enhance crop growth (Zhang et al., 2023). Identifying the genes that confer specific characteristics is crucial for

advancing our understanding of plant–environment interactions and accelerating crop development. The ultimate goal is to identify genes and mechanisms that influence crop productivity, a central objective in plant genomic research (Abebe et al., 2023). Various methodologies have been devised within genomics to pinpoint and characterize genes responsible for desired traits in crops. Techniques like genome and transcriptome sequencing, microarray analysis, RNA-seq gene expression profiling, and map-based cloning are employed to uncover these candidate genes (Pevsner, 2015; Li et al., 2021; Khan et al., 2023). However, understanding the complex interplay between genetic information and observable traits remains a formidable challenge in the realm of crop science (Gao et al., 2023). The emergence of high-throughput techniques and advanced plant phenotyping platforms in recent years has brought newfound efficiency and precision to the assessment of multiple plant traits. These innovations enable us to gain insights into how different environmental conditions impact various aspects of plant biology, including growth, development, and reproduction (Metje-Sprink et al., 2020; Prakash et al., 2022).

A critical bridge between genomics and phenomics is functional genomics. This approach involves delving into the functional aspects of genes and their interactions within living organisms. Techniques like gene knockouts, which intentionally deactivate specific genes to observe resulting phenotypes, are instrumental in this pursuit. This method has been extensively applied in crop legumes, where it has contributed to the development of cDNA libraries, the production of expressed sequence tags (ESTs), gene expression analysis, and the extraction of functional data (Yang et al., 2013; Pevsner, 2015). Furthermore, the field of bioinformatics offers a powerful avenue for synthesizing and analyzing the vast amount of data generated by both genomics and phenomics. Through sophisticated computational

methods, bioinformatics integrates disciplines like computer science, biology, statistics, and artificial intelligence to address intricate biological questions at the molecular level. By leveraging data from genome sequencing, gene expression profiling, and high-throughput phenotyping, we gain valuable insights into the genetic underpinnings of observable traits (Pevsner, 2015; Montesinos-López et al., 2021; Zhang et al., 2023). In essence, the synergy between omics approaches and phenotyping provides a comprehensive perspective on the intricate relationship between an organism's genetic makeup and its observable characteristics. Also, omics approaches provide comprehensive and multi-dimensional insights into the molecular and genetic underpinnings of phenotypes (Yang et al., 2013; Prakash et al., 2022; Interdisciplinary Plant Science Consortium, 2023). These advancements not only shed light on the molecular mechanisms underlying desired traits in crops but also hold promise for developing more productive crop varieties capable of thriving in challenging environments (Khan et al., 2023). They enable us to better understand the complexity of biological systems, identify biomarkers for diseases, predict responses to treatments, and unravel the intricate relationship between an organism's genes, environment, and observable traits, ultimately advancing our knowledge of biology and medicine.

5. Epigenetic modifications

Epigenetics, an enthralling realm within genetics, has enriched our comprehension of how genes influence traits, a puzzle perplexing scientist for decades (Varotto et al., 2020). It extends genetics by unravelling how genes interact with their products to shape plant traits (Waddington, 2012). In contemporary molecular biology, its scope has narrowed to scrutinize DNA-related processes regulating phenotype, and transcending DNA sequence. This field's success lies in applications like leveraging epigenetics in plant breeding and tracing heritable marks across generations to enhance crop traits (Slotkin, 2016). Inherited yet nonconforming to traditional patterns, modifications like DNA methylation, histone tweaks, chromatin remodeling, and small RNA activity drive this change (Varotto et al., 2020). DNA methylation, particularly, holds promise as a source of crop fitness variation. It influences vital traits—seed dormancy, flowering time, yield—and its partially heritable patterns unveil epigenetics' role in plant evolution and domestication (Liu, 2003; Zhang et al., 2013; Song et al., 2017). Grasping DNA methylation empowers breeders to craft favorable changes while curbing undesirable epigenetic shifts stemming from breeding practices (Stroud et al., 2013; Stelpflug et al., 2014; Zhang et al., 2014; Han et al., 2018; Lin et al., 2019).

In recent times, there have been remarkable advancements in the field of plant epigenetics, particularly in the area of histone post-translational modifications (PTMs) and DNA methylation. However, more recently, attention has turned to the chemical modifications occurring on RNA molecules, such as 5-methylcytosine (m5C) and N6-methyladenosine (m6A), which have emerged as a novel layer of epigenetic marks. These findings have been particularly evident in model plants like *Arabidopsis thaliana*, shedding light on the intricate mechanisms by which these RNA modifications influence gene expression. As research has progressed, these novel epigenetic marks have also

been identified in important horticultural species like tomato (*Solanum lycopersicum*) and poplar (*Populus trichocarpa*), expanding our understanding of their roles beyond model organisms. Recent research has uncovered DNA methylation's crucial role in governing important agricultural traits such as heterosis, fruit ripening, and stress responses (Kathiria et al., 2010; Furner and Matzke, 2011; Kou et al., 2011; Meyer, 2011; Xing et al., 2015; Wang et al., 2016; An et al., 2017). DNA methylation in plants is vital for processes like fertilization, gametogenesis, and developmental crosstalk with histone modifications (Johannes et al., 2009; Verhoeven et al., 2010). Long non-coding RNAs (lncRNAs) are significant players in the epigenetic control of gene expression. Cao and colleagues initially detected 2 857 lncRNAs from existing RNA-seq data in potato plants. They further focused on lncRNAs that exhibited differential responses (DELs) in a resistant potato variety when faced with *Phytophthora infestans* infections, the causal agent of late blight disease. Using the GENIE3 algorithm, which employs a random forest approach, they established the directional regulatory connections between these DELs and their target genes. By employing enrichment analyses, this approach enabled the us to deduce the potential involvement of these DELs in enhancing potato resistance against *Phytophthora infestans*. Jubair et al. introduced a novel approach. Their transformer model, capitalizing on genetic marker relationships, outperforms existing methods, emphasizing the transformer's potential in genomic prediction. Notably, they streamline transformer training and gene identification for disease resistance by innovative marker selection. This research employs machine learning to identify plant resistance proteins, enhancing pathogen adaptation and reducing susceptibility. Machine learning has been used to discover various epigenetic modifications in plants, uncovering novel insights into gene regulation, stress responses, and developmental processes (Fig. 5).

Numerous machine learning tools have emerged to identify resistance proteins, yet refinement is needed. Chen et al. have introduced an advanced tool that surpasses current ones by employing a stacking algorithm and factoring in residue pairwise energy. This advancement deepens insight into plant-pathogen adaptation and aids in cultivating disease-resistant crops. In recent times, machine learning has demonstrated its capability to handle intricate data, providing a platform to unravel the genetic and epigenetic foundations of vital agricultural traits. DNA methylation patterns in *Arabidopsis thaliana* were examined using machine learning, leading to the discovery of conserved methylation signatures (Takuno and Gaut, 2012). A similar approach may have been employed to investigate histone modification patterns in plants (Zhang et al., 2006). Another study applied machine learning to predict and analyze transcription factor binding sites in *Arabidopsis*, shedding light on the regulatory DNA landscape (O'Malley et al., 2016). Additionally, a study utilized machine learning to predict Chromatin Accessibility (Zhang et al., 2023). Although not plant-specific, this example showcases the use of machine learning to predict chromatin interactions, which could potentially be adapted for plant research.

6. Machine learning approaches for trait discovery

Machine vision technology has found successful applications across various agricultural domains, including but not limited to

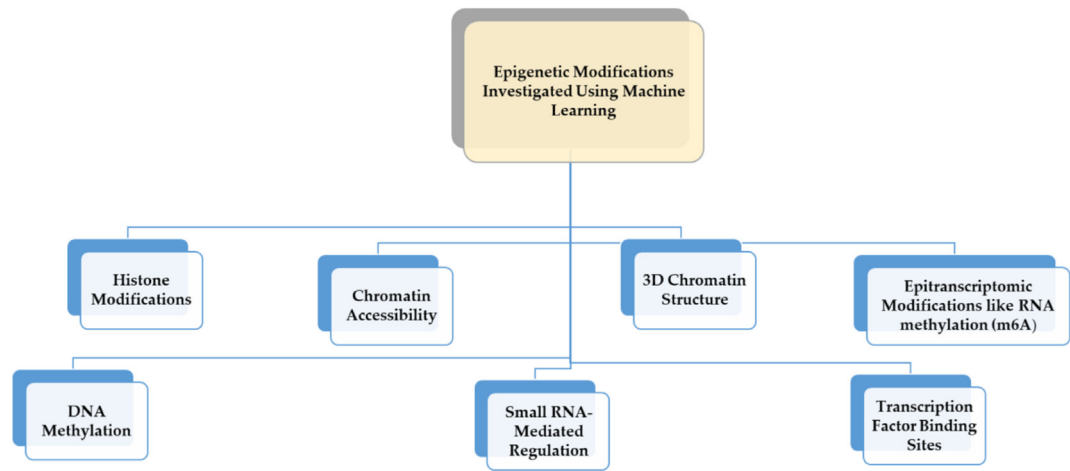


Fig. 5 Various epigenetic modifications explored through the application of machine learning (ML) techniques

yield prediction, assessing the physiological response of plants to stressors, enhancing precision farming, sorting and categorizing fruits, and facilitating automated phenotyping (Diaz-Garcia et al., 2016). ML approaches are becoming increasingly important in plant biology research, particularly in the area of plant trait discovery. Machine learning models can be trained to predict plant traits based on environmental variables, and to analyze plant images and genomic data to identify genetic and environmental factors that affect plant growth and development. These approaches can also be used to automate plant phenotyping and collect large-scale phenotypic data sets, which can help to identify new plant traits important for crop productivity and resilience. It can be used to analyze plant images and extract features such as leaf area, chlorophyll content, and leaf shape (Zhang et al., 2023). This can be useful for studying plant development and for identifying genetic and environmental factors that affect plant morphology (Wallace et al., 2018; Eraslan et al., 2019). Modern breeding pipelines employ two distinct paths, each suited to specific types of traits. Data-driven modeling is used for quantitative traits, which are primarily determined by genetic background, while the causal genes of polygenic traits, which are determined by specific genes with major effects, are explicitly characterized to enable beneficial alleles to be pyramided (Ferrão et al., 2023).

Machine learning and artificial intelligence algorithms can be used to identify patterns and relationships between genetic and

phenotypic data. The rapid growth in data capture and machine learning techniques has empowered scientists to efficiently obtain, organize, analyze, and interpret biological data. This analytical approach aims to uncover hidden, non-trivial, and intriguing patterns that can have significant implications for various biological processes and applications. Gene expression profiling is the process of simultaneously measuring the activity of thousands of genes to obtain a comprehensive overview of cellular function, and the analysis of this data using machine learning or statistical methods can reveal intrinsic patterns that aid in understanding the underlying causes of important traits (Barah et al., 2021; Danilevicz et al., 2022). The utilization of the technologies mentioned above has resulted in the accumulation of vast quantities of gene expression data, offering valuable insights into diverse biological processes within living organisms. This wealth of data provides a foundation for tackling various challenges through gene expression data analysis. For these analysis, appropriate statistical and machine learning techniques including data clustering, association mining and classification are widely involved (Fig. 6) (Barah et al., 2021; Ferrão et al., 2023; Yan and Wang, 2023).

In the field of plant biology and precision-designed breeding, genome editing has emerged as a potent approach for addressing single-gene traits. However, the harnessing of multi-omics data has become increasingly critical, and machine learning (ML) and deep learning (DL) are poised to play pivotal roles. ML

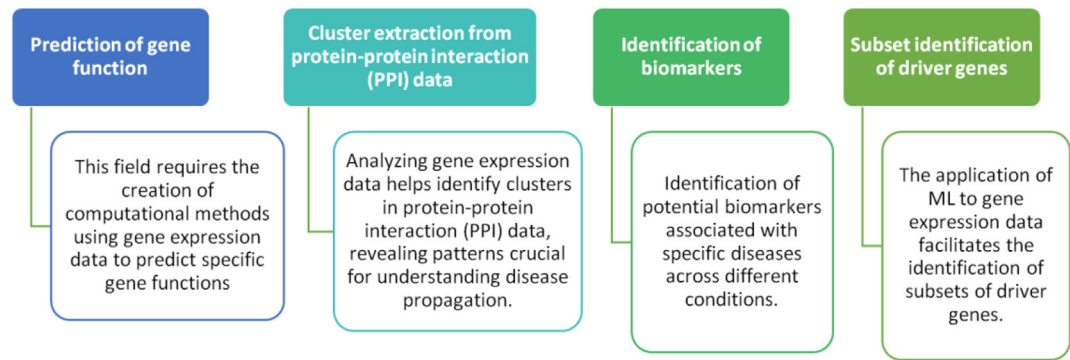


Fig. 6 Key issues that can be effectively addressed through gene expression data analyses with ML techniques

applications extend across large-scale omics research, encompassing the prediction of genetic elements, molecular structures, and regulatory components like promoters, enhancers, TF-binding sites, and epigenetically modified regions. Nonlinear techniques, such as convolutional neural networks and feed-forward deep neural networks, have proven valuable for improving genomic selection (GS) by accounting for environmental interactions and subtle marker interactions. These methods offer more precise predictions for high-dimensional datasets, illuminating connections between related traits. While traditional ML techniques and mixed linear models remain accurate for smaller datasets, DL excels at feature extraction from extensive datasets, accounting for feature interaction effects. Expanding beyond genomic best linear unbiased prediction (GBLUP) methods holds promise for more accurate phenotype predictions in GS problems, ushering in a new era of precision breeding (Pérez-Rodríguez et al., 2012; Montesinos-López et al., 2018; Jubair et al., 2021; Danilevicz et al., 2022). Fig. 7 illustrates the synergy between machine learning and plant biology, showcasing how the computational power of machine learning enhances the analysis of complex plant data and contributes to advancements in agriculture, crop improvement, ecological understanding, and sustainable resource management.

In tandem with these advances, the integration of various gene regulatory network algorithms and machine learning techniques has emerged as a powerful strategy for identifying and validating crucial genes and mutations related to specific plant traits. Prioritizing candidate genes, even within quantitative trait loci (QTL) identified through genome-wide association studies (GWAS), has been greatly improved through techniques such as penalized regression, Bayesian approaches, gradient boosting machines, and deep learning. Specialized tools like

QTG-Finder have been developed to harness machine learning models for post-GWAS analysis in plants, further enhancing the accuracy of gene prioritization (Díaz-García et al., 2016; Cui et al., 2020). Deep learning models, well-suited for handling complex, unstructured imaging data, have revolutionized plant phenomics and precision agriculture through the application of transfer learning and pretrained deep learning model architectures. These advancements have the potential to significantly enhance genotype-to-phenotype (G2P) prediction in plant breeding, particularly for complex traits and under challenging environmental conditions (Varshney et al., 2005; Wallace et al., 2018; Park et al., 2019; Danilevicz et al., 2022; Ferrão et al., 2023). Genomics-assisted breeding, powered by machine learning models like convolutional neural networks and Bayesian approaches, has the capacity to unlock new frontiers in predicting complex traits across a variety of crops, enabling the development of flavorful varieties and enhanced agricultural outcomes.

The integration of phenomics, genetics, and ML stands as a promising avenue for optimizing phenotypic traits through the application of high-throughput phenotyping platforms (Zhang et al., 2023). In recent years, substantial progress has been made in the development of these platforms, which encompass a variety of configurations, including ground-based and aerial systems. Ground-based platforms, ranging from fixed installations to portable setups, offer the capacity to directly measure morphological characteristics such as color, size, shape, and architecture of plant parts. These traits can provide critical insights into plant growth and development. Aerial platforms, such as satellites and unmanned aerial vehicles, offer an alternative perspective by capturing large-scale data, although they may face limitations in terms of resolution and payload (Duan et al., 2011; Danilevicz et al., 2022; Yan and Wang, 2023). The convergence of

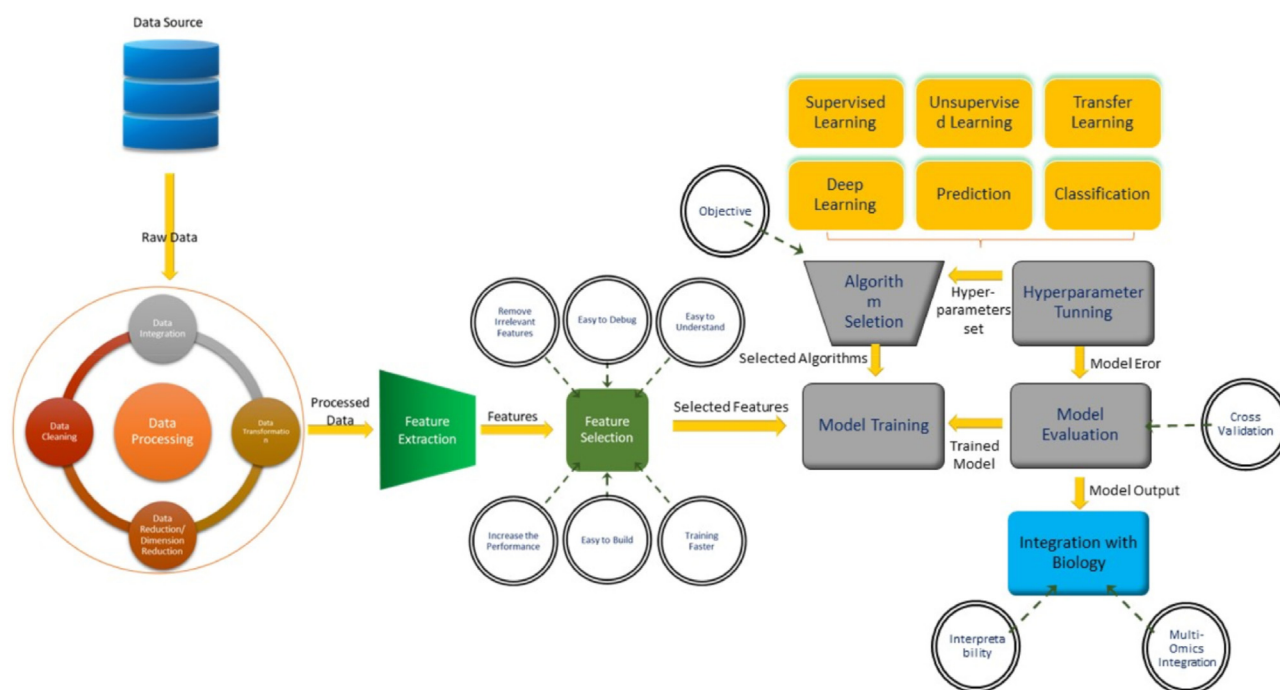


Fig. 7 The systematic application of machine learning techniques to plant biology research, encompassing data acquisition, processing, feature extraction, model training, and biological integration

phenomics, genetics, and ML takes advantage of the vast datasets generated by high-throughput phenotyping. By incorporating genetic information, we can unravel the genetic basis of observed traits, identifying specific genes associated with desired characteristics. Machine learning algorithms, adept at recognizing intricate patterns within complex datasets, play a pivotal role in deciphering the relationship between genomics and phenomics. This integrated approach enables the creation of predictive models that link genetic variations to distinct phenotypic outcomes, thus facilitating the selection of crop varieties with optimal traits for specific environments or conditions (Araus and Cairns, 2014; Barah et al., 2021; Yan and Wang, 2023; Zhang et al., 2023). The amalgamation of these disciplines empowers precision agriculture and targeted breeding efforts, ultimately leading to the development of crops that exhibit enhanced productivity, resilience, and adaptability. As advancements continue to refine high-throughput phenotyping technologies and analytical techniques, the integration of phenomics, genetics, and ML emerges as a transformative strategy in shaping the future of agriculture and crop improvement (Ferrão et al., 2023).

7. HTP for precision farming

In order to increase agricultural output and satisfy the expanding demands of the human population, it is crucial to establish the link between genotype and phenotype. This will help food production maintain pace with population expansion. In order to understand how genes and characteristics interact, phenotyping, which includes observing and quantifying physical properties in plants, is equally as crucial as genotyping. Therefore, to achieve the optimum phenotype and provide plants with the ability to produce superior and steady yields in a changing environment, advances in technology and “omics” techniques are also being utilized. In the field of molecular plant

biology, these methods are frequently employed to investigate cellular functions, genetic regulation, and interactions with environmental changes (Deshmukh et al., 2014; Rahaman et al., 2015). Phenomics, unlike genomics, cannot fully characterize the entire phenome due to its dynamic and complex nature. However, advancements in high-throughput and high-dimensional phenotyping have made it possible to collect specialized characteristics. Throughput refers to the number of individual units measured at specific levels of plant organization, while dimensionality refers to the range of phenotypic traits measured across different spatial and temporal scales and categories, such as plant structure, physiology, and performance (Dhondt et al., 2013). Our ability to predict phenotypes has greatly improved due to advances in genotype-phenotype mapping and the rapid pace of trait discovery. We can simulate biological processes throughout time and at different dimensions by combining data from phenotypic and genome-wide techniques. Plant studies have incorporated genetic research approaches that are useful for learning about genomes, such as GWAS and the mapping of QTL. Comprehensive phenome-wide data allow for the characterization of all potential phenotypes, including structural, physiological, and performance-related traits (like biomass per hectare and seed yield) under various environmental conditions for a given genotype. This enables the study of plant similarity or dissimilarity across the entire population. They have been broadly adopted for gene mapping (Topp et al., 2013; Yan and Wang, 2023). We can measure and quantify a variety of plant features using advanced phenotyping, including physical, chemical, and physiological variables. The ability to discover and select the most desirable qualities in crops, such as resistance to pests and diseases, drought tolerance, and increased yields, is made possible by this method, which has grown in importance in modern horticulture (Table 1).

Table 1 Major challenges and Limitations associated with an integrative approach

	Phenotyping	Genomics	Machine learning
01	Machine learning models might struggle to accurately capture and predict the intricate interactions.	Genomics offers extensive DNA data, yet understanding gene functions is challenging. Many genes have complex roles not easily deducible from sequences.	Plant science demands robust ML with sizable, high-quality datasets. Challenges arise from diverse plant species, experimental variations, and data collection limitations
02	Collecting phenotypic data is often labor-intensive and time-consuming, leading to limited datasets.	Accurately predicting the phenotype solely from genomic data is considerable challenge.	ML models occasionally overfit training data, excelling on it but struggling to apply it to new, unfamiliar data.
03	Fluctuations in environmental conditions can complicate impacts on traits, creating difficulty in precisely connecting phenotypic variations.	Numerous genes possess uncertain or multifaceted functions, necessitating thorough experimental validation for comprehensive functional annotation.	ML models often identify correlations in data, but they might not uncover true causal relationships.
04	Identifying the most informative features (trait) can be challenging and subjective, impacting the model's performance.	Unraveling the genetic underpinnings of quantitative traits governed by multiple genes demands advanced techniques due to their challenging nature.	ML application requires collaboration between experts in both biology and ML. Lack of understanding between practitioners can hinder progress.
05	The environmental variations can have significant impacts on traits that might be missed by phenotyping methods	Genomic sequencing might not capture all types of genetic variation, such as large structural variations, insertions, deletions, and copy number variations.	Complex ML models, such as DNN and CNN can lack interpretability. It might be challenging to understand how the model arrives at its predictions

With the fast development of facilities and algorithms, light detection and ranging offers a potent new tool for 3D phenotyping. A great deal of effort has been put into utilizing LIDAR in agriculture and horticulture field to explore static and dynamic changes of structural and functional traits. Moreover, these developments enhance 3D plant modeling across many spatial–temporal scales and disciplines, making it simpler and less expensive to associate genes with environmental practices and analyze environmental practices, which provides fresh perspectives on breeding and management. LIDAR has enormous promise for forestry, horticulture, and grass phenotyping in addition to agricultural phenotyping. Although plant modeling and phenotyping have significantly improved owing to LIDAR, its potential for use in breeding and management has not yet been completely investigated (Topp et al., 2013; Lin, 2015; Colaço et al., 2018; Jin et al., 2021). Overall, improved phenotyping is a vital tool for modern horticulture, allowing growers and plant breeders to increase crop output, quicken breeding processes, improve precision farming, and encourage more environmentally friendly agricultural techniques. It's essential to choose the correct tools for different phenotyping tasks. High throughput phenotyping is essential in horticulture as it allows for the recognition and description of desirable characteristics in crops. Precise phenotyping enables the choice of superior varieties that exhibit enhanced productivity, disease resistance, and quality (Fig. 4). It also contributes to a deeper understanding of the genetic and environmental factors that influence crop performance, supporting targeted breeding and sustainable cultivation methods in horticulture. High-throughput phenotyping has gained significant popularity in the field of horticulture for assessing and characterizing a wide range of traits. These traits encompass diverse aspects such as morphology, physiology, biochemistry, yield potential, and responses to both biotic and abiotic stresses (Abebe et al., 2023; Sheikh et al., 2023). Advanced phenotyping enables plant breeders to identify promising crop varieties with desired traits, leading to increased food security and improved quality of life for farmers. This figure highlights the potential benefits of advanced phenotyping, including accelerated breeding efforts, precise assessment of plant properties, and enhanced precision horticulture. It showcases how advanced phenotyping can aid in reducing reliance on synthetic inputs, optimizing resource utilization, and promoting sustainable and environmentally friendly horticulture practices. Additionally, improved phenotyping contributes to a better understanding of plant responses to diverse environmental conditions, potentially leading to new discoveries.

8. HTP for smart horticulture

In recent years, the field of plant biology and horticulture has witnessed remarkable progress in HTP technologies, transforming the way we understand and improve crops. Although HTP greenhouse experiments cannot entirely replace field evaluations, they offer valuable insights into trait discovery and development, particularly for ornamental plants and vegetables. Automation and non-invasive imaging-based platforms have gained traction, proving successful for monitoring and phenotyping within production pipelines (Neumann et al., 2015). Moreover, technologies like ultrasonic and LiDAR sensors are

revolutionizing digital horticulture, enabling accurate measurements of canopy structure, while image based HTP methods are revolutionizing how we rapidly quantify traits, advancing both precision horticulture and phenotyping across horticultural crops (Colaço et al., 2018; Abebe et al., 2023).

A driving force behind these advancements is the integration of machine learning and artificial intelligence (AI) into plant phenotyping. AI is reshaping gene identification and validation for specific traits, enhancing the precision of breeding efforts (Ferrão et al., 2023). This combination of AI and high-throughput physiological phenotyping, referred to as “Physiolomics” is facilitating rapid assessment of dynamic physiological traits under stress conditions, contributing to a deeper understanding of plant responses (Lin et al., 2019). Simultaneously, AI's capabilities are being harnessed to predict consumer-preferred flavors and guide breeding strategies, responding to evolving market demands for tastier and more nutritious crops (Ferrão et al., 2023). Amidst these innovations, the horticulture industry is poised for a significant transformation through the paradigm of smart horticulture. Leveraging cutting-edge technologies like AI, big data, and the Internet of things, smart horticulture envisions a holistic approach across the entire production chain. This includes smart breeding, cultivation, transportation, and sales, all aimed at maximizing productivity, minimizing resource use, and ensuring sustainable growth (Zhang et al., 2013, 2023). This shift towards data-driven decision-making and technology-driven precision reflects a promising future for horticulture, where innovation and optimization will be pivotal in addressing global agricultural challenges. In present, the field of horticulture and plant biology has witnessed a remarkable transformation fueled by HTP technologies, ML, and AI. These advancements are bridging the gap between basic scientific research and practical applications in crop improvement. For instance, in a study focusing on Indian pennywort, high-throughput phenotyping was used to optimize irrigation schedules, resulting in improved crop productivity and quality. This illustrates how the integration of phenomics and technology can provide actionable insights for enhancing the cultivation of medicinal plants (Theerawitaya et al., 2023; Karunathilake et al., 2023). The application of HTP phenotyping extends beyond medicinal herbs. In tree cultivation of apple, the utilization of UAV-LiDARs for rapid 3D scanning and architectural trait assessment exemplifies how technology can streamline the evaluation of fruit tree cultivars. This approach, compared to traditional methods like TLS, offers a high-throughput solution for assessing architectural traits, demonstrating the fusion of genetics, phenomics, and advanced technology in fruit tree breeding (Rojas-Bustos et al., 2023; Kwon et al., 2024).

Moreover, the importance of advanced phenotyping technologies in addressing global agricultural challenges is underscored by their potential to enhance crop productivity. By employing robotics, high-tech sensors, and bioinformatics tools, we can uncover the genetic basis of complex traits associated with plant growth and development. This integrated approach of genotyping and phenotyping not only contributes to a deeper understanding of gene functions and environmental responses but also provides relevant solutions to increase crop production. These developments are pivotal in translating basic scientific knowledge into practical strategies for addressing food security and

sustainability concerns (Kumari and Munjal, 2023). The integration of phenomics, genetics, and cutting-edge technologies is driving a profound transformation in horticulture and plant science. These multidisciplinary approaches are not only optimizing cultivation practices but also offering insights into genetic traits and stress responses. This convergence of basic science and applied research is poised to revolutionize crop improvement, address global agricultural challenges, and shape the future of sustainable agriculture.

9. Challenges and limitations

Advancements in phenotyping technologies have led to the establishment of numerous phenomic facilities around the world, dedicated to capturing precise data on various traits of plants throughout their growth cycle. These facilities primarily operate within controlled environments and utilize robotics, automated image acquisition, and analysis to gather this phenotypic data (Pieruschka and Schurr, 2019). These approaches often involve different types of sensors, cameras operating across different wavelengths, and versatile platforms such as moving plants along tracks, suspending sensors from cables, or even using drones to collect signals from plant populations (Sanaeifar et al., 2023). Despite these technological advancements, challenges persist in effectively using these tools to understand the complex interactions between plants and their environment, particularly in response to stress. Plants are highly responsive to a multitude of signals from their surroundings, including factors like light intensity, humidity, CO₂ levels, and soil moisture (Rosenqvist et al., 2019). How plants react to different stress is both dynamic and adaptable. Complicating matters, environmental conditions tend to be unstable and change rapidly, even within controlled settings. For example, plants undergoing drought stress will quickly exhibit varying levels of soil moisture due to differences in their transpiration rates. Furthermore, even under seemingly uniform conditions (such as consistent greenhouse lighting), measurements taken at different times can show discrepancies due to natural fluctuations in light intensity throughout the day. This variability underscores the limitation of studying isolated traits or conducting measurements on single dates across multiple genotypes, especially under stressful conditions (Bochner, 2003). The comprehensive understanding of plant traits necessitates acknowledging the dynamic interplay between plants and their environment, requiring multiple measurements taken over time to truly capture the intricate responses (Topp et al., 2013; Guo et al., 2018; Arab et al., 2019).

Variables like fluctuating cloud cover, shifting angles and intensities of sunlight, and variations in wind strength all present difficulties for the algorithms utilized in automated phenotyping. Plant traits, which are often the result of intricate interactions between multiple genes and the environment, contribute to the complexity of the task. Delving into the genetic foundations of these quantitative traits requires the application of advanced statistical methods due to their inherently challenging nature (Singh et al., 2021; Gill et al., 2022). While machine learning models excel at identifying correlations within data, they might not necessarily uncover true causal relationships. Therefore, grasping the underlying biological mechanisms and causal

connections is of paramount importance for deriving meaningful insights in the field of plant science (Machwitz et al., 2021; Ninomiya, 2022). Several challenges and limitations that arise from this integrated approach are summarized in Table 1. In essence, while the integrated approach to plant phenotyping offers tremendous potential for advancing our understanding of plant traits and responses, it is essential to recognize and address these challenges to ensure the reliability and meaningfulness of the insights gained.

10. Conclusion and future prospects

The convergence of physiology, genomics, and machine learning has ignited a transformative era in plant trait discovery, presenting unparalleled opportunities for understanding and enhancing plant traits essential for agriculture, environmental resilience, and ecosystem sustainability. This synergy enables us to unravel intricate relationships between genetic makeup, physiological mechanisms, and environmental responses, elucidating traits that govern plant growth, stress resistance, and productivity. However, as we navigate this cutting-edge landscape, policy implications surrounding data sharing, collaboration, and regulations come to the fore. Striking a balance between open data sharing for scientific progress and safeguarding intellectual property rights is pivotal. Collaborative efforts across academia, industry, and governing bodies are imperative to establish frameworks that encourage equitable data access, stimulate innovation, and ensure ethical research conduct. Regulatory measures should evolve iteratively to address challenges posed by this dynamic field, upholding data privacy, fair usage, and responsible AI deployment. In essence, the fusion of these scientific disciplines holds promise for a greener future, underscoring the urgency of fostering a holistic approach that harnesses scientific advancement while upholding ethical and regulatory considerations.

Machine learning has the potential to connect fundamental science and practical plant breeding by utilizing biological knowledge and omics data to create precision-designed breeding strategies. These strategies can be knowledge-driven, using molecular design to achieve specific breeding goals, or data-driven, using genomic design to analyze large sets of data. In general, the integration of genomics, phenomics, and machine learning shows great potential for precision-designed plant breeding. The future of crop improvement and production lies in the integration of these technologies to develop crops with improved yield, disease resistance, nutritional content, and other important traits, ultimately leading to more sustainable and efficient food production.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

Basic Science Research Program supported this research through the National Research Foundation of Korea (NRF), funded by the Ministry of Education (2019R1A6A1A11052070).

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