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Omics-driven plant breeding through phenomics-enviromics crosstalk

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Abstract

Genomics, including all molecular omics, is driven by molecular data, while phenomics and enviromics rely on phenotypic and environmental data. Yet phenotyping is often conducted under poorly characterized environments, limiting the interpretation of phenotypic variation and constraining genetic gain. Integrating high-throughput phenotyping with envirotyping is hence vital to resolve genomic effects. This Perspective introduces phenomics-enviromics (PE) crosstalk as a framework for coordinated data collection and integration to advance plant breeding. Satellites, unmanned aerial and ground vehicles, and controlled indoor facilities are establishing the basis for synchronous, high-throughput PE crosstalk to enhance interpretability, prediction, and crop resilience.

Introduction

Technology advancements are accelerating scientific innovation for ensuring global food security. Achieving stable food production becomes vital to feed the ever-growing population of the world [1], yet it is endangered by crop diseases and pests [2], soil salinity and alkalinity [3], limited genetic diversity, extreme climate changes [4], and declining arable land [5]. The genetic enhancement of crops therefore offers a sustainable approach to mitigate the challenges.

Traditional plant breeding, though successful, requires integrated scheme to address yield gaps and climate change challenges [6-8]. Selecting of high performing genotypes has relied on phenotypic evaluation in multi-environment trials (METs) [8], while advances in omics technologies (for instance, genomics, metabolomics, proteomics, transcriptomics, and epigenomics) have generated large, complex datasets. Standardisation of these datasets is essential to enhance detection of polygenic effects, nonlinear interactions, and uncovering emergent system-level patterns that support scalable, predictive biology beyond small-sample inference. Emerging multi-omics, specifically single-cell approaches, has been offering a vital promise for advancing plant breeding [9-11] by uncovering essential principles controlling growth, development, and various stress responses [12] with a comprehensive, stage-specific insights into plant metabolism and gene expression [11]. For instance, chromatin heterogeneity study in a single cell epigenomics demonstrated by bisulfite-converted randomly integrated fragments sequencing in maize microspores facilitates identification of heterogeneous sites [13]. Artificial intelligence (AI) technologies increasingly empower predictive breeding by translating molecular discoveries into validated models and scalable experimental systems [12,14]. Genome editing supports rapid elite trait introgression and crop domestication [15], while genomic prediction [16,17], crop growth modeling, and whole-genome prediction (using full set of genetic material of an individual species) accelerate genetic gain and enhance an end-to-end crop performance for more productive, sustainable agricultural system [8]. Examples of this application include advanced AI-based biomolecular modelling [18] and prediction of plant complex traits from multi-omics data [19]. During this process, high-throughput phenotyping (HTP) is facilitating the evaluation of genomic combination and genetic variation by integrating genotype to phenotype. An accurate prediction of plant trait dynamics whose heritability varies less through time using genetic markers and HTP in maize and *Arabidopsis* [20], exemplifies this application.

Phenotypic performance of a plant is determined by its genotype, the environment, and their interaction [8]. Despite the massive amounts of genotypic (including multi-omics) and phenotypic datasets have been generated, environmental factors remain comparatively under-characterized and are often treated as a "black box" rather than being resolved into specific drivers of phenotypic variation. Phenomics-enviromics (PE) crosstalk, the interaction between these two components is therefore essential for transforming plant breeding through synchronous phenotyping and envirotyping. In this perspective, we define the crosstalk as a negative or positive interaction, data integration, synchronic performance, and sharing in technologies, platforms and facilities between phenomics (large-scale phenotyping of a given individual species) [21,22], and enviromics (studying all environmental variables affecting plant growth and development) [23,24]. Plants do not respond to biotic or abiotic stress conditions independently, but via non-additive signaling interactions [25-27]. A real-time phenomics and enviromics (continuous, automated acquisition, processing, and integrated phenotypic and enviromic analysis during the growth and development of plants) [25] can capture these interactions by identifying the authentic environmental factors that breeders can assess the same plants simultaneously under real stress combinations in a coordinated PE crosstalk pipeline. An accurate crop prediction therefore requires multi-scale measurements integrated with environmental factors, because various stress conditions interact across cells, tissues, organs, individual plants, and populations.

Supported by AI and big data, PE crosstalk can advance high-precision tri-typing (genotyping, phenotyping, and envirotyping) technologies to systematically collect and analyze genotypic, phenotypic, and envirotypic variables [23,28] (Fig. 1). AI-powered breeding robots equipped with advanced sensors represent a new frontier by automating enviromic-phenotypic data collection, analysis, and breeding decisions across both field and controlled environments [29-31]. As PE crosstalk evolves, breeding is shifting from selection to prediction, integrating omics with PE to predict plant performance in diverse environments [32-34]. AI-driven algorithms and robotic platforms establish real-time decision-making, transforming breeding fields into dynamic environments where biotic and abiotic stresses are continuously monitored and superior genotypes are efficiently selected. In this perspective, the emerging role of AI is highlighted in enhancing every technology that facilitates PE crosstalk for the crop improvement. We discuss key technical limitations and potential concerns. Finally, we present a perspective on PE crosstalk, suggesting that integrating these technologies with AI will transform plant breeding.

Phenotyping and envirotyping in the era of omics

Phenotyping and envirotyping act as dual cornerstones. Phenotyping defines crop performance, while envirotyping shapes phenotypic expression. The two approaches function synergistically. Distinct from other routine omics strategies, phenotyping serves as the fundamental pillar and envirotyping acts as its contextual modulator. Their synergistic interaction collectively determines the performance of crop plants.

Phenotyping as a foundation in the era of omics

Phenotyping, the measurement of trait expression of a genotype at a specific developmental stage, serves as the foundational anchor of omics since it sets the pace for genetic understanding of trait expression and its interaction (Fig. 2). Tracking measurable phenotypes along plant's developmental timeline provides critical intuition into genotypic performance [35].

The full set of phenotypes expressed by a genotype, the phenome [27], is influenced by environmental variables. Unlike the static genotype, phenotype is dynamic, reflecting environmental effects and genotype by environment interaction (GEI). Studying the phenome is therefore vital to understanding plant functional genomics [23,25,36].

Advances in HTP technologies have revolutionized the collection and analysis of phenotypic data [36,37] (Table 1). Automated imaging sensing technologies now facilitate the acquisition of data on yield, resistance to abiotic and biotic stresses, and quality traits across various scales. These innovations empower rapid, high-precision, and scalable analysis, potentially enhancing the capacity to identify valuable genetic traits [38].

Phenotyping facilitates marker-trait associations mainly by linkage mapping and genome-wide association studies. These associations are crucial for understanding the genetic basis of traits, identifying functional alleles, and developing molecular markers for plant breeding. Continuous advancements in phenotyping techniques are thus essential for genomics and efficient genomic selection (GS) [35] and genomic-enviromic selection (GES)—a predictive breeding approach that jointly models environmental factors and genome wide markers [24,39] (Fig. 1).

Envirotyping as a contextual modulator in the era of omics

Before enviromic data were integrated into breeding applications, GEI was used to explain phenotypic variations (genomic effects) unexplained by breeding experiments, including genotype-specific responses across environments and performance inconsistencies often attributed to experimental errors. However, in reality (i.e. in the field), crops experience various, largely unmeasured environmental factors that change throughout the growth cycle [40], complicating the traditional GEI analysis. While approaches such as partial least squares can associate trait expression to specific weather parameters at discrete growth stages in crops such as wheat [41], the approach is rarely applied to MET data. Phenotyping has long dominated plant omics, whereas environmental factors have been seldom measured, although envirotyping has recently emerging as an essential counterpart in the era of omics.

Recent plant breeding increasingly emphasizes the necessity to characterize environmental conditions as thoroughly as genotyping and phenotyping. Environmental factors vigorously influence crop production by affecting processes from gene expression to metabolism throughout the growth and development of a plant [28]. A comprehensive understanding of the plant's environment improves genetic mapping and cloning, regulates gene expression, and underpins phenotyping and production protocols, thereby accelerating genetic improvement and enhance crop productivity.

Envirotyping provides a comprehensive characterization of environmental factors influencing plant growth and development, complementing phenotyping. This comprises measurements such as land surface temperature and a wide range of top-soil characteristics defining the environmental situations of a testing site [42]. While phenotyping reveals the genetic basis of traits, envirotyping provides necessary environmental context, enhancing the accuracy and interpretability of phenotypic data. For instance, a large-scale, multi-environment hybrid maize study leveraged automated machine learning to integrate environmental and genomic data, demonstrating that dimensionality environmental parameters aligned with crop developmental stages can effectively quantify environmental effects on phenotype [43]. As such, envirotyping can be regarded as a contextual modulator of interpretation in the omics era (Fig. 2).

Spatiotemporally structured enviromic data can predict patterns of genotypic performance under diverse conditions analogous to the use of linkage disequilibrium in genetic studies to identify associations between DNA segments [23]. Enviromics has already been applied in plant breeding programs. For example, climate-smart enviromic selection guidelines have been used to adapt elite common bean germplasm to various climatic conditions in Brazil [44]. High-resolution, high-throughput envirotyping (HTE) through satellite sensors, ground-based probes, and indoor facilities provide detailed spatiotemporal envirotypic information that, when combined with phenotypic data, enhances the accuracy of breeding prediction models and strategies [23,24] (Table 1).

As a third typing technology, envirotyping provides a third-dimension dataset that may precisely match genotypic and phenotypic data for individual plants or plots in plant breeding programs to elevate breeding efficiency by enhancing selection and prediction accuracy. Furthermore, envirotyping allows the designation of MET efficiency by optimizing selection of experimental sites and genotypes, reducing the reliance on extensive field trials, maintaining resources, and reducing cost of phenotyping [23]. For example, optimized METs in the Southern US rice belt revealed reduced trial sites that maintain a significant prediction accuracy and minimal phenotyping costs [45]. Through refining cultivar recommendations and categorizing genotype selection for specific environments, envirotyping enhances crop adaptation, performance, and resilience [44].

***In planta* and *ex planta* envirotyping**

Plants are affected by both *in planta* and *ex planta* environments, and their interactions, and thus, a given genotype has an ability to produce variable phenotypes across environmental situations thereby a dynamic dialogue between genes and the environment is reflecting a plant phenotype [25,46] (Fig. 2). A range of possible programs are provided by a genotype, though internal hormonal networks interpret external environmental signals to decree a biological response path. The internal environmental factors such as chemicals, temperature, nutrients, moisture or hydrostatic pressure, and acid pH are mostly caused by signal transduction and material exchange with external environments [27,28]. For instance, a single-nucleotide—C to T natural variation resulted in an increased gene expression and drought resistance in upland rice [47], revealing the function and effect of an internal environmental factor.

Ex planta or external environmental factors are those surrounding the plant with a direct effect, including biotic factors (such as pathogens, pests, and weeds), soil factors (soil class, texture, soil water holding capacity, soil composition, and soil salinity), climate (precipitation, wind, temperature, and radiation), and cropping system (crop rotation, intercropping, and agronomic practices). A biochar amendment, a suitable supplement for improved wheat yield sustainable production in saline environments [48], exemplifies an external environmental factor influencing plant phenotype.

Current status of phenotyping-envirotyping interaction

For a long time, the lack of synchronized phenotyping and envirotyping has made phenotypic data collected across laboratories, locations, and years (seasons) difficult to integrate, compare, and analyze comprehensively. Plant breeding is shifting from a genotyping centered approach to a comprehensive approach that integrates phenotyping and envirotyping within the genotype-phenotype-environment (G-P-E) triangle [23,28] to unlock complex trait variation. Even though genotyping has become high-throughput and affordable, major advances now lie on accurately capturing the 'P' and the 'E' and modeling their dynamic interactions [49]. HTP and efficient HTE across METs, supported by hyperspectral, light detection and ranging (LiDAR), multispectral, and thermal imaging, along with remote sensing, GIS platforms, and meteorological networks, are enabling trait prediction by converting raw sensor data into biologically interpretable environmental effects [50]. AI-based breeding platforms are scalable computational framework interfaces that support data-driven breeding decisions. For instance, an automated workflow for genomes-to-fields is providing multi-location and multi-year G-P-E datasets to reveal how curated envirotyping markedly enhances the prediction of flowering and grain yield traits in maize [49].

Innovative phenotyping and envirotyping technologies

The advent of multimodal HTP and HTE technologies marks a paradigm shift in accessing natural genetic variation across multi-omics and phenotypes for efficient selection of superior genotypes . These approaches, mostly based on advanced optical imaging sensors have progressed from modest measurements to multi-modal analyses spanning individual plants, field plots, and physiological to microscopic scales under different phenotypic and environmental conditions [51]. Platforms such as remote sensing satellites, unmanned aerial and ground vehicles (UAV and UGV), and gantry systems are commonly deploying to provide small-scale to field-based phenotyping and envirotyping [52] (Table 1). Applied to whole-genome sequenced and genome-edited plants [53], these technologies generate detailed datasets on shoot and root traits in controlled environments [54] or in situ observation [55], to support functional genomics and crop development. For instance, characterization of root phenotyping of 9,000 worldwide maize genotypes and wild relatives identified *ZmHb77,* gene conferring drought resistance in the lateral root system [56]. On the other hand, HTP of 368 maize genotypes identified 10,080 traits indicating drought resistance, along with 2,318 candidate genes and 1,529 QTL [57].

Enhanced phenotyping technologies involve collaboration between computer scientists, biologists, engineers and statisticians to facilitate accurate 3D plant and canopy structure modelling, vital for aboveground phenotyping, by engaging high-resolution 3D cameras [58], LiDAR [59], and light-field cameras [60]. Effective integration of these technologies can expand the scale of physiological trait evaluation and support more precise assessment of plant quality traits. For instance, 3D photosynthetic traits quantification for light use efficiency, stress detection, and yield prediction in wheat was conducted using the integration of multispectral and LiDAR data [61]. Automated ground robot, TerraSentia, equipped with advanced multi-sensor and AI-assisted analytics were used to measure various traits in maize across diverse fields in Canada and USA [62]. On the other hand, an indoor phenotyping robot capable of scoring agronomic and physiological traits was used to predict adaptive traits in the field for hybrid maize [63].

High-throughput, precise and innovative technologies developed for phenotyping have seldom been applied to envirotyping (see “Shared typing technologies”). Some of these technologies can be directly adopted for environmental data collection, whereas others require further improvement for envirotyping purposes. Although massive enviromic data are available for large-scale METs and locations via climate and GIS systems, targeted envirotyping of specific environmental factors still needs to be developed, supported by dedicated envirotyping technologies and facilities. This will enable synchronous phenotyping and envirotyping, thereby facilitating PE crosstalk.

Phenomics-enviromics crosstalk

What is phenomics-enviromics crosstalk?

Molecular marker-based genomic prediction has been broadly used in plant breeding, but it is frequently environment-specific and does not incorporate other data layers that explain trait variation, particularly enviromics [23,24]. Likewise, phenomics has often been implemented independently of enviromics, with limited consideration of environmental factors affecting phenotypes. Enviromics was introduced to thoroughly study the full range of environmental variables affecting crop performance [64] and GEIs across local environments to enhance selection efficiency and adaptation by uncovering environmental and environment-linked variation.

Classical MET-based GEI frameworks decompose phenotypic variance across categorical site–year environments, genotypes, and interaction components using limited end-point trait measurements and discrete environmental classifications, limiting biological interpretation and predictive robustness across untested environments. While these approaches are well established and remain powerful for estimating stability and adaptability, it is inherently limited in capturing the continuous, dynamic nature of environmental variation and the spatiotemporal development of traits [28,50]. PE crosstalk, in contrast, leverage high-resolution spaciotemporal phenotypic datasets with both continuous environmental factors and covariates to model genotype-specific reaction norms with a mechanistic inference, transforming conventional GEI from descriptive variance components into predictive, mechanistic modelling across explicit environmental factors and gradients [24,28,50]. This framework replaces categorical environmental descriptors with continuous environmental sensing, substitutes static phenotypes with spatiotemporal trajectories. Where this framework differs is primarily at the level of data integration and resolution, improving predictive accuracy and deeper biological interpretability, particularly how environmental factors around plants would affect phenotyping, rather than introducing a new statistical paradigm beyond established GEI modelling. PE crosstalk is hence to describe an explicit association of high-throughput and multi-dimensional phenotype evaluations with a widely characterized environmental data so that models can predict and explore environmental effects and GEIs as an operational clutch of modern plant-breeding.

A potential transformative application of combining G-P-E has led GES, a promising approach for efficiently exploiting natural diversity in crops, as demonstrated in barley breeding [39]. In parallel, multiplex nanosensor strategy provides an evidence of signal integration crosstalk at the whole-plant level under multiple stresses, offering a powerful way to decode plant signaling networks and realize acclimation and defense responses through molecular signaling dynamics [65].

Why does phenomics-enviromics crosstalk?

Plant breeding has shifted beyond genomics (genotyping the complete set genetic material of an individual) and sequencing alone to an integrated approach that includes enviromics and phenomics [23] addressing the limitations of genomics in predicting phenotypes in diverse environments [23,49]. For instance, an enviromic assembly approach has enhanced the accuracy and reduced the costs linked to genomic prediction of yield plasticity in crops such as maize [49] and wheat [66]. The holistic breeding approach of integrating genotype-by-environment-by-management (G × E × M) dimensions via predictive modeling allows to anticipate crop performance a way to close yield gaps and ensure sustainability [8,23,62]. Although breeding strategies that incorporate GEI features have enhanced selection efficiency, prevent prediction bias, and improved genetic gain [23,24,27], integrated agronomic practices strongly influence the expression of genotypic potential in crops [8,62]. All environmental variables affecting phenotypic expression, the envirome [23], need to be explored for understanding environmental effects and GEIs.

Enviromics has received little attention, resulting to less efficient selection and prediction [23,24,27]. Genotype performance across environments highlights the necessity to integrate environmental information into breeding programs, as phenotypic variation remains partially explained [8,49]. Although almost all omics data are molecular involving DNA, RNA or proteins, which can be called molecular omic or moleomic data, phenomics and enviromics provide non-molecular, associated with phenotypes and envirotypes. Molecular omics alone often fails to stipulate where, when, and under what environmental scenarios these molecular processes influence performance of a whole-plant. Integrated molecular omics with phenomics and enviromics via an appropriate AI-based models, however, provides the necessary spatiotemporal and environmental context.

Phenomics provides the physiological manifestation that links the molecular data to yield, and enviromics describes the environmental conditions defined by all environmental factors. Collectively, the molecular signatures are converted into actionable and environmentally contextualized trait mechanisms for breeding.

Future development in phenomics-enviromics crosstalk

The future of plant breeding is progressively defining by the PE integration to accelerate genetic gain. From autonomous field robots to satellite constellations, emerging platforms are generating multi-scale datasets that assist breeders link environmental effects and GEIs with unprecedented precision. Cost-effective high-resolution phenotyping and envirotyping can also be implemented through satellite-derived environmental factors and covariates (see "Shared typing technologies") and reanalysis of climate datasets. Consecutively, AI-assisted envirotyping robots could provide automated high-throughput, at plot and plant-level measurements in the field [28]. In contrast to phenotyping technologies, which must be standardized separately for each crop species and target trait, envirotyping can be standardized by envirotype, allowing multiple crops at the same location to share nearly the same tools, protocols, and environmental datasets.

Future large-scale, standardized synchronous phenotyping and envirotyping, multi-omics data, will generate multidimensional G-P-E-M big data that exceed the analytical capacity of conventional genetics and statistical models. Fully exploiting these datasets for breeding therefore requires AI-driven analytical and predictive frameworks, integrated interpretation of phenotypes, environmental effects per se (a historically neglected dimension), and GEI. Such PE crosstalk can only emerge from comprehensive, synchronized HTP and HTE datasets; otherwise, analyses remain restricted to traditional covariance-based GEI approaches.

The data deluge has, in turn, driven the innovation of sophisticated AI solutions, such as large language models (LLM) and AI-agent based systems capable of integrating generative synthesis, predictive analytics, complex logical inference, and autonomous decision making [31,34]. For example, platforms such as AutoGP [67], DeepPGDB [68], Smart Breeding [69], and BreedingAIDB [70] platforms are offering user-friendly and scalable computational framework interfaces to support data-driven breeding. These advances demonstrate that the PE crosstalk powered by robotics, remote sensing, and AI is the cornerstone of next-generation, data-driven, and climate-resilient crop improvement.

Integrated phenotyping and envirotyping for omics and precision breeding

Prediction of phenotypic traits largely relies on high-throughput genotyping and DNA sequencing technologies. These technologies assist GS and GES [24,39], corresponding with the genotype to phenotype (G2P) or genotype-envirotype to phenotype (GE2P) paradigms (Fig. 2). Accordingly, this integration improves plant breeding precision by more attested predictions, efficient utilization of resources, and enhanced cultivar recommendations (Fig. 3). For example, integrated environmental variables with genomic marker data can be used to develop prediction models accounting for local adaptation in crops, substantially enhancing the prediction of adaptive traits [39].

Over the last decade, substantial technological improvement and genetic architecture studies discovered that a significant proportion of heritability remains unexplained [71]. This "missing heritability" can largely be recovered by utilizing large-scale populations with extensive genetic variation and functional genes/alleles, combined with high-density molecular markers or high-precision sequencing [72].

Current breeding programs call for new technologies

Plant breeding has shifted from individual genes, genotypes, and environmental sites into a data-driven paradigm [73-75], calling for new technologies. Taking the fact that the distinct heterogeneity features of different omics layers and the data deluge, integrating multi-omics data remains a bottleneck [76,77]. Advanced technologies have emerging to facilitate an efficient use of data, such as semantic mapping, data mapping, extract-transform-load (ETL), and data modeling [24,77]. Such recent developed technologies should be designed for scalability to address heterogeneity and data management.

AI and deep learning (DL) algorithms play a magnificent role to capture nonlinear data generation, analysis, and integration of different data sources to empower genomic breeding [24,29,30]. For instance, an integrated AI method, integrating climate variables, soil data, and satellite-based vegetation indexes, have been used to enhance prediction of crop yield [73]. Integration of multi-omics data plays a vital role to predict plant traits in *Arabidopsis* [19], soybean [9], and potato [75]. The acquisition of high-throughput of complex traits, coupled with advanced sensors and imaging technologies, and automated phenotyping data analysis, are driving the development of phenomics [23,24,26,78]. Phenome and its assisted selection are offering a non-destructive and cost-effective approach for QTL mapping of yield trait, significantly reducing breeding cycle in rice [79], and facilitates rust and senescence prediction in maize [80]. This progression, coupled with envirotyping, has led to the expansion of phenotypic variations across environments in aligning with genomics and enviromics [49].

Shared typing technologies

To enhance the PE crosstalk using shared data, synchronous envirotyping and phenotyping must be prioritized. This ensures optimal utilization of interacted datasets for training plant breeding models and constructing next-generation decision-making systems. Most existing platforms and facilities can be adapted to collect both phenotypic and enviromic data, making possible the integrated precision HTP and HTE (Table 1).

Satellites can act as a promising platform for both phenotyping and envirotyping in plant breeding, although most studies have focused on phenotyping rather than envirotyping. Their major perceived limitation has been insufficient spatial resolution, exclusively for individual plants or specific experimental plots. Advances in high-resolution remote sensors could enhance the future precision HTP and HTE systems [78].

On the other hand, the capabilities of satellites for envirotyping are markedly well-suited for global characterizations of target environments. Mapping of various soil health indicators, such as texture and degradation [81], organic carbon [82], salinity level [83], moisture content [84], fertility status and nutrient availability [85], and heavy metals [86], has been effective through satellites.

However, higher resolution envirotyping is required at the single plot level, where limitations may exceed those faced in phenotyping. A prime example is the evapotranspiration phenotyping limited by the absence of thermal bands and low spatial resolution in many satellite system [87]. To address this outcome, approaches estimate evapotranspiration and crop water requirements using optical satellite bands, such as surface albedo and leaf area index, often combined with evapotranspiration models. Numerous studies leverage red and red-edge bands to predict crop coefficients, which then combined with evapotranspiration estimates to assess crop water requirements [88].

Spatial resolution can be enhanced by the combination of different imaging sensors. For instance, the integration of multispectral and color images [89], optical and radar bands [90], and optical and thermal bands [91], has proven useful for both phenotyping and envirotyping. Besides, low resolution limitations can be enhanced by employing appropriate machine learning (ML) algorithms [92]. For example, random forest algorithms have been applied to estimate within field grain yield of wheat using Sentinel-2 data [93]. Moreover, high-resolution Landsat-8, Sentinel-2, and Planet CubeSat, exploiting fusion of multi-satellite data and ML approach, were used in tracking the growth cycle of maize, by providing a daily leaf area index with greater spatial resolution [94].

Nevertheless, spatial resolution remains challenging in satellite-based systems, making it difficult to monitor experimental plots, individual plants, and their particular environmental factors. High-spatial resolution satellites offer a potential solution for crop phenotyping and within-trial envirotyping; for instance, some provide panchromatic resolution of about 0.5 m per pixel, multispectral imagery at 1–2 m, and radar resolution approximately near 1 m [89], often with revisit times as short as 24 hours. However, broader adoption is limited as many of these high-resolution platforms are commercially owned and not openly accessible to end users [95].

Spectral resolution is a critical feature of satellites, beyond spatial and temporal resolution as it determines the precision of plant physiological properties [95]. Insufficient spectral resolution, such as lack of red-edge wave and broad spectral bands, may hinder crop growth accuracy, yield estimation, water status, heavy metal stress, and nitrogen status [88,96,97]. Nevertheless, temporal gaps created by cloud cover, high spatial resolution deficit, and inequitable real-time data access coverage to every institution are not yet achievable without an extensive investment to deploy satellites in the agricultural system.

Although high-resolution satellite imagery data plays a vital role in breeding, real-time and affordable public access is limited by security, regulatory, and economic restrictions. Many satellites offered access under paid licensing models that some public-sector breeding programs are unable to access at an affordable cost [98]. Consecutively, high-resolution remote sensing satellites are imposed regulatory controls by national governments to protect security interests [99]. Moreover, countries mostly embargo real-time, open satellite imagery data access to some sensitive areas, raising privacy concerns as it provides military intelligence and conflict monitoring information [100].

Phenotyping is transforming from traditional manual measurements and visual scoring to high-throughput, precision remote-sensing approaches. Aerial and ground platforms such UAVs and UGVs, together with satellites and indoor facilities, now deliver detailed, high-resolution data on plant growth and development (Table 1). Integration of multiple imagers/sensors has enhanced the monitoring crop status, stress responses, and yield predictions. For example, multispectral, hyperspectral, and RGB combinations to measure wheat grain yield [101-103], and hyperspectral and thermal sensors detecting early-stage *Xylella fastidiosa* infections in olive trees [104] have been deployed.

Although technologies for envirotyping may appear relatively limited, most phenotyping platforms can be adapted with environmental sensors to capture air, soil, and stress-related data (Table 1). However, envirotyping generally lacks the fine granularity of phenotyping. This underutilized potential remains across nearly all facilities, with satellite sensors providing particularly immense promise for large-scale environmental monitoring [23]. However, challenges of precision and resolution persist, underscoring the need for further advances to match the phenotyping detail and support PE crosstalk.

Phenomics-enviromics across fields and controlled environments

The Space-Sky-Ground-Indoor network, integrating UAVs, UGVs, satellites, and indoor facilities, will be a key advancing plant breeding in both field and controlled environments (Fig. 4). By synchronizing phenotypic and envirotypic data, it supports robust PE crosstalk. AI-driven breeding platforms can then merge G-P-E data to optimize prediction breeding performance across environments [69]. Such synchronized envirotyping and phenotyping relied on continuous, real-time data collection from sensors and observations, while historical climate data combined with real-time phenotypic data further improve prediction accuracy. These capabilities are essential for climate-smart crop enhancement.

Scalable frameworks are quantifying environmental impacts like soil carbon stock changes and greenhouse gas emissions at field level [105]. The Climate Corporation and EOSDA Crop Monitoring platforms provide wide datasets for vegetation health assessments, soil moisture monitoring, and efficient resource use. Through integrating UGV, UAV, and satellite imagery data, higher precision enviromic data is achieved [32].

Modern breeding programs connect multi-environment and multi-trait data to moderate field phenotyping while maintaining high prediction accuracy [106]. Bayesian multi-environment and multi-trait models associate traits across years, enhancing correlations, prediction accuracy, and the development of biologically related yield and growth models. Integration enviromic data into such models is a logical next step for enhancing genomic-enviromic prediction [24]. More importantly, PE crosstalk combines advanced modeling with multiscale crop models to optimize genetic gain. Random regression models can predict genotype performance across limited sites, while multiscale models integrate genetic enhancements with crop management to improve productivity [107]. High-resolution environmental data further provide deeper understanding of environmental and genetic effects and their interaction, fostering the development of high-performing, resilient crops.

AI-assisted robots for phenotyping and envirotyping

Facilities and platforms required for precision and HTP and HTE must be supported by automatic systems, such as robotics [108]. Typing technologies are evolving through four generations: beginning with single-functional platforms (G1.0), advancing to multi-functional platforms (G2.0), one platform for all tasks (G3.0), and AI-driven platform (G4.0) (Table 2), as developed for phenomics. In the manual typing stage, data acquisition relied on direct human observations or as much using basic tools designed for specific tasks. The first generation (G1.0) of typing technologies was single-functional, capable of collecting only one type of data at a time. This necessitates using multiple manual protocols or robots for different tasks, such as seed counting, seed sizing, and plant height measuring, often varying across species.

The second generation (G2.0) introduced multi-functional protocols or robots capable of performing either one type of typings across various crops or multiple typings for a single crop. The third generation (G3.0) envisions an ideal “one-for-all” platform equipped with interchangeable probes and sensors. Such a platform or robot would handle phenotyping and envirotyping tasks across all plant species.

To achieve the fourth generation (G4.0) versatility, robots must replicate human behaviors during data collection. Tasks include navigating fields and plots, shaking or touching plants, tasting seeds or fruits, counting seed or fruit numbers, measuring plant height, and scoring responses to abiotic and biotic stresses (Table 2). These capabilities require robots to be equipped with AI to simulate complex human actions and make real-time decisions.

Benefits of integrating phenotyping and envirotyping

Breeding programs should integrate genomic, phenotypic, and envirotypic data, as environmental factors alone have been indicated to explain more than half of yield variation in crops. In a soybean trial across India, for instance, envirotypic covariates of 20 years of climate data in multi locations defined mega-environments, revealing the dominant environmental drivers yield production in soybean [109]. The combination of envirotyping with phenotyping ensures capturing environmental variations more completely, enhances model predictive accuracy, and supports optimal site selection and genotype-by-environment matching in fields [23] (Fig. 3).

Envirotyping also eases breeders explore GEIs, detecting specific environmental factors manipulating trait expression [28]. Traditionally, GEI analyses treated the environment as a secondary factor. By treating the E as an independent and equally significant dimension alongside G, P, and M, a comprehensive 3D analysis of G × E × M interactions become possible [8,23,62]. Crop management covariates like fertilizer nitrogen management and plant density [8,110] can be applied to exclusively understand G × E × M interactions [8,62].

This approach decomposes E and GEIs into distinct components, revealing precise environmental influences on traits and their interplay with genetic components and proper crop management strategies. Future research should prioritize methodologies that treat environmental variables as structured, quantifiable data streams alike to genomic data, assisting systematic exploration of environmental effects and their contributions to GEI.

Advanced models, holding the equation $P_t=G+E+P_i+M+GEI+P_iGI+GMI+P_iEI+EMI+P_iMI+P_iGEI+\ldots+P_iGEMI+error$, explicitly model major factors and their interactions, where P_t denotes the phenotype for the target trait t, and P_i denotes the phenotypes for all non-target traits. The variables in bold represent vector or matrix ones. The M can be included as a part of E in the model framework [23,28,62]. This transcends traditional frameworks, which depend greatly on MET data and treat GEI and other interaction items as an aggregated term. The anticipated shift provides a detailed understanding of crop-environment dynamics, enhancing predictive accuracy.

Panenviromics, panphenomics, and their integration

Panenviromics—characterization of all environmental factors across species, and panphenomics, which profiles all genotypes for a species, represent broader approaches to understand interactions between environmental factors and phenotypic traits across species and developmental stages (Fig. 2). These methodologies support large scale, multidimensional analysis of genomic effects, environmental influences, and phenotypic expression across various omics layers [23]. Panphenomics, however, represents a contrasting scenario where phenotypes exhibit fundamental differences across species due to distinct morphological, physiological, and developmental architectures. Even within a species, phenotypic expression varies markedly within genetic background, developmental stage, and environment, reflecting phenomic data highly species- or genotype-specific and challenging through cross-species comparisons.

Panenviromics, on the other hand, represents environmental characterization as a unique case where different species can share identical monitoring platforms and datasets when co-located in the similar geographic location or environmental site [50].

Panenviromics hubs on a uniform studying of environmental profiles, such as climate, soil, and geographical parameters regardless of which species inhabit that environment [28]. This property makes enviromic data highly transferable across taxonomic boundaries, enabling standardized envirotyping for multi-species communities, particularly for major environmental factors. Conversely, panphenomics focuses on large-scale phenotypic analyses, comprising observable morphological, behavioral, developmental, physiological, and molecular (DNA, RNA, and protein) profiling [111,112]. This perspective extends the concept of panenviromics to include internal and external environmental factors of plants across time, space, and species that may share similar environments at the same or different times (Fig. 2).

Omnibiology and panomics

In this Perspective, we use the term "omnibiology" to refer to a holographic biology framework that encompasses the complete spectrum of biological information across all living systems. Derived from the Latin prefix "omni-" (meaning "all" or "every"), omnibiology represents an integrative paradigm that seeks to capture, catalog, and comprehend the totality of biological data, from molecular structures to ecosystem-level interactions, within a unified conceptual and analytical framework. Unlike traditional reductionist approaches that isolate specific biological components, omnibiology emphasizes the interconnectedness of all biological entities and processes, treating life as a comprehensive, multi-layered information system where genomes, phenomes, and enviromes form an inseparable continuum [113].

The "pan-" prefix in omics denotes the comprehensive inclusion of diversity within or across species. However, significant conceptual and methodological differences exist among these panomic approaches.

Panomics at the molecular level (excluding phenomics and enviromics), particularly genotyping platforms, can be standardized and shared across different species. The same technological infrastructure, whether for genome sequencing, transcriptome profiling, or proteome analysis, can be applied universally because the fundamental molecular structures (DNA, RNA, proteins) are conserved across life forms. This cross-species compatibility allows researchers to utilize shared analytical pipelines and reference databases [114].

Enviromics interacts with all other omics layers, serving as a universal modulator of biological information. Environmental factors influence all other omics disciplines, though the magnitude and mechanisms of their effects vary across molecular levels. Epigenomic layers demonstrate the most environmental responsive, with DNA methylation, histone modifications, and chromatin accessibility changes rapidly in response to environmental cues. In contrast, DNA-level omics (genomics) remain relatively stable, as genetic sequences are generally invariant within an individual's lifetime [50]. This variation in environmental sensitivity across omics layers requires careful consideration of environmental factors and covariates in integrative biological studies.

These distinct properties of different omics layers, ranging from the stability of genomic data to the dynamic nature of transcriptomic and metabolomic information, create substantial difficulties in integrating and analyzing multi-omics datasets. Reconciling these disparate data types into coherent biological interpretations requires sophisticated statistical frameworks and computational approaches [113,114].

Balancing precision and cost

Achieving more precision in HTP and HTE often requires sophisticated, costly technologies. Precision in data collection is essential to ensure the relevance and reliability of breeding information and reduce bias in predictive models. While higher precision is always desirable, the associated expenses must be balanced to avoid prohibitive costs. For instance, a panicle neural radiance fields, PanicleNeRF, was developed to reconstruct a rice panicle 3D model with high precision and at an affordable cost [115].

As more environmental conditions are included in a phenomic study, the complexity and the resolution of the phenome increases [35]. This growth in data complexity affects many aspects of PE crosstalk, including data management, analysis, and interpretation (Fig. 3). High-resolution data in both phenotyping and envirotyping help breeders to identify the environmental factors most significantly affecting traits of interest. Integrating these high-resolution datasets can make breeding programs more effective.

Integrating panenviromics and panphenomics

The panphenomics and panenviromics integration provides a holistic understanding of genomics, enviromics and GEI to the manipulation of complex traits of a genotype. This approach calls immense promises to enhance crop breeding, predict plant responses, and enhance ecosystem functionality.

Traditional plant breeding often studied a single or a limited number of traits, offering incomplete performance view of a plant. This approach captures snapshots rather than a comprehensive understanding of a plant's life cycle. To address these limitations, the concepts of the phenome (envirome) and panphenome (panenvirome) have been introduced, drawing parallels to the genome and pangenome frameworks.

The ultimate goal of ML in plant breeding is to model the panphenome by integrating data from the pangenome, the full genome of individuals of an organism [116], and panenvirome (Fig. 2). Advanced sensors and computer vision technologies are potential to capture extensive data for this purpose. However, capturing the phenomic-enviromic information and their crosstalk is challenging. Both fields need robust experimental design and substantial funding; their integrating further amplifies challenges by requiring large datasets and more complex modeling schemes (Fig. 3). To minimize this complexity, it is better to focus on key factors and use streamlined models for developing practical breeding strategies.

Omics research often strives to measure all elements within a given “ome”, but fully capturing every possible trait and environmental factor for a single genotype is nearly impossible. This is due to the potential interactions a given genotype may experience through time and phenology with different environmental factors. As such, either phenomics or enviromics does not fundamentally require complete measurements, though future advancements may bring this closer to reality [24,35].

Researchers should identify critical interactions between phenotypic traits and environmental factors to construct predictive crop-performance models (Fig. 3). Once complete phenomic and enviromic measurements become feasible, breeding models can be developed on synchronously collected data for every genotype. Achieving this requires high-performance computing and AI to extract data and deploy the models effectively.

PE crosstalk plays a vital role in understanding phenomic and enviromic effects, GEIs, and broader G-P-E relationships. Integrating multidimensional G-P-E data with advances in spatiotemporal multi-omics and single-cell omics technologies is pushing the boundaries of plant breeding [24,117]. This approach creates vast datasets requiring advanced analytical tools (Fig. 3 and 4). For instance, time-controlled transcriptomics have been used to study flowering time regulation in rice, detecting major genes participated in photoperiod sensitivity [118]. Likewise, single-cell omics technologies support evaluation of molecular profiles in intricate tissues, showing cellular heterogeneity in response to environmental cues [117]. In *Arabidopsis* roots, single-cell transcriptomics revealed discrete gene-expression patterns within cell types [119], while spatial transcriptomics in stressed rice leaves identified regulatory appliances underlying functional specialization [120].

The shifting from analyzing individual traits in a single environment to panphenome modeling across the panenvirome is a major driver in plant breeding. By integrating G-P-E data, comprehensive predictive models are created, offering a more holistic view of crop-performance and better prediction. Full-dimensional, full-parameter, and streamlined optimization models [24,121,122] capture complex biological systems for high-resolution predictions.

DL and AI further enhance predictive capacity (Fig. 2). DL and deep kernel methods have been effectively employed to genome-based prediction in crops across multiple environments [122]. Integrated G-P-E models use multi-omics datasets and AI to deepen grasp of intricate interactions [24]. High-throughput and advanced ML technologies can accelerate breeding programs to develop climate-smart and high-performing cultivars. For instance, ML algorism versus linear models were used for yield and flowering time prediction of untested maize hybrids where ML inevitably captured a complex non-additive GEIs [123].

Crop improvement driven by genomics-enviromics-phenomics triangle

Enviro-phenomics, defined as integrated enviomics and phenomics through coupled, synchronized envirotyping and phenotyping of the same genotype or set of genotypes. Multi-omics, including transcriptomics and metabolomics, facilitates identify stress-adaptive traits and strengthen PE crosstalk (Fig. 1 and 2). These perceptions support the development of crop varieties matched to sustainable agricultural systems while enhancing genetic merit through integrative omics [78]. As a multidisciplinary context, enviro-phenomics offers a quantitative basis for plant breeding by combining environmental and genetic data [23]. This also allows identify optimal environmental circumstances for specific genotypes, enhancing genotype-environment suitability and efficient breeding.

Omics interactions: triangle and pyramid

The omics-enviromics-phenomics triangle: at the core of biological systems lies a fundamental triangular relationship among molecular omics (excluding phenomics and enviromics), enviromics, and phenomics. Here, "omics" encompasses genomics, transcriptomics, proteomics, metabolomics, and epigenomics, molecular layers that capture biological information from DNA to functional molecules. These three components form an inseparable triad that governs organismal structure and function [124]. Molecular omics provide the genetic and biochemical blueprint, enviromics delivers the external context, and phenomics represents the observable outcome of their interaction. This triangular framework captures the dynamic interplay between internal biological potential and external environmental forces in shaping phenotypic expression [125].

The omics pyramid with enviromics at the apex: when considering all omics layers collectively, a hierarchical pyramid structure emerges. All molecular omics constitute the polygonal base of this pyramid. Enviromics occupies the apex position because it influences every other omics layer without exception [126]. Environmental factors modulate gene expression, protein synthesis, metabolic fluxes, and epigenetic modifications, making enviromics the universal modulator of biological information. This pyramid architecture underscores that environmental context serves as the overarching filter through which genetic potential is ultimately realized, highlighting the centrality of enviromics in integrative biological studies.

Enviro-phenomics-driven crop improvement

Omics provides precise selection of traits by integrating ML and big data, enhancing selection accuracy, accelerating breeding cycles, and strengthening breeding strategies [122]. For instance, integrated genomic and multi-environment data allowed precise prediction of maize grain yield and moisture content [127], while genomic ML enhanced soybean seed quality trait [128].

Multi-omics approach helps discover regulatory systems underlying complex traits remained unexplored via single-omics [19,61]. Proteomics, specifically, has become a vital layer for identification of functional effectors, including post-translational modifications, that are mostly unseen to DNA/RNA-based evaluation [129]. For example, an antibody-based method along with isobaric labeling identified 17,940 ubiquitinated lysine loci from 6,453 proteins of rosette leaves, seedlings, and primary roots in *Arabidopsis* [129]. Even though large-scale proteomics remained technically time-sensitive and demanding, mass spectrometry advances are steadily improving throughput and reproducibility. Proteomics revealed a vital promise when applied to complex traits with low-heritability like disease or drought resistance where transcriptional regulation alone is unable to capture main post-translational mechanisms [130]. Collectively, strategical integration of proteomics within multi-omics pipelines, signifies a high-value to speedup molecular breeding and precision agriculture.

Generalized enviromic models in plant breeding

Generalized enviromic models use multiple regressors for environmental factors, annual grain crop productivity, and photoperiod-dependent flowering time [19,131]. High-resolution platforms evaluate variables such as evapotranspiration, soil properties, climate, and meteorological data at experimental site and plant level [28,66] (Table 1). These data assist establishing efficient breeding system and recurrent selection by detecting superior parents and cross combinations for specific environments.

Enviromic models also allow the use of genetic germplasm resources by directing the rescue of materials with location-specific phenotypes. Long-term grain yield prediction trials in sorghum for example, revealed strong GEIs, mainly seasonal and spatial driven variability in water supply that caused sorghum to inconsistently rank across locations and years in north-eastern Australia [132]. Reaction norm models [133] and enviromic models provide robust statistical frameworks for this purpose [134]. However, when field experiments are significantly reduced (i.e. limited training data), these models may struggle to select genotypes that maintain average yield performance [135].

Genotypic imbalance in such scenarios can be managed with specific experimental designs for effective selection, even with limited trials. For such models, performing more trials with less replications is often more effective than fewer trials with more replications [136]. Combining data from multiple environments utilizing predictive error variance or Bayesian methods to estimate ambiguity enhances predictive capability [137]. This approach allows for more informed cultivar selection in specific environments.

AI-driven data integration, modeling, and prediction

Advanced data-mining algorithms and DL approaches are necessary to ease the complexity of multi-omics characterized by varying formats, dimensions, and scales [77]. AI-derived and cloud computing methods facilitate G–E–P data integration, optimize plant breeding predictions, and enhance decision-making processes [25,138] (Table 1, Fig. 2). The complexity and diversity of environmental data, as we do for phenomics, is addressed by a systematic ETL process [24]. This comprises collecting data from diverse sources such as weather stations, sensors, satellites, and climate repositories, standardizing it for consistency, and loading it into analytical environments for detailed analysis (Table 1). The Genome-to-Field Initiative uses multivariate analysis to investigate GEIs, characterize genetic and environmental structure, investigate association of key agronomic traits with environmental factors, and establish benchmarks for genomic prediction models in maize [49]. Google Earth Engine and other platforms facilitate this process by integrating surface measurements, satellite observations, and climate model data to offer comprehensive envirotypic information [139]. With an integrated satellite imagery, soil information, and seasonal weather conditions, Google Earth Engine platform was used to reveal a robust framework to predict wheat yield [73].

Comprehensive environmental data platforms, such as modern era retrospective analysis for research and applications, version 2 (MERRA-2) and ERA5, are important in global-scale climate reanalysis, involving atmosphere, ocean waves, land surface, and other climatic factors [140,141]. Additional platforms such as NCEP/NCAR Reanalysis and the Copernicus Climate Change Service (C3S) enhance climate research and weather forecasting [141]. To handle such vast datasets, cloud-based ML computational resources, supported by high performance computing and cloud services like Google cloud, Amazon Web Services, and Azure are required [138,142] (Table 1, Fig. 4).

Robust packages for data extraction, manipulation, and integration into enviromic models are offered from python and R ecosystems. Python libraries like Sentinelsat and pyModis are effective for extracting satellite data, while R packages like NASA POWER and raster manage climatic and geospatial data [143].

Conventional predictive approaches, such as Bayesian and mixed models, complemented by advanced AI and ML techniques, are prompting a paradigm shift in plant breeding and geoprocessing. AI enhances mapping accuracy, predictive modeling, and spatial pattern recognition, revolutionizing environmental monitoring, disaster management, and agricultural decision-making [144].

Emerging AI techniques, such as artificial neural networks, and joint learning algorithms such as XGBoost and random forests, have revealed superior performance in predicting geological and agricultural properties in comparison to other algorisms [145]. The synergy between geoprocessing and AI, often referred to as GeoAI, holds enormous potential for addressing sustainable land management.

AI techniques in geosciences and geotechnical engineering have been successful, and similar applications in plant breeding could reform crop improvement [146]. Through ML techniques, such as neural networks, AI helps learning from complex data and generating valuable predictions, bypassing the limitations of traditional approaches. AI also simplifies data acquisition for crop breeding, facilitating the development of robust predictive models [34,144] (Fig. 3).

Moreover, deployment of cloud-based ML models has become a cornerstone in the modernization of precision agriculture, leveraging the computational efficiency, flexibility, and scalability of cloud platforms [138,147]. Deployment of serialized models along with pre- and post-processing pipelines are making possible the real-time inferences. Such models can be updated and optimized whenever a new dataset become available, including data collection across seasons, years, populations, and species. This approach allows secure, continuous up to dated, and monitoring to ensure models remained accurate through time. For instance, a cloud-based platform incorporating ML with agronomic and real-time environmental data transforms crop recommendation model, providing crop recommendations tailored to regions and commercial needs in India [138].

AI-driven imputation for envirotypic data

Envirotypic datasets often experience from missing values due to sensor malfunctions, network disruptions, or incomplete data collection. Missing data creates biases, and reduces predictive accuracy of models. Traditional imputation methods, such as Multivariate Imputation by Chained Equations (MICE) and k-nearest neighbors (KNN), can be used to fill these gaps. While effective in certain contexts, these approaches often struggle with complex and high-dimensional data. Advancements in ML approaches, such as missForest employing random forests for iterative imputation, outperform conventional techniques by lowering errors while managing mixed data types more effectively [148].

In recent advancements, physically constrained ML frameworks ensured that imputed values remain realistic and adhere to natural constraints, significantly enhancing the reliability of envirotypic models [149,150]. Such frameworks are complementing by cloud-based data processing systems enabling large-scale, near real-time imputation of missing values. These systems also offer compatibility and scalability across datasets (Table 1, Fig. 4).

Envirotypic data may be wholly absent for some specific sites, plots, or genotypes due to non-existence of envirotyping activities. Such scenario needs imputing for entire locations of genotypes depending on information from similar or neighboring areas. Nearest-neighbor interpolation and advanced time-series imputation approaches are effective. For example, eight time-series data imputation methods, including mean, median, MICE, KNN imputation, multi-directional recurrent neural network, self-attention-based imputation for time series, transformers, and bidirectional recurrent imputation for time series, have been utilized to predict air quality [151]. Similarly, enviromic factors such as longitude, latitude, and elevation can be used to predict environmental characters at any given sites [24,28]. The accuracy of these predictions improves when data from nearby locations are included.

However, some enviromic factors are highly variable, sensitive, and difficult to impute with precision. For such cases, advances in high-resolution envirotyping tools and facilities are making it increasingly feasible to measure these factors at the scale of single plots or plants. This progress reduces reliance on imputation for critical variables, enhancing the overall quality of envirotypic datasets.

AI-driven imputation methods are transforming plant breeding by addressing the challenges of data sparsity and imbalance (Fig. 3). By ensuring complete and accurate environmental datasets, these methods help breeders to optimize genotype selection, refine predictive models, and match genotypes to specific geoclimatic conditions with greater precision. Incorporating crop growing conditions from the fields such as environmental monitoring and water resource management, plant breeders can adopt advanced imputation techniques to tackle challenges unique to agriculture. Decision-making capabilities are improved by such techniques to develop robust predictive models.

Integrated breeding strategies using enviro-phenomic information

The integration of enviro-phenomic information into breeding platforms is transforming current plant breeding by combining numerous advanced technologies. For example, integrating enviro-phenomic information in off-season breeding nursery speed up generation advancement by changing target environments and controlled off-season nurseries [152]. HTP, HTE, networking, and data management are vital for enhanced plant breeding (Fig. 2). Marker-assisted selection (MAS), GS, and GES accelerate generation cycles in off-season, where cultivars can be developed and subsequently examined in target environments.

Vast time-series trait data generated by HTP and HTE technologies should be interpreted with detailed environmental data to reveal a true biological interpretation of a genotype [24]. By prioritizing large-scale and rapid data collection, field-based and controlled-environment platforms can capture plant traits at various layers from canopy to cellular levels [27,153]. Integrating these approaches with aeronautics, computing, robotics, and automation has led to the HTP systems equipped with aerial, ground-based, and microscopic platforms to characterize traits from field to tissue scales [62,154,155]. Microscopic systems for precise imaging of cellular and subcellular features [155], ground-based platforms for quantifying individual plant traits [62], and aerial phenotyping systems [156] are collectively monitoring pathological, physiological, and morphological traits to accurately evaluate stress responses and crop-performance.

The initial step in the enviromics basis for plant breeding is defining the target population of environments (TPE), the set of envirotypes and their frequencies within a region of breeding where performance of genotypes is evaluated [23]. Within the availability of geospatial and GPS technologies for civilians, environmental variability can be quantified at field, farm, and regional scales [23]. Once the TPE is defined, phenotypic data across various environments should be analyzed to capture necessary envirotypic variation [50]. Advanced environmental and improved soil sensors facilitate simultaneous phenotyping and envirotyping, producing an integrated dataset that associates environmental heterogeneity along with genotype performance. For instance, enviromic evaluation of climate-driven adaptation in common bean has identified critical developmental stages and climate limits, guiding climate-smart variety selection [44]. Integrating soil and meteorological data with phenotypic information also enables ML and modeling approaches to predict disease and pest risks, monitor nutrient use efficiency, and predict crop performance across environments.

An integrated approach combining gene transfer, doubled haploid (DH) technology, speed breeding, and GS has been suggested to modernize plant breeding [152,157]. Enviromic assembly, which incorporates environmental data into models of whole genome prediction models, reveals promise in tropical maize [158]. This approach uses environmental databases to support climate-smart decisions, lower field costs, and enhance prediction of future scenarios. An integrated P-G-E approach further enhances return on investment.

DH technology accelerates breeding by rapidly developing pure lines [159]. Advances in gene editing and cloning for DH induction in maize have made DH programs feasible in both monocotyledonous and dicotyledonous crops [159]. Together with environmental monitoring and plant growing systems [27,160], speed breeding can attain six to nine generations every year in some species [161,162], and when combined with GS, MAS, and DH, it may substitute conventional field breeding while reducing reliance on field experiments and winter nurseries.

Seed chipping (removing a small part of a seed for DNA extraction before sowing) and non-destructive genotyping, as vital components of seed-based high-throughput genotyping approach, also accelerated breeding cycle [163-165]. This genotyping method provides high-quality DNA, while germination viability is maintained in major crops such as maize [163], groundnut [164], soybean [165], and pigeonpea [166]. Seed-based genotyping integrated into GS and GES is currently speeding up breeding frameworks, cost-efficient screening, and decision-making through genotyping and predictive modeling at the early stage of plant growth or before planting.

Prospects and challenges

Future of panphenomics and panenviromics

Plant breeding is increasingly driven by the holistic panphenomics and panenviromics integration, a data-rich framework linking environmental effects and GEIs. Panphenomics integrates quantifiable traits of plants from molecular and cellular features to landscape and canopy phenotypes across growth stages and environments, developing a combined phenome atlas through multi-sensor data capture, temporal modeling pipelines, and AI-aided data integration such as dynamicGP [20]. Likewise, panenviromics is compiling comprehensive environmental profiles (such as soil, hydrology, weather, and management), transforming them into enviromic markers to be modeled along with genomic data [50].

The development of omnibiology, encompassing high-dimensional, structurally complex big data that integrates moleome, phenome, and envirome information, has created computational demands far exceeding current classical computing capabilities [167]. Future quantum computers, leveraging superposition and entanglement principles, offer a paradigm shift for processing such massive multi-omics datasets. Additionally, emerging energy technologies, including nuclear energy and advanced sustainable power sources, may provide the necessary infrastructure to support these computational advances. This convergence of quantum computing and next-generation energy systems could ultimately overcome the modeling and simulation challenges inherent in holistic biological systems analysis.

AI and AI-driven intelligent breeding

AI, ML and AI-driven models play a critical role in analyzing and processing large-scale G-P-E datasets, thereby, the data deluge produced, in turn, is driving sophisticated AI innovations such as LLMs and AI-agent based autonomous decision in plant breeding [31,34]. Robust algorithms enhance environmental classification accuracy allowing breeders to design effective METs and optimize site selection [109,121,168]. Integrated G-P-E systems demonstrated significant genetic gains in breeding programs [24,169]. AI-driven advances, such as Joint Genomic Regression Analysis (JGRA) and Critical Environmental Regressor via Informed Search (CERIS), indicated a great promise in crop performance prediction across environments [169,170]. Moreover, various breeding platforms offered scalable and user-friendly computational framework interfaces are now supporting data-driven AI-based breeding decisions.

By further advancing AI-driven intelligent breeding, we will not only unravel the complex mechanisms of G-P-E interactions but also pave the way for next-generation molecular design and precision breeding that is essential for future extraterrestrial agriculture. As gene functions and regulatory sequences are elucidated, and G-P-E interactions governing trait expression become fully understood, numerous crop traits can be precisely engineered and developed by molecular breeding within plant factories. This knowledge drives a paradigm shift in plant breeding from traditional field-based selection to controlled indoor manufacturing [171]. Such advancements are critical for establishing bioregenerative life-support systems in space habitats, enabling sustainable food production in lunar and Martian bases [172]. This transition supports humanity's progression toward becoming a multiplanetary species.

PE crosstalk in modern plant breeding

The adoption of precision HTP and HTE, assisted by advanced robotics and AI technologies, is set to reform omic study and plant breeding. By escalating our understanding of environmental effects and GEIs and optimizing breeding strategies, PE crosstalk can navigate extensive advancements in crop design and engineering. The synergy integration of multi-omics with advanced technologies is revolutionizing themselves and plant breeding into predictive science. It bridges molecular mechanisms with field, plot, and even an individual plant scale of environmental dynamics, pioneering precision PE crosstalk, while enviro-phenomic data make multi-omics more functionally interpretable. Integrating high-resolution envirotypic data helps capture the detailed environmental factors at site-specific levels, granting enhanced granularity in data collection [28,49].

By integrating G-P-E datasets, breeders can simulate environmental effects and GEIs across scales and predict performance of a genotype under future climatic conditions [23].

Just as AlphaFold revolutionized protein structure prediction [18] and AlphaGenome enabled genome sequence-based functional prediction [173], all-purpose AI-driven breeding robots integrated with multifunctional pipelines, encompassing typing, prediction, and selection, are poised to transform crop breeding. These integrated systems combine high-throughput genotyping, AI-assisted phenotype prediction, and automated selection into continuous pipelines, enabling autonomous breeding cycles that operate with minimal human intervention [31,34].

Despite its highlighted potential, several challenges must be addressed to fully harness the PE crosstalk:

1. Data standardization and integration: aligning diverse datasets collected across phenotyping and envirotyping platforms and scales is necessary to create comprehensive databases. To enhance the large-scale data landscape, approaches have been deployed for plant breeding to manage heterogeneous data, bridge resources distribution, develop accessible, findable, reusable, and interoperable data process [174,175], and establish a public programming interface.

2. Advanced model development: enviro-phenotypic autonomous sensor streams, high-resolution imagery, and -omics datasets are massive, producing multi-dimensional and heterogeneous data that demand advanced computing environment and model development [23,24]. Current models must evolve to integrate feature selection dimensionality reduction, and prediction performance within the combined G-P-E space. There are limited models that accommodate the high dimensionality and complexity of G-P-E data across time and space.

3. Full spatiotemporal data utilization: development of models with the capability of utilizing enviromic dataset from MET sites to individual plants is required. The current performing methods, such as CERIS and JGRA, have limitations to fully capture data variability, revealing that AI-driven approaches are highly required to combine G-P-E data [23,170].

4. Scalability and accessibility: ensuring the scalability of advanced technologies to worldwide breeding programs is special important, predominantly in scarce resource regions. Precision HTP and HTE often requires sophisticated technologies incurring significant costs. Affordable and accessible solutions, such as open data initiative to share protocols and datasets, must be prioritized for widespread adoption.

The integration of enviro-phenomics with AI-driven technologies and a comprehensive understanding of PE crosstalk promises to create a new era of omics and plant breeding. Bypassing the existing challenges helps develop resilient, high-performing crop cultivars. PE crosstalk corresponds to a transformative approach, bridging the G-P-E gaps to foster predictive, manageable, and technology-driven omics and breeding systems. Advanced technologies, such as robotics, machine learning, and high-throughput sensing platforms can accelerate developing climate-smart crops, ultimately contributing to the global food security.

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Author contributions

Y.X. and H.L. co-led the conceptualization; H.L., Y.X., S.G., and T.W.G. drafted and revised the manuscript, and created the figures and tables; and W.L., J.W., Z.H., M.P.R., J.L.A., and S.H. contributed to the revision, creation of some figures, and tables. All authors contributed to the development of the manuscript.

Competing interests

The Authors declare no competing interests.

Table 1. **Platforms, techniques (sensors/imagers) used in phenomics and enviromics.**

Platform	Techniques and application examples	Reference
Indoor facilities	RGB imagers, stereo vision and SFM, multispectral, hyperspectral, thermal, chlorophyll fluorescence sensors/imagers for assessing plant growth, height, biomass, total area, architecture, photosynthetic performance, water and nutrient status, disease occurrence, chemical compositions and quality traits among other phenotypic traits. Most UGVs/stationary field platforms can be also set up indoor and used in phenomics and enviromics.	176-178
UGVs/stationary field platforms	RGB imagers, stereoscopic vision and SFM, multispectral, hyperspectral, thermal, chlorophyll fluorescence, and LiDAR sensors/imagers for predicting crop yield or assessing crop growth, plant height, biomass, structure, phenology, photosynthetic characteristics, leaf area index, crop water and nutrient status, biotic disorder impacts, crop quality or chemical composition, among other phenotypic traits; air and soil environmental variables, PPFD, evapotranspiration enviromic variables.	178-181
UAVs	RGB imagers, SFM, multispectral, hyperspectral, LiDAR, chlorophyll fluorescence, thermal sensors for predicting crop yield, crop growth, biomass, phenology, plant height, canopy structure, leaf area index, water and nutrient status, photosynthetic performance, pathogen detection, weed detection, plant numbers, plant disease, vegetation indices, plant species composition, leaf stomatal conductance, heat stress, crop quality characteristic, chemical composition; environmental factors including soil properties, spray drift, water stress, nitrogen fertilization, atmospheric chemical composition, surface reflectance, and evapotranspiration conditions are amenable for evaluation.	182-185
Satellites	VIS, NIR and SWIR bands, multispectral, hyperspectral, RADAR, thermal optical sensors, and LiDAR to predict yield or assess crop growth, water or nutrient status, biotic disorder impacts, vegetation indices, plant health, biomass, and canopy phenotypic traits; whereas, soil composition, moisture discrepancies, surface albedo, ocean salinity, environmental quality, atmospheric variables, air pollutants, thermal variations, solar energy, fire emission estimation, evapotranspiration, weather forecasting, precipitation, water vapor, biotic and	186-190

	abiotic stresses such as drought, heat, heavy metal enviromic traits.

RGB: red, green, blue; LiDAR: light detection and ranging; UGV: unmanned ground vehicle; VIS: visible; UAV: unmanned aerial vehicle; NIR: near infra-red; SWIR: short-wave infrared; RADAR: radio detection and ranging; SFM: structure from motion; PPFD: photosynthetic photon fluence density.

Table 2. Robot platforms for phenomics and enviromics generations 1.0 to 4.0.

Generation	Platform	Sensor	Application
G1.0: single functional	Individual platforms such as, UGVs and UAVs used one at a time	Individual sensors, such as, RGB camera, temperature, humidity, and CO_2 level monitors, used one at a time.	Phenomics for individual traits and enviromics for individual environmental characters.
G2.0: multi-functional	Multi-platforms systems, including UGVs, UAVs, satellites, and hybrid robotics systems, used separately.	Multiple-sensors with specific functions, such as RGB cameras, hyperspectral, multispectral, LiDAR, thermal cameras, soil moisture, nutrient, environmental, and weather sensors, used separately.	Phenomics for multiple-traits and enviromics for multi-environmental characters, performed separately.
G3.0: one for all	One robot designed to fulfil all purposes.	Replaceable and interchangeable sensors with diverse functions.	Phenotyping all traits and envirotyping all environmental variables, performed by a single robot.
G4.0: AI-driven	One robot designed for all purposes, fully supported by AI.	A unified sensor system supported by AI, capable of performing all required functions.	Fully mimics all activities of breeders in the field or facilities, including observation and selection, using AI-driven robotics.

UGV: unmanned ground vehicle; UAV: unmanned aerial vehicle; RGB: red, green, and blue; LiDAR: light detection and ranging; AI: artificial intelligence.

Figure legends

Fig. 1. Genomics-Phenomics-Eviromics (G-P-E) triangle in plant breeding. Above: The conventional G-P-E relationship can be visualized as an incomplete triangle, lacking a direct relationship between phenotype and envirotype, excluding envirotypic data. This approach has evolved into a new framework, the “golden triangle”, incorporating genotyping, phenotyping, and envirotyping within a multidimensional framework across populations, plant species, time, and space. This includes different developmental stages for a specific population or species. Below: The phenome is shaped by genome and envirome. The genome-phenome relationship has been extensively studied through multi-omics approaches, forward and reverse genetics, and plant breeding strategies such as domestication, phenotypic selection, and genomic selection. Establishing the phenome-envirome relationship requires advancements in functional enviromics, including envirotyping, enviromics and panenviromics (which involve all environmental factors across relevant species), G-P-E interaction analysis, genomic-enviromic prediction, and phenomic-enviromic (PE) crosstalk, all supported by big data and artificial intelligence (AI). Created in BioRender. Gao, S. (2026) https://BioRender.com/9uonyam

Fig. 2. AI-driven integration of genomics, phenomics, and enviromics for accelerated crop breeding. Phenotyping drives breeding by identifying traits of interest in plant breeding and genetic engineering. Envirotyping and genotyping provide essential environmental and genomic contexts. The genotype to phenotype model focuses on direct genetic influences on traits, while the genotype and envirotype to phenotype model incorporates G-P-E factors, offering a more comprehensive explanation of trait expression. AI-driven integration of G-P-E-M data accelerates breeding through enhanced predictive models, enabling faster testing and deployment of new crop varieties. AI and ML algorithms played a magnificent role to capture nonlinear data forms, analysis, and integrating from different sources to enable the omics breeding. This "breeding factory" approach reduces time-to-market, enhances productivity, and facilitates streamlined commercialization of improved cultivars. Created in BioRender. Gao, S. (2026)

https://BioRender.com/nxeltiw

Fig. 3. AI-driven application of genomic-phenomic-enviromic (G-P-E) data in plant breeding. In the first step, G-P-E data are processed using dimensionality reduction and data fusion techniques. The fused datasets are then input into AI model equipped with multiple hidden layers, enabling them to learn complex relationships between variables. These models predict key agronomic traits such as yield or stress tolerance, guiding more precise breeding decisions. This approach facilitates the detection of desirable genotypes and populations, streamlining the development of enhanced crop cultivars. Created in BioRender. Gao, S. (2026) https://BioRender.com/ptuh897

Fig. 4. Integration of phenotyping and envirotyping in the Space-Sky-Ground-Field-Indoor network for the next-generation of plant breeding. The network shapes the basis for next-generation plant breeding, combining phenotyping and envirotyping to urge innovation. This integrated network manages data from several sources, like satellites, unmanned ground vehicles (UGVs), aerial vehicles (UAVs), indoor facilities, and other platforms. By enabling the comprehensive collection of phenotypic and environmental data across varied conditions, the network allows phenomics-enviromics (PE) crosstalks, laying a basis for advanced breeding strategies. Created in BioRender. Gao, S. (2026) https://BioRender.com/ptuh897. Satellite and winged UAV icons designed by Freepik from Flaticon; UAV icon designed by Luvdat from Flaticon.

Editor's Summary

Genomics, phenomics, and enviromics constitute the G–P–E triangle in plant breeding, yet enviromics and its interaction with phenomics remain underexplored. Here, the authors introduce phenomics–enviromics (PE) crosstalk and discuss its coordinated data-collection and -integration into next-generation plant breeding.

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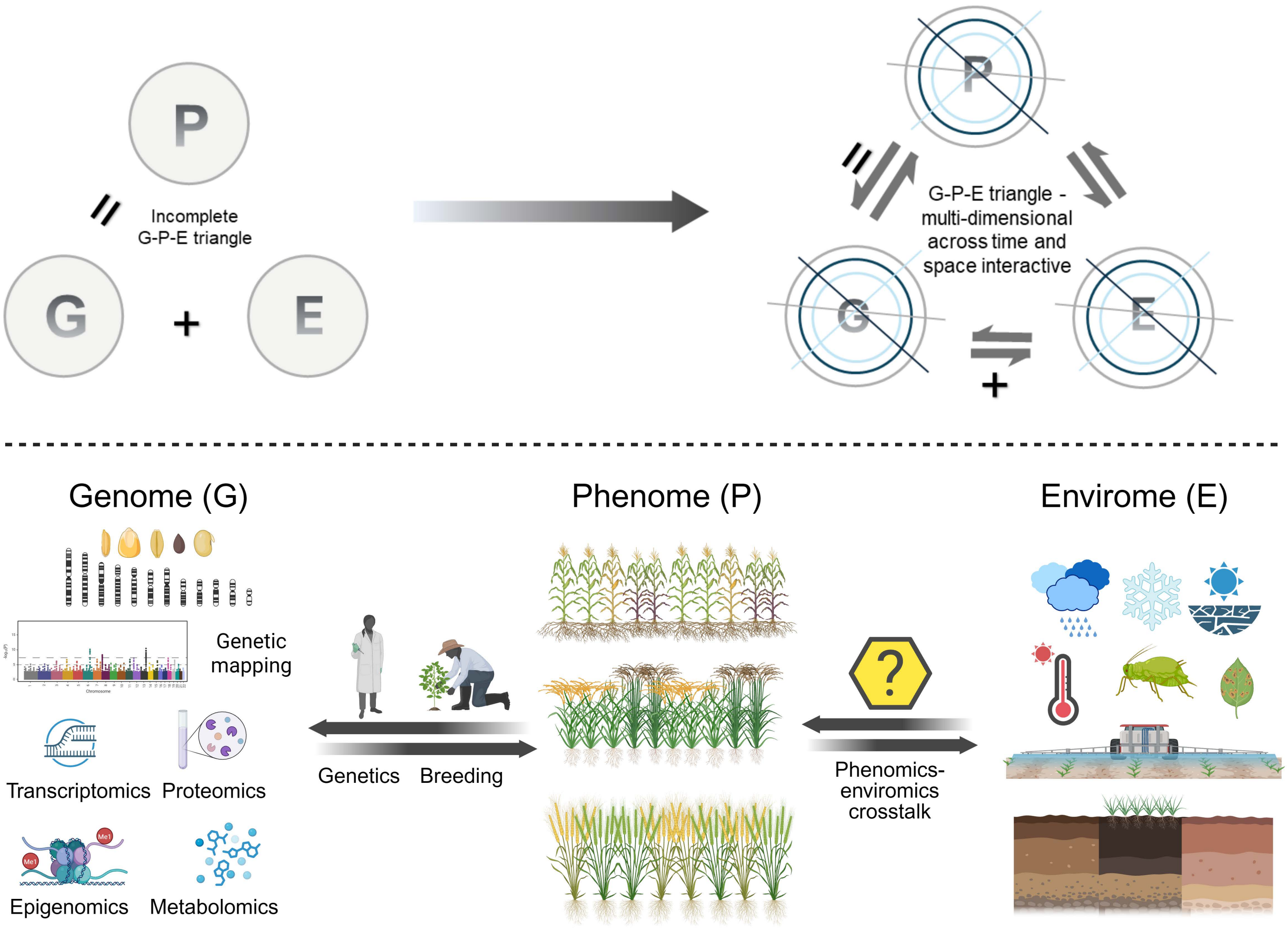
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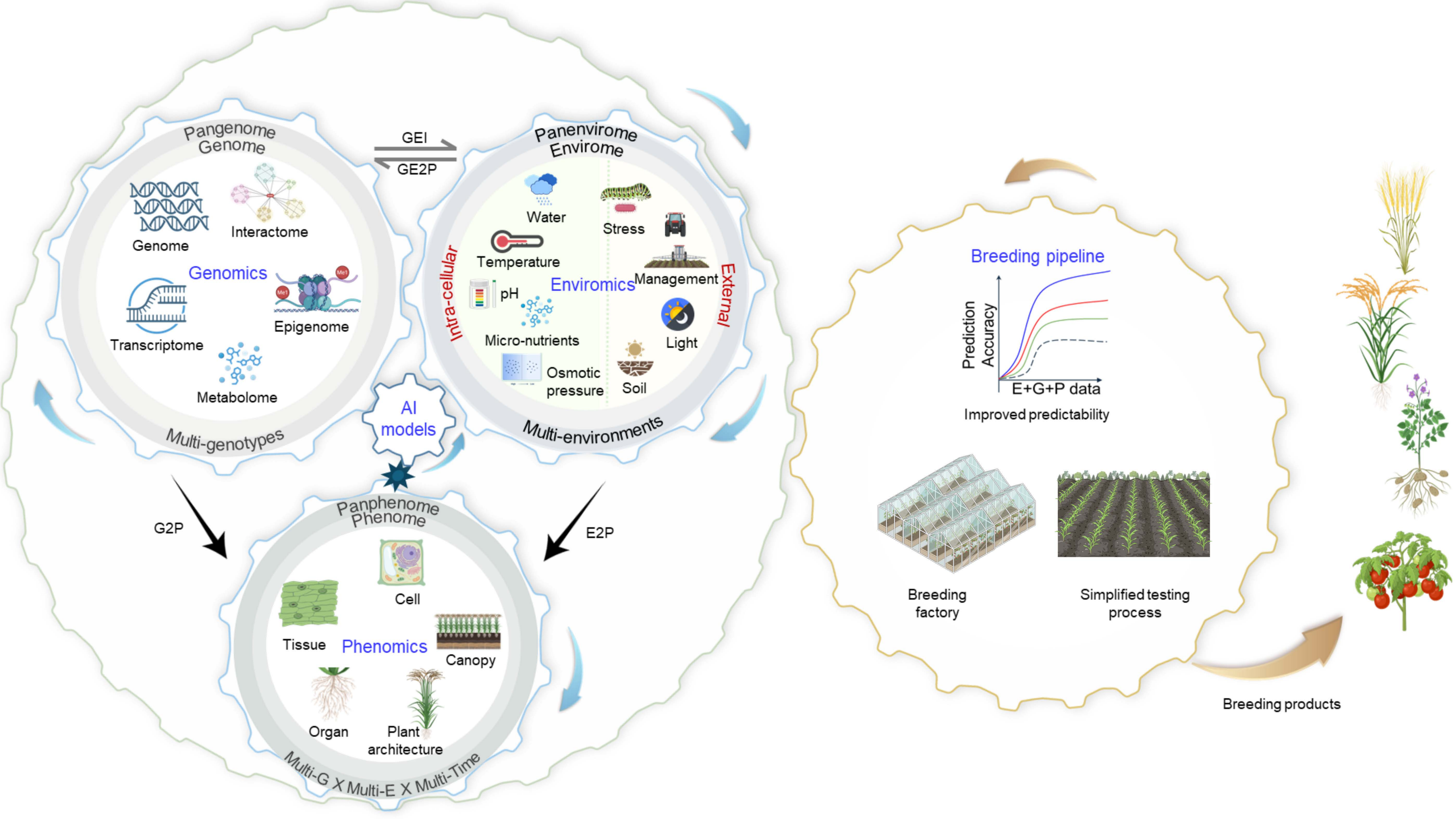
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Intra-cellular
External
Micro-nutrients
Light
Osmotic pressure
Soil
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G2P
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Panphenome
Phenome
Cell
Tissue
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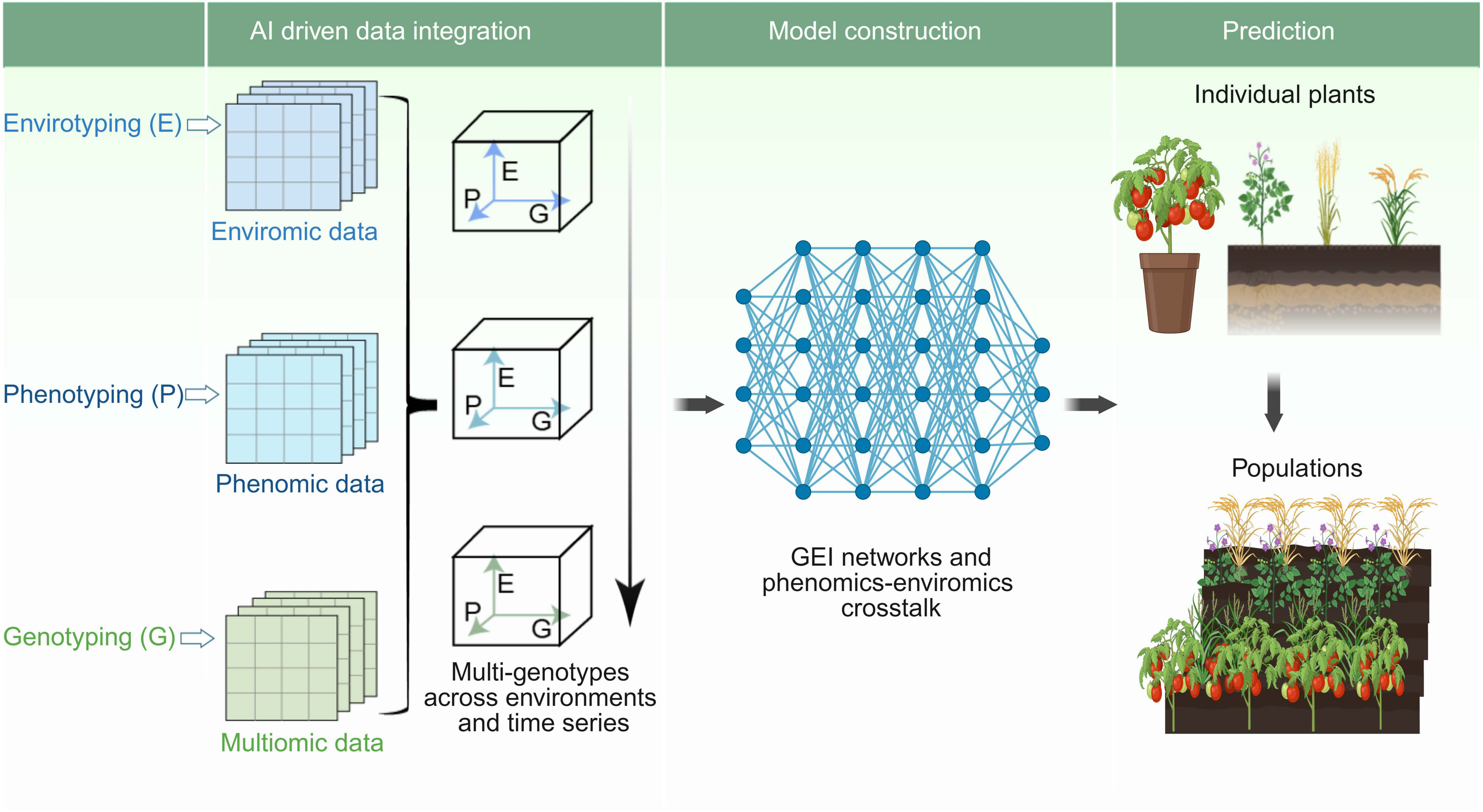
Simplified testing process
Breeding products


AI driven data integration
Model construction
Prediction
Envirotyping (E)
Enviromic data
Phenotyping (P)
Phenomic data
Genotyping (G)
Multiomic data
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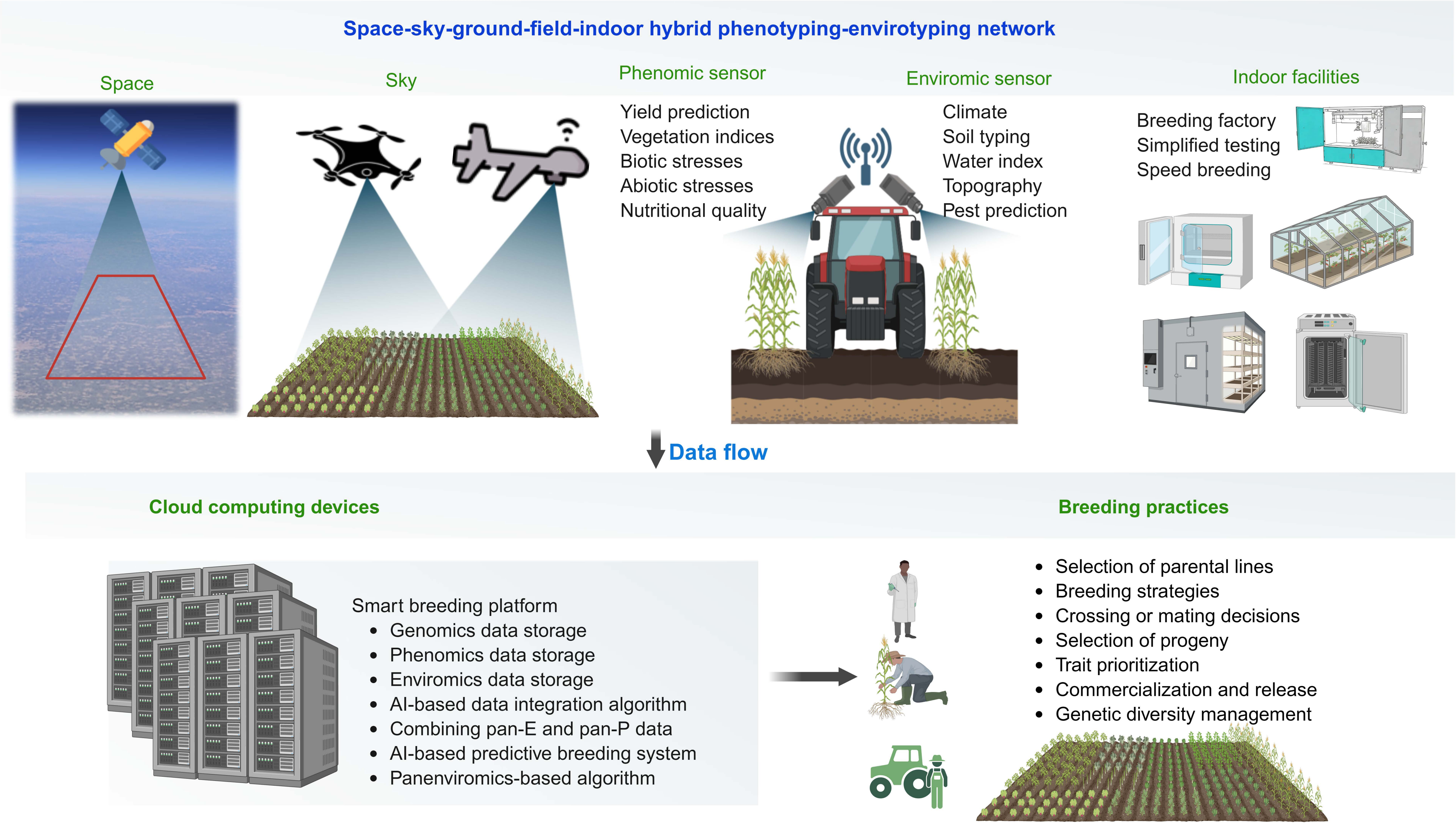
Multi-genotypes across environments and time series
GEI networks and phenomics-enviromics crosstalk
Individual plants
Populations


Space-sky-ground-field-indoor hybrid phenotyping-envirotyping network
Space
Sky
Phenomic sensor
Yield prediction
Vegetation indices
Biotic stresses
Abiotic stresses
Nutritional quality
Enviromic sensor
Climate
Soil typing
Water index
Topography
Pest prediction
Indoor facilities
Breeding factory
Simplified testing
Speed breeding
Data flow
Cloud computing devices
Smart breeding platform
Genomics data storage
Phenomics data storage
Enviromics data storage
AI-based data integration algorithm
Combining pan-E and pan-P data
AI-based predictive breeding system
Panenviromics-based algorithm
Breeding practices
Selection of parental lines
Breeding strategies
Crossing or mating decisions
Selection of progeny
Trait prioritization
Commercialization and release
Genetic diversity management