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Sreehari V Santhosh
Division of Plant Physiology, Indian Agricultural Research Institute, New Delhi, Delhi, India

Pradeep Krishnamurthy
Division of Plant Physiology, Indian Agricultural Research Institute, New Delhi, Delhi, India

Neethu RS
Division of Agricultural Statistics, IASRI, New Delhi, Delhi, India

Corresponding Author:
Sreehari V Santhosh
Division of Plant Physiology, Indian Agricultural Research Institute, New Delhi, Delhi, India

From Phenotype to Phenomics: Multidimensional Classification of Plant Traits

Sreehari V Santhosh, Pradeep Krishnamurthy and Neethu RS

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Abstract
Phenotypic traits represent the observable outcomes of interactions between plant genetic architecture and environmental conditions and form the foundation for understanding plant growth, adaptation, and productivity. With the rapid advancement of high-throughput phenotyping and phenomics platforms, trait evaluation has evolved from isolated measurements toward integrative, data-driven frameworks capable of capturing structural, physiological, and functional plant responses across spatial and temporal scales. However, the expanding diversity of measurable traits and analytical approaches has created a need for a coherent conceptual framework that organizes phenotypic traits in a biologically meaningful and experimentally practical manner. This review addresses this gap by synthesizing existing knowledge and presenting a comprehensive classification of plant phenotypic traits based on measurement strategy, including direct and surrogate traits, as well as biological organization, developmental stage, functional relevance, environmental responsiveness, and genetic control. Particular emphasis is placed on the growing role of surrogate image-derived traits as scalable proxies for complex physiological processes, enabling rapid, non-destructive phenotyping across large populations. By integrating traditional trait concepts with modern imaging technologies, sensor systems, and data analytics, the review highlights how multidimensional trait classification strengthens genotype-phenotype interpretation, improves experimental design, and accelerates precision breeding efforts. Ultimately, this synthesis provides a unified perspective linking phenomics technologies with plant biology, offering a conceptual and methodological foundation for advancing crop improvement and developing climate-resilient agricultural systems.

Keywords: Plant phenomics, phenotypic traits, trait classification, high-throughput phenotyping, genotype-phenotype relationship, plant development, crop improvement, multi-omics integration, precision breeding, plant stress responses, image-based phenotyping

Introduction
Phenotypic characteristics are the outward appearances of an organism which are results of highly complex interactions between the genetic structure and the environment, the manifestation of genotype functioning at the spatial and temporal scales (Houle *et al*., 2010; Cobb *et al*., 2013) [15, 39]. Morphological, physiological, biochemical, and developmental characteristics are some of the traits in plants, which confer growth, adaptation, productivity, and response to stress, depending on the diverse environmental conditions (Furbank and Tester, 2011; Walter *et al*., 2015) [28, 88]. The combination of phenotypic traits and phenomics makes up a complex system of studying plant biology, under which a systematic classification of properties in various orthogonal dimensions allows detailed characterization of the traits and enhances the use of these characteristics in breeding (Araus & Cairns, 2014; Yang *et al*., 2020) [3, 92]. The combination of high-throughput technologies in phenotyping has essentially changed the measurement, analysis and interpretation of traits to be performed in real-time, non-destructively, and at large scale using imaging vehicles, remote sensing and computation analytics (Fahlgren *et al*., 2015; Li *et al*., 2014) [22, 54]. Modern phenomics is therefore helpful in bridging the genotype x phenotype relationships by allowing the quantitative evaluation of complex traits over developmental stages and environmental gradients and thereby accelerates crop improvement and systems-level insight into plant functioning (Houle *et al*., 2010; Yang *et al*., 2020) [39, 92].

Classification of phenotypic traits

Phenotypic traits classification allows developing a systematic way of sorting observable plant traits, which results in a better understanding of the biological functionality and the effectiveness of the crop research and breeding programs (Furbank and Tester, 2011; Cobb *et al*., 2013) [15, 28]. Phenotypic traits may be categorized according to how they are measured, how they are organized biologically, how they develop, whether they are functional or not, and their genetic makeup (Figure 1). A very common differentiation is one of direct and surrogate traits. Direct measurement is used to quantify direct traits, and surrogate traits serve as indirect measures of complex physiological processes that are hard to measure in practice, especially on a large scale (Araus and Cairns, 2014; Reynolds *et al*., 2023) [3, 67]. The characteristics can also be divided into levels of biological organization, where morphological, physiological, biochemical and molecular categories are identified. These groups are the levels of increasing complexity and include observable structural features to gene expression and regulatory networks, which overall define plant performance (Pieruschka and Schurr, 2019) [64]. Developmental stages of classification, including seedling, vegetative, and reproductive stages, allow making a stagespecific determination of growth and yield formation and making a connection between initial vigor and ultimate productivity (Poorter *et al*., 2016; Sadras and Richards, 2014) [65, 72]. Further agronomic benefits can be gained through functional association of traits into categories of growthrelated, stress-associated and yield-related, which allow the relationship of phenotypes with resource use efficiency, stress adaptation, and harvestable output (Blum, 2011; Passioura, 2012) [8, 63]. Also, the characteristics can be differentiated in terms of their variation type (quantitative or qualitative), their genetic basis and stability, which are critical to choosing the right statistical model and breeding strategies (Falconer and Mackay, 1996; Bernardo, 2020) [7, 23]. Such classification models integrated into contemporary phenomics systems make it possible to obtain a multidimensional perspective on genotype x phenotype correlations, promoting the discovery of genes, enhancing breeding accuracy, and achieving the creation of climate-resistant crops (Yang *et al*., 2020; Tardieu *et al*., 2017) [80, 91, 92].

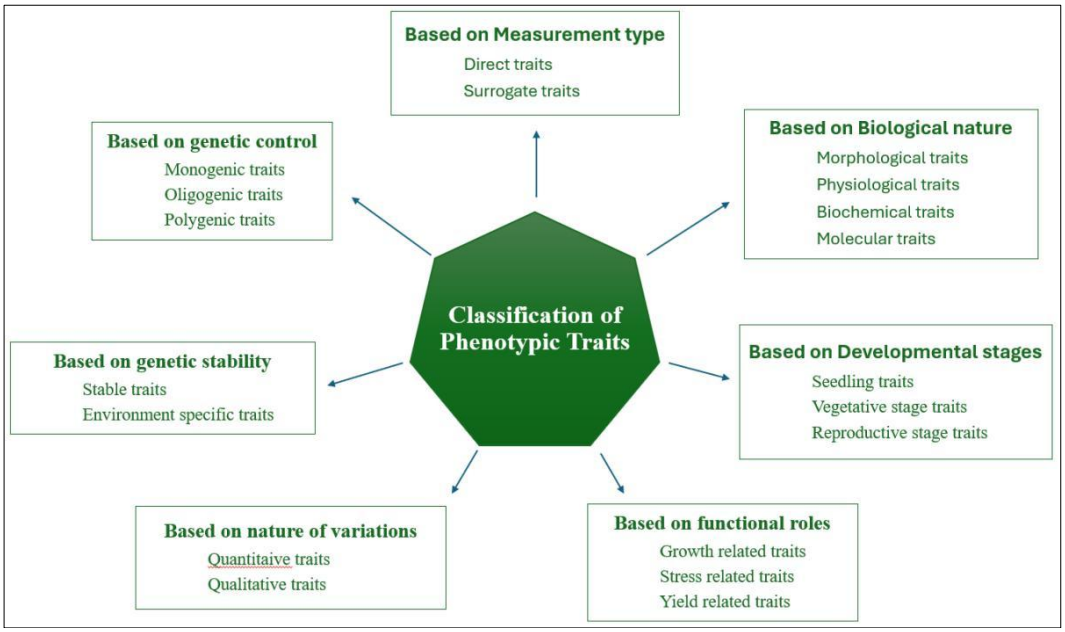

Fig 1 Illustration of the classification of phenotypic traits on different basis

Direct and Surrogate traits

The differentiation between direct and surrogate traits as measured by the approach is emphasized by classification and has gained more and more prominence in high-throughput phenotyping. This difference is especially significant in terms of experimental design, where surrogate traits are used to acquire data quickly and without destruction and at scale when direct measures are either very labor-intensive or even destructive.

Direct traits are acquired by direct quantification without the use of inference or modeling. They can be the height of plants, leaf area, and the structures of canopies. New imaging capabilities, including RGB imaging, three-dimensional reconstruction, and automated phenotyping systems, have provided a major boost in the quality and throughput of structural trait measurement by providing detailed computerized representations of the plant architecture (Esser *et al*., 2023; Zhang *et al*., 2024) [21, 98]. Image analysis based on machine learning also allows morphological features such as leaf size, venation patterns and projected leaf area to be extracted en masse, enhancing reproducibility and scalability (Lagergren *et al*., 2023) [52]. Moreover, spectral and fluorescence imaging methods allow direct measurements of pigment composition, photosynthetic efficiency, and structure characteristics in controlled and field conditions (Pieruschka and Schurr, 2019; Zhang *et al*., 2024) [64].

In contrast surrogate traits are used as an approximation of processes occurring within the body that are hard to measure in practice. As an example, thermal infrared imaging canopy or leaf temperature has become one of the common indices to predict stomatal conductance and water status of a plant due to the strong correlation between transpirational cooling and gaseous exchange (Plant Phenomics Consortium, 2024; Tardieu *et al*., 2017) [31, 80]. This method facilitates effective screening of vast groups of water-use efficiency and does

not use the destructive sampling to screen a sample (Jones *et al*., 2009; Jones. 2004) [45, 47]. On the same note, systems of integrated phenotyping, in which transpiration measurements, environmental data, and modeling are combined, can also be used to obtain indirect estimates of stomatal behavior, which is a convenient alternative to the tedious manual measurements without compromising predictive capability (Zhao *et al*., 2019) [100]. Hyperspectral reflectance indices are also used as proxy indicators of biochemical characteristics, such as nitrogen status, chlorophyll content, and metabolic pigment shifts and, therefore, allow identifying physiological stress early before the appearance of any visible symptoms (Zhang *et al*., 2024) [98]. Direct and surrogate traits when used together in the pipelines of phenomics enable parallel characterization of structural, physiological, and functional responses, thus enhancing both genotype x phenotype analyses and precision breeding (Furbank & Tester, 2011; Yang *et al*., 2020) [28, 92].

Morphological, physiological, biochemical, and molecular traits

Phenotypic traits according to biological organization have been broadly classified into morphological, physiological, biochemical and molecular levels. Though these categories are mostly displayed in a hierarchical manner, they are very interrelated and play an important role in the growth, development and adaptation of a plant.

Morphological features include structural and architectural features including: plant height, leaf morphology, number of tillers, canopy structure, and architecture of the root system (Fiorani and Schurr, 2013; Pieruschka and Schurr, 2019) [27, 64]. The development of imaging technologies has substantially strengthened morphological phenotyping. As an example, X-ray computed tomography can be used to have a non-destructive visualization of root architecture and spatial distribution of crops like maize at the early development stages (Kojima *et al*., 2025; Chauhan *et al*., 2025) [12, 48]. On the same note, RGB imaging and LiDAR-based UAV are popular in monitoring canopy height dynamics and biomass accretion in crops such as wheat and sorghum in the field where large-scale and high-resolution phenotyping can be conducted (Ten Harkel *et al*., 2019; Maimaitijiang *et al*., 2020) [57, 81].

Physiological characteristics distinguish functional mechanisms behind the growth and use of resources in plants, such as photosynthesis, stomatal conductance, transpiration efficiency, chlorophyll fluorescence, and thermal regulation (Reynolds *et al*., 2023) [67]. Sophisticated highthroughput phenotyping systems with combination of gas exchange, fluorescence imaging, and automated environmental regulation today makes it possible to continuously monitor plant responses to abiotic stressors, including drought and heat (Li *et al*., 2021; Tardieu *et al*., 2017) [1, 80]. An example of this is chlorophyll fluorescence imaging, which is widely employed to measure the functionality of photosystem II and identify the initial stress responses of crops, including rice and barley (Brestic and Zivcak, 2013; Herritt *et al*., 2020) [10, 38]. The thermal imaging is also used extensively to measure the transpiration dynamics and stomatal behavior of different genotypes (Jones, 2018) [46].

Biochemical characteristics indicate a metabolic composition and enzymatic activities on which physiological functioning and stress responses are based. These are the primary and secondary metabolites, antioxidants, and enzyme kinetics (Fernie and Schauer, 2009) [26]. Metabolomics techniques have made metabolic pathways to be characterized in detail. A good example is the explanation of montbretin A biosynthesis, an anti-diabetic that is made in montbretia corms under the coordination of enzymatic reactions (Irmisch *et al*., 2020) [42]. Latest developments in massspectrometry and nuclear magnetic resonance spectroscopy have also linked a set of specific metabolite patterns with drought resistance and nitrogen use efficiency in crops including maize and rice, with biochemical characteristics being seen as intermediate phenotypes between genotype and agronomic performance (Kumar *et al*., 2017) [51].

Molecular characterizations are based on the degrees of gene expression, regulatory circuits, and protein interactions, which include transcript abundance, epigenetic control, and signaling pathways (Choudhary *et al*., 2015; Jamil *et al*., 2020) [14, 44]. Transcriptomic and proteomic techniques have been developed to identify stress-responsive gene networks that are linked to crop traits such as drought and salinity tolerance in crops, such as rice and soybean (Lenka *et al*., 2011; Huang *et al*., 2014; Fang *et al*., 2025) [24, 25, 41, 53]. Recent technologies like single-cell RNA sequencing and phosphoproteomics can provide cell-type-specific responses and signaling cascades behind adaptive phenotypes in greater detail (Ryu *et al*., 2019; Choudhary *et al*., 2015) [71].

Seedling, vegetative, and reproductive traits

Phenotypic trait classification according to developmental stage gives a time structure to study plant growth and performance since the expression of traits is markedly different at different stages of ontogeny. The different developmental stages are related to different physiological priorities and, therefore, stage-specific trait assessment is required in determination of adaptation and productivity. The classification of traits into seedling, vegetative, and reproductive groups allows following the performance of plants over time in a systematic manner and designing the phenotyping strategies of a specific stage (Fiorani and Schurr, 2013; Tardieu *et al*., 2017) [27, 80].

Characteristics at the seedling stage are mainly linked with initial establishment and activity i.e. germination, coleoptile length, hypocotyl length and initial root system architecture. These characteristics play a key role in dictating crop establishment, acquisition of resources and competition in the field (Halperin *et al*., 2017) [35]. The development of high-throughput imaging has made it possible to quantify the dynamics of seedling growth and root development in large-scale crops like maize, rice, and wheat, automatically. The methods have enabled the discovery of genetic variation in the relation to drought tolerance at an early stage and efficiency in nutrient uptake (Atkinson *et al*., 2019) [5]. Specifically, digital root phenotyping and X-ray computed tomography have offered comprehensive information on root branching models and soil discovery methods, which are closely associated with water acquisition in the state of stress (Kojima *et al*., 2025; Chauhan *et al*., 2025) [12, 48].

The characteristics of the vegetative stage are mainly linked with the biomass growth and canopy, such as the number of tills, the rate of stem elongation, the length of internodes, the growth of leaves, and the canopy structure (Sen *et al*.,

2026; Poorter *et al*., 2016) [65, 73]. The application of timeseries phenotyping with the use of UAV-based RGB and multi-spectral imaging has made it possible to monitor vegetative development in breeding populations of large sizes continuously. It enables to estimate growth rates, leaf area index, and radiation use efficiency in the field (Maimaitijiang *et al*., 2020; Ten Harkel *et al*., 2019) [57, 81]. Parallel, physiological characteristics (like transpiration efficiency and photosynthetic capacity) are more frequently measured using integrated phenotyping systems that are based on image-integrated environmental sensing to enable extensive characterization of genotype-specific responses to water availability and temperature (Reynolds *et al*., 2023) [67].

The characteristics that are directly connected to the formation of the yield include flowering, anthesis-silking interval, spike or panicle structure, the effectiveness of pollination, the rate of grain filling, and the development of seeds (Fan *et al*., 2025; Sadras and Richards, 2014) [24, 72]. The latest breakthroughs in high-resolution phenotyping and machine learning have increased the accuracy of tracking of reproductive timing and floral development, which has led to the insight of the sensitivity of stress responses to critical reproductive transitions in crops such as maize and rice (Zhao *et al*., 2019; Millet *et al*., 2019) [60, 100]. An example of such an indicator can be the anthesis-silking interval, which has been widely adopted as a measure of drought tolerance in maize as the greater male and female flowering synchrony results in better kernel set in water-stressful environments (Messina *et al*., 2019) [58]. Moreover, hyperspectral imaging has also made it possible to monitor grain filling without being destructive, as well as to anticipate yield components, which has allowed correlating the reproductive characteristics with physiological performance at the subsequent developmental stages (Ge *et al*., 2019) [13]. Altogether, the ontological division of traits in developmental stage adds a time aspect to the analysis of phenotype. This system can be used to dissect genes at specific stages and breeders get a detailed method to concentrate on traits that are most important at a particular stage of crop growth.

Functional role of phenotypic traits

The functional role of phenotypic traits is an effective way of classifying phenotypic traits to enable a correlation between the plant phenotype and agronomic performance. In this method, the traits are clustered based on their involvement in development of the plant, tolerance to stress and development of yield, thus making it easier to interpret biologically at different stages of development as well as under different environmental circumstances. Functionally, there is functional classification, which separates traits into growth-related, stress-related, and yieldrelated traits and provides a systematic means of ranking traits when used in phenomics-based breeding programs.

Characteristics related to growth are mainly an expression of the vigor of plants, acquisition of resources, and development of plant canopies that together dictate the extent of biomass accumulation and competitive capacity. The most important indicators are the rates of biomass production, the index of the leaf area, and the dynamics of the plant heights, which impact the efficiency of radiation interception (Singh *et al*., 2019) [76]. Recent developments in high-throughput phenotyping have made it feasible to use temporal growth processes based on RGB and LiDAR imaging to quantify a dynamic canopy architecture in crops like wheat and sorghum (Li *et al*., 2022) [2]. Root architecture characteristics such as root length density, root growth angle, and lateral root proliferation are even more accepted in this category because they form the central determinants of water and nutrient intake (York, 2019) [93]. Furthermore, physiological indices like chlorophyll content index, photosynthetic efficiency, and canopy temperature depression can be considered as inclusive indicators of growth performance of crops under field conditions (Araus and Kefauver, 2018; Zhang *et al*., 2023) [4, 97]. Hyperspectral imaging also supplements this framework by allowing to measure the nitrogen status and pigments composition hence connecting biochemical characteristics to the growth dynamics in varied environments (Banerjee *et al*., 2021) [6].

Stress-related characteristics characterize the process through which plants can be tolerant or avoid abiotic and biotic stresses and have increasingly become a point of interest in relation to climateresilient agriculture. Other physiological characteristics like osmotic adjustment capacity during drought-mediated by the buildup of compatible solutes, such as proline and soluble sugars are still the major indicators of stress tolerance (Song *et al*., 2025) [78]. The most common method of measuring an oxidative stress response in cereals and legumes is the use of biochemical markers, such as antioxidant enzyme activities of superoxide dismutase, catalase, and peroxidase (Hasanuzzaman *et al*., 2020) [36]. Recent phenotyping methods are more dynamic, including stomata conductance, transpiration efficiency, and canopy spectral index as a quicker proxy of drought and heat resilience (Driever *et al*., 2023) [20]. One of the most common traits reviewed by heat stress resilience is the membrane thermostability, pollen viability, and the ability to maintain stay-green phenotypes under terminal heat stress (Jagadish *et al*., 2015) [43]. Stress-reactive phenotypes like the production of heat shock proteins and genes controlled by abscisic acid (ABA) also enhance the connection between physiological reactions and genomic regulations at the molecular level (Zandalinas *et al*., 2022) [96]. Functional indicators like ion homeostasis characteristics, such as sodium-to-potassium ratio and levels of sodium exclusion, are more frequently employed as functional indicators in barley and rice crops under salinity pressure (Lenka *et al*., 2011; Huang *et al*., 2014; Rodríguez Coca *et al*., 2023) [41, 53, 68].

Yield-based characteristics directly define harvestable production and thus, are the major objectives in crop enhancement programs. Traditional yield parameters, such as the number of grains per panicle, the harvest index, and weight of the average tuber, are still traditional productivity indicators (Rozentsvet *et al*., 2022) [70]. Nonetheless, modern models are adopting more source-sink relationship characteristics like grain filling rate, assimilate partitioning efficiency, and spike fertility index (Rosati *et al*., 2023) [69]. Thousand grain weight, spike or panicle structure, and kernel set efficiency are some of the attributes that are closely related to yield stability in changing environmental conditions in cereal crops (Powell *et al*., 2012) [66]. Improvements in the field of phenomics allowed to acquire automated yields-related proxies, such as the processes of canopy senescence and reproductive biomass estimation, by applying UAV-operated imaging systems (Yang *et al*., 2017) [91]. Besides that, such quality-related characteristics

as protein level, starch structure, and oil content are also becoming part of this category, as their financially important characteristics are at par with the traditional indicators of yield (Sreenivasulu and Wobus, 2013) [79].

Quantitative and Qualitative traits

The patterns of variation of phenotypic traits have the ability to be effectively classified depending on the patterns of variation within populations that they are used to depict the differences in genetic architecture, inheritance, and modes of analysis. In general, traits could be classified as either quantitative or qualitative, which is still the cornerstone of genetics, crop, and contemporary phenomics.

Quantitative traits are continuously varying and are generally governed by numerous genes that have minute additive effects that may be interacting with environmental factors. Familiar ones are the yield of grain, flowering duration, plant stature, biomass development, and root structure (Fan *et al*., 2025) [24]. These characteristics typically have near-normal distributions in the process of their segregation because of their polygenic nature and environmental impact. In turn, they must be analyzed by means of complex statistical and genomic methods, such as mixed linear models, genomic prediction, and Quantitative Trait Locus (QTL) mapping (Occelli *et al*., 2024) [62]. Research on the domestication of wheat has shown a consistent change in morphological characteristics, including leaf biomass, seed mass, and tillering, as an element of a complicated genetic control due to both evolutionary and human-made selection (Shan & Osborne, 2024) [74]. On the same note, the use of phenotypic measurements in crops like watermelon has indicated a consistent variability and an approximate normal distribution of phenotypic traits like flowering period and fruit production, further confirming that they are quantitative (Kumar *et al*., 2025) [50]. Further discovery of genomics and high-throughput phenotyping, especially genome-wide association studies, indicated that most agronomic traits are controlled by a number of loci with minor effects instead of a few major genes (Plants Special Issue Editorial, 2023) [67]. In addition, there are integrative methods, which involve phenomics, environmental variables, and genomic data, which are being employed to predict trait performance in different environments.

Qualitative traits, on the contrary to the former, exhibit discrete phenotypic classes and are generally regulated by one or a few major genes, which are based on Mendelian patterns of inheritance. These traits tend to be less affected by environmental deviation and can be defined into a series of groups, including whether it has pubescence or not, the types of kernel texture, pigmentation, or whether it has a waxy or non-waxy endosperm (Gaur *et al*., 2024) [31]. The categorical variation of rice germplasm characterization based on Distinctness, Uniformity, And Stability (DUS) descriptors is represented by the differences in the characteristics of leaf pubescence and plant stature (Dat *et al*., 1978; Busov *et al*., 2008) [11, 17]. A qualitative trait that has been described well, especially in rice is the waxy phenotype that is controlled by the Waxy gene that biosynthesizes amylose, which primarily impacts grain texture and cooking quality, but the pleiotropic effects can also impact the related biochemical properties (Wu *et al*., 2021) [90]. Likewise, kernel texture in maize which can be in the flint, dent, sweet, or waxy categories is defined by a few loci, and therefore, it is easy to classify and select these aspects in breeding programs (Gangadhar Karjagi *et al*., 2025) [29]. Qualitative traits can also be used extensively in marker-assisted selection, identification of varieties, and genetic purity because of their predictable patterns of inheritance.

Although this is the case, there is no necessarily a boundary between quantitative and qualitative traits. The modifier genes or the pleiotropic effects of some traits traditionally viewed as qualitative, and major-effect loci may have a strong impact on some quantitative traits. This classification is more and more being handled in contemporary breeding of plants as a continuum, and not a dichotomy. By bridging the gap between classical Mendelian genetics and quantitative genomics, it has been possible to understand trait architecture in a more subtle way and devise better approaches to better crop development in difficult environments.

Stable and Environment-specific traits

The phenotypic traits may be also categorized according to their stability of expression within the different environments. There are also those traits that are highly stable and have little Genotype X Environmental (GxE) interaction and therefore, tend to be quite constant in different agro ecological settings. These characteristics are thought to be good selection criteria when breeding. There are not many examples of seed coat color, qualitative morphological descriptors, and some structural traits the expression of which is highly dependent on the genetic code (Li *et al*., 2022) [2]. Crops such as cassava and cowpea have been shown to have a stable expression of traits such as root characteristics and yield components across locations and seasons by using multiple environments, showing that the traits are highly genetic controlled (Adugna *et al*., 2022; Ghazy *et al*., 2025) [2, 33]. On the same note, tomato tomato research utilizing AMMI and GGE biplot techniques has revealed that there are hybrids that show stable expression of horticultural attributes across more than two environments, which will be suitable to be expanded to more environments (Tiwari *et al*., 2025) [83]. High clonal repeatability of fiber properties and growth characteristics is further evidence that genetically stable phenotypes do exist in perennial species like *Populus tomentosa* (Wu *et al*., 2021) [90].

Environment-specific traits, on the contrary, are very much affected by the environment and show high levels of phenotypic plasticity. Such characteristics tend to appear in specific situations of stress, including the leaf rolling associated with the drought, the responses to heat stress, osmotic adjustment, and metabolic alterations that depend on the pressure (Song *et al*., 2025) [78]. Maize experimental trials in varying moisture conditions have revealed that the degree of variation in yield and stress tolerance characteristics with changes in water availability is strong, and GxE interactions are obvious (Singamsetti *et al*., 2021) [75]. Also, studies have demonstrated in *Arabidopsis thaliana* that seed dormancy and longevity are different among genotypes in reaction to environmental factors such as temperature and light during growth, suggesting that genetic pathways are activated by the environment (He *et al*., 2014) [37]. Such a type of environment-specific expression is highly related to adaptive phenotypic plasticity, which allows plants to maximize performance under changing

environments but also makes selection more complicated, as traits are expressed differently in different test environments (Des Marais *et al*., 2013) [18].

To overcome this obstacle, recent phenomics methods are becoming more and more multienvironmentally data-driven, in order to free up the stable genetic effects through environmentallyinduced variation. This allows prediction of traits performance more accurately and allows the establishment of both broad and specific adapted crop genotypes.

Genetic control of phenotypic traits

The phenotypic traits have the potential to be categorized in terms of their geneticability; in terms of the number of genes which they regulate, in terms of their genomic location, and the sea magnitude of their influence as well. This classification is valuable in terms of trait architecture and it has a direct effect on the selection of breeding strategies and methods of analysis. The traits may be classified broadly as monogenic, oligogenic, or polygenic, indicating more genetic complexity.

Monogenic traits are governed by a single gene whose impact on phenotype is strong and their inheritance is usually of the Mendelian type. These traits are also quite simple in their genetic structure, and therefore, relatively mapable, and are easily applied to marker-assisted selection. The typical examples of monogenic traits are the race-specific resistance to disease controlled by the resistance (R) genes that encode Nucleotide-Binding Leucine-Rich Repeats (NLR) proteins. The most significant examples are the Pi54 gene that provides the rice with the resistance to blast and Lr34-related resistance in wheat (Krattinger *et al*., 2009) [49]. Genome editing has further confirmed monogenic control of various agronomically significant traits. As an example, rice semi-dwarfism is controlled by SD1 gene to a large extent, and fruit-ripening in tomato is strongly affected by transcription factor called RIN (Li *et al*., 2020) [55]. Moreover, the application of CRISPR-Cas-based alteration of susceptibility genes has made it possible to obtain long-lasting disease resistance across various crops, and the concept of monogenic traits is practically applicable to crop enhancement (Zaidi *et al*., 2017) [95].

Oligogenic traits take up an intermediate position and are regulated by few genes or major Quantitative Trait Loci (QTLs), with a moderate effect each. Although they still could be affected by the environmental factors, being relatively simple in their genetic structure, these traits can be subject to a focused breeding intervention. The best example that is well characterized is the SUB1 locus in rice that improves submergence tolerance by regulating the ethylene-responsive transcription factors (Zhang *et al*., 2025; Achary *et al*., 2021) [1, 97]. Oligogenic traits have been demonstrated to be oligogenic in maize, wherein there are major-effect QTLs that regulate root architecture and water uptake efficiency, which determine drought tolerance (Messmer *et al*., 2009; Varshney *et al*., 2021) [59, 86]. And likewise, in wheat, there are few genomic regions that tend to be affecting specific traits such as grain protein content and the date of heading (Distelfeld *et al*., 2012) [19]. The methods of integrative combination between QTL mapping and phenomics data are becoming more and more popular to describe such traits, as well as to fill the gap between simple Mendelian and highly complex quantitative inheritance.

The most complex forms of characteristics are polygenic those caused by a combination of the effects of a large number of loci with little influence. Such attributes tend to exhibit a gradual change and seriously rely on environmental factors. Major agronomic traits, including grain yield, nitrogen-use efficiency, biomass accumulation, and abiotic stress tolerance, are polygenic in nature, as a rule (Muthurajan *et al*., 2025; Wallace *et al*., 2018) [61, 87]. Genome-Wide Association Studies (GWAS) have since identified hundreds of loci with an accumulative effect on the eventual trait (Hu *et al*., 2019; Tibbs Cortes *et al*., 2021) [40, 82] that provide support to the genetic basis of yield stability and stress adaptation in crops (sorghum, maize, and wheat). Polygenic interactions among multiple metabolic and developmental processes also control a few complex physiological properties such as photosynthetic efficiency and the formation of canopies (van Bezouw *et al*., 2019) [84]. To address the gap and maximize such traits, the new generation breeding programs rely increasingly on the genomic prediction schemes that take into account the overall traits of the genome-wide markers to enable individuals to choose those who have beneficial combinations of small-effect alleles (Crossa *et al*., 2017) [16].

Conclusion

The recent technological innovations have made possible the incorporation of several dimensions of phenotypic classification in the same analytical system. The morphological, physiological, biochemical, and molecular features can now be described simultaneously and this provides a more detailed picture of plant performance. The crossroads of Artificial Intelligence (AI) and the high-throughput phenomics has aided the ability of drawing biologically relevant results in multidimensional datasets that are accumulated at different stages of development and under different environmental conditions (Yang *et al*., 2020) [92]. Hyperspectral images have been demonstrated as highly predictive of quality features and stress responses and can be trained together with time-resolved phenotypic features using deep learning models, and can simultaneously measure structural, physiological, and biochemical traits when water is scarce (Yu *et al*., 2022) [94]. Similar progress has been achieved in crops, including wheat and rice, with convolutional neural networks trained on multispectral and RGB images having succeeded in predicting multidimensional attributes of biomass accumulation, nitrogen status, and stress resistance, demonstrating the opportunities of data-driven phenomics in multidimensional trait analysis (Liakos *et al*., 2018) [56].

The high-throughput systems of phenotyping have also facilitated the comprehensive quantification of interacting and dynamic characteristics in large scale and have addressed continuous analysis of growth and development of plants. Image-based phenotyping systems placed in controlled settings, as well as in the field, have the capability of measuring a very large number of phenotypes, such as the dynamics of plant height, canopy structure, growth rates, and the temporal response to environmental dynamics. They have made it possible to obtain a deeper understanding of the genetic makeup of the sophisticated agronomic characteristics (Fan *et al*., 2025) [24]. The combination of robotics, sensor networks, and cloud-based tools of analytical analysis has also increased phenotyping scales and reproducibility and has surpassed the restrictions

in the long term (Furbank and Tester, 2011) [28]. Also, it was possible to correlate several phenomics databases with genome-wide association analysis and genomic prediction models, thereby identifying candidate genes that predict various aspects of traits variably, thereby increasing precision breeding strategies (Tibbs Cortes *et al*., 2021) [82].

Genome editing technologies, particularly, the CRISPR-Cas technology has introduced a powerful functional validation component to the phenotypic classification, making the precise manipulation of complex phenotype genes possible. As an example, the loci editing of GW2 in rice has demonstrated significant pleiotropic responses of grain size, yield dimensions, and stress responses that demonstrate how single genetic manipulations can alter the various dimensions of phenotypic responses ((Zhang *et al*., 2025; Achary *et al*., 2021) [1, 97]). Similar studies have been carried out on flowering-time, plant-architecture, and abiotic-stress-tolerance gene networks in tomato, maize, and wheat, thereby connecting molecular activities with observable phenotypes (Chen *et al*., 2019; Gao, 2021) [13, 30]. High-resolution phenotyping platforms enable genome editing that can be followed by iterative hypothesis generation, validation, and optimization, and can speed up the functional genomics and crop improvement research (Varshney *et al*., 2021) [86].

This AI plus high-throughput phenotyping plus sophisticated sensing technology plus, lastly, genome editing is transforming the analysis of phenotypic traits into a multidimensional systems framework. It is a hybrid approach that can be applied to scale up genotype-phenotype relationships across environments to support predictive breeding and yield climate-resilient crops through data-driven and precision agriculture (Yang *et al*., 2020; Varshney *et al*., 2021) [86, 92].

Way forward

The combination of the structured trait frameworks and the use of the new technologies of phenomics and multi-omics will play a more important role in the further development of the phenotypic trait classification. The given type of integration is already enhancing the knowledge of genotype-phenotype association in an extensive variety of environmental conditions. Combined with remote sensing, automation, and artificial intelligence, high-throughput phenotyping platforms are changing the conventional trait evaluation methodologies of a small number of measurements on a plant into a dynamic large-scale monitoring system that could record and process the response of plants across space time (Yang *et al*., 2020) [92].

The interaction of genomics, transcriptomics, proteomics, metabolomics and phenotypic data will enable the accumulation of complex regulatory networks in the process of plant growth, development and adaptation of stress. This kind of understanding at systems level must enhance the discovery of genes and their functional validation (Weckwerth *et al*., 2020) [89]. At the same time, machine learning predictive models and computer modeling of crops will enhance the accuracy of breeding because they are able to predict the phenotype with genomic and environmental information and do it effectively prior to experimental testing in the field (van Dijk *et al*., 2021) [85].

Genome editing technologies will continue to take center stage considering that they will offer one of the ways of rapid validation and targeted improvement of the candidate genes identified in the environment of the analysis presented by phenomics. These tools will accelerate the crop-enhancement pipelines to increase the stability in the yield, resource-utilization quality, and climate-resilience (Varshney *et al*., 2021) [86].

Overall, the integration of the application of the phenotypic classification with the use of the most advanced phenomics and multi-omics solutions makes it one of the pillars of the nextgeneration breeding strategies, and its contribution to sustainable agriculture and global food security is dramatic.

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