Chapter 6
Applications of High-Throughput Phenotypic Phenomics

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Contents

Introduction of Phenomics

Phenomics is the study of the phenome with the goal of characterizing phenotypes in a rigorous and formal fashion and linking them to the genes and gene variations that cause them (alleles). The study of plant development, performance, and composition is known as plant phenomics. Phenotyping technologies are used in forward phenomics to "sieve" collections of germplasm for important traits. The

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C. S. Prakash et al. (eds.), *Sustainable Agriculture in the Era of the OMICs Revolution*,
https://doi.org/10.1007/978-3-031-15568-0_6

sieve or screen may be high-throughput, completely automated, and low-resolution, with higher-resolution, lower-throughput measurements following. Abiotic or biotic stress challenges may be used in screenings, which must be repeatable and physiologically relevant. Reverse phenomics is the detailed dissection of attributes that have been found to be valuable to disclose mechanistic insight and use this mechanism in new techniques. A physiological characteristic may need to be reduced to biochemical or biophysical processes and subsequently to a gene or genes.

High-Throughput Phenomics (HTP)

Phenomics is the study of multidimensional phenotypes with high throughput and correct achievement at different (cell, tissues, organs, individual plant, plots, and field) levels during the developmental stages of a crop. The phenotypic performance of crops is totally dependent upon the interaction between genotypes and environmental factors such as climatic factors, biotic and abiotic factors, and management methods of crops. In other words, phenomics can be defined as the whole study of high dimensional phenotypes. To improve the crop and understand the plant biology, its necessary to obtain data on all main features of phenotype in detail, as shown in Table 6.1.

Phenotypic Technologies

The phenotypic traits can measure exactly through the fast growth of harmless or nontoxic senses and advanced techniques of imaging in which visible, thermal infrared, fluorescence, 3D, and hyperspectral imaging, as well as tomographic imaging using magnetic resonance imaging (MRI) or X-ray computed tomography (CT) are involved. The number of high-throughput phenotyping (HTP) platforms can increase with the help of different technologies like sensing technologies, automatic controlled technologies, computers, robotics, and aeronautics for crop phenotypic traits inquiry. Numerous phenotypic platforms for the traits of the crop at numerous application scales are developed by scientists. In this chapter, there are three types of phenotypic platforms: microscopic, ground-based, and aerial phenotyping platforms split on the bases of imaging levels, which permit the representation of phenotypic traits at the different levels (tissue level, individual plant level, plot level, and field level). For the highly developing field of phenomics and giving rise to an increasing amount and diversity of data, high-throughput technologies are generally used. Turn off the extent data into the

Table 6.1 Various imaging tools and techniques used for different traits phenotyping

Sr. no.	Imaging tools and techniques	Traits to be measured/phenotype
1	Visible light	Shoot biomass, yield attributes, leaf morphology, ear traits, and root traits are all factors to consider
2	RGB imaging	Growth dynamics, chlorosis and necrosis, simple pigmentation, senescence, projected structures, surfaces, shoot colors, roots, seeds, leaf spots, growth dynamics, chlorosis and necrosis, simple pigmentation, and senescence
3	MRI, CT (X-ray)	Internal structures, in-soil structures, volumetric data, root development, and metabolites are all examples of internal structures
4	Thermal infrared	Index of the surface of the leaf, temperature of the leaf, insect state infestation, sheet and canopy water status
5	Laser, stereo imaging, time of flight imaging	Deep 3D structure, leaf angle, leaf area, plant height, cover, biomass amount, and structural composition are all factors to consider
6	Hyperspectral	Moisture content, leaf wellness, panicle health, wheat quality, pigments composition, and other factors.
7	Multispectral imaging	Minimal pigmentation, discontinuous spectrum reflection, includes NIR
8	PAM-fluorescence, wet chemistry, destructive sampling	Advanced studies of plant physiological functions and processes, including photosystem II activity, metabolite and phytohormonal profiles, enzyme activities
9	Fluorescence imaging	Leaf disease severity ratings, leaf health status, and more. Photosynthetic performance, quantum yield, non-photochemical quenching, leaf disease severity ratings, leaf health status, and more. Photosynthetic system (indirect), biomass development, nitrogen content, and senescence are some of the topics covered in this paper
10	Thermal imaging	Temperature of the leaf or canopy surface, relation to stomatal conductance, and biotic and abiotic stress responses
11	3D imaging	Turning structure; sheet corner distributions; canopy structure; root architecture; height
12	MRI	Water content, morphometric parameters, etc.
13	Hyperspectral imaging	Senescence, water, chlorosis/necrosis, continuous spectral reflectance, including NIR, immediate physiology, advanced pigmentation, and specialized specific pigments, such as xanthophyll related to biochemical composition and photosynthesis, senescence, water, chlorosis/necrosis
14	PET	Solute content, metabolites content, etc.
15	Fluorescence imaging	Photosynthetic machinery and associated metabolism, predicted leaf area, research of leaf stress owing to biotic and abiotic causes, snapshots of photosynthetic performance, and senescence

beneficial forecast and perception the artificial intelligence (AI) acts as a game changer. Although we need specialized programming skills and deep knowledge about machine learning, deep learning and ensemble learning algorithms are used to understand this artificial intelligence.

HTP Methods

RGB Imaging

RGB camera or RGB imaging method is mostly used to measure the morphological effects of plants (caused by its cost efficiency and ease of insertion). RGB cameras consist of an infrared blocking filter (VIS camera) that can detect the light wavelength of 400–700 nm instead of customer cameras. For the measurement of the color of every pixel, this camera used different color sensors (red, green, and blue). Scientists concluded that the model's prediction accuracy could be enhanced by adding other elements such as the growth date (Golzarian et al., 2011) or more anatomical or physiological characteristics in a more complex model (Chen et al., 2014). Because of its cost-effectiveness and ease of installation, the RGB camera approach is the most extensively used technology for measuring plant morphological features. RGB cameras (VIS cameras) include an infrared blocking filter that detects light wavelengths between (400 and 700 nm), unlike consumer cameras. The VIS camera measures through red, green, and blue color sensors as shown in Fig. 6.1.

Near-Infrared Imaging

In different topics, the highest reflectance is in the near-infrared wavelength range (700–1400 nm). This near-infrared imaging (NIR) attribute is employed to confirm plant transformations during drought stress.

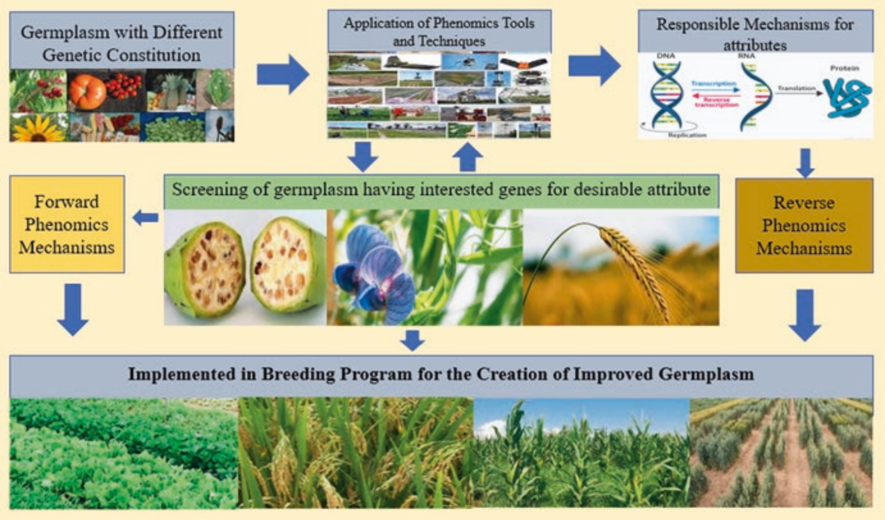

Fig. 6.1 High-throughput phenotyping technology concept

Hyperspectral Imaging

Hundreds of thousands of bands per pixel are detected by hyperspectral sensors, which cover the visible (400–700 nm), NIR (700–1000 nm), and SWIR (1000–2500 nm) wavelength ranges. Even though the data's physical complexity mandates the use of high-performance analytical processors, sensitive detectors are required, and also pictures may be recorded at high resolution with restricted spatial coverage to distinguish reactions to different pressures and large data storage capacity.

Fluorescence Imaging

With the fluorescence sensors, we can easily test the photosynthetic ability of the crop, and it can be tested by the estimation of chlorophyll fluorescence. For example, the excretion of unessential energy by the plant in the form of fluorescence.

Applications of High-Throughput (HTP) Phenotypic (Phenomics)

According to Soulé (1967), the word phenome implies an entire phenotype like genome manifestation in a certain location (Houle et al., 2010; Chen et al., 2014). As a result, a plant phenotype in an agricultural system must be viewed as the outcome of complicated G*E*M interactions (Houle et al., 2010). The word phenomics was coined in 1997 (schork, 1997) and was described as the methodical study of phenotypes at an organism-wide ranging like genomics and the various further omics technologies (Houle et al., 2010). The set of morphological, physiological, and recital-associated features of a genotype in the environment is known as the phenotype (Dhondt et al., 2013). In other disputes, phenomic is an inclusive wide-ranging study of high-dimensional phenotypes that is vital for the generation of meticulous data on all important aspects of phenotypes and for an improved understanding of plant biology and crop improvement. Therefore, the phenotyping system not only includes tools for performing phenotypes on its own but also plants in a specific environment, from the tightly controlled condition of the climatic chamber to the natural environment of the field it also means to grow (Dhont et al., 2013). The throughput of a plant phenotyping system relates to the number of individual units at a given organization. Steven A., a UC Berkeley and LBNL scientist, invented the term phenomics to describe the scientific study of phenotypes. As a result, it is a multidisciplinary field of study that includes biology, data science, engineering, and other disciplines.

Phenotypic Technologies

Multidisciplinary collaboration and some of the initial developments were targeted toward assessing genetically modified crops on a large scale (Reuzeau et al., 2005). Plant refurbishment approaches, Trait Mill, a suite of proprietary bioinformatics tools, a high-throughput gene engineering system, Crop Design (Belgium) established a HTP stage that was utilized to detect morphometric characteristics. (aboveground biomass, plant shape, and plant color) that might have an impact on yield. TraitMill's details, as well as the trial methodology and results, were inappropriately kept confidential (Reuzeau et al., 2005).

High-Throughput Phenomic Methods

Scanalyzer 3D platform:

Hairmansis et al. (2014) and Neilson et al. (2015) reported that the Scanalyzer 3D platform was created by Lemna Tec in Germany, and it has been implemented in numerous countries. Computer-controlled conveyor systems are installed at the Plant Accelerator (Australian Plant Phenomics Facility, University of Adelaide, Australia), automated weighing–watering devices, imaging stations, *Near-infrared (NIR), fluorescence* (at near-infrared wavelengths between 700 and 1400 nm, the green portions of plants had the maximum reflectivity), and *Hyperspectral imaging* (hundreds of thousands of bands per pixel are detected using hyperspectral sensors, which cover the visible spectrum) (Mathieu et al., 2015).

RADIX Imaging Marié et al. (2016) and Jeudy et al. (2016) examined the RhizoTubes (an automated "plant-to-sensor" platform including 1200 rhizo tubes to acquire the RSA in about 6–8 weeks) and RhizoSlide (a rhizoslide platform used to screen the shoots and roots of 200 maize plants) (Le Marié et al., 2016).

Quantitative Plant Morphology Detection Through Phenomics

To maintain future food security, it is critical to developing crop tolerance to abiotic stresses and new pests brought on by climate change. The growing use of gene editing, as well as the continuous utilization of natural genetic diversity, present excellent prospects for producing novel alleles and selecting natural sources of genetic variation for crop development. This necessitates the examination of hundreds of lines growing in a variety of environments. At the same time, breakthroughs in DNA marker assays and sequencing technology have enabled genotyping to achieve this throughput at a reasonable cost, similar innovations provide an urgent demand for high-throughput and meaningful phenotypic data. The purpose of plant phenomics, which we describe as the study of the development of plants, is to achieve this and implementation of a set of tools and methodologies that are used to achieve three key objectives—gathering data on the structures, functions, and performances of huge groups of plants, as well as their surroundings; analyzing, organizing, and storing the generated datasets; and constructing models that can untangle and recreate plant activity in a variety of settings. Plant phenomics has advanced significantly in the last decade, with new sensors and imaging approaches being developed for a variety of features, organs, and conditions. When it comes to turning sensor data into knowledge, however, data handling and processing remain significant obstacles (Tardieu et al., 2017).

Plant phenotyping is the study of complex plant characteristics such as growth, development, tolerance, resistance, architecture, physiology, ecology, and yield, as well as the fundamental assessment of quantitative parameters that serve as the foundation for more sophisticated aspects. Photosynthetic efficiency, root shape, biomass, leaf features, fruit traits, and yield-related aspects direct measuring parameters in the plant phenotype, including biotic and abiotic stress response. To enable current genetic crop development, there is a necessity for more effective and reliable phenotyping data, given the fast development of high-throughput genotype screening for associated growth, yield, and resistance to various biotic and abiotic stresses in plant breeding and genomics. Currently, expert visual evaluation is used to assess phenotypic features for disease resistance or stress in breeding programs (Yang et al., 2020). This takes time and may result in prejudice between experts and experimental duplicates as shown in Fig. 6.2.

It will be a huge challenge for plant science and crop development to ensure that crop production is sufficient to meet the needs of a human population that is predicted to reach more than 9 billion by 2050. This aim is difficult to achieve because crop output increases at a 1.3% annual rate, which is insufficient to keep up with population growth. High-yielding, stress-tolerant plants can be selected

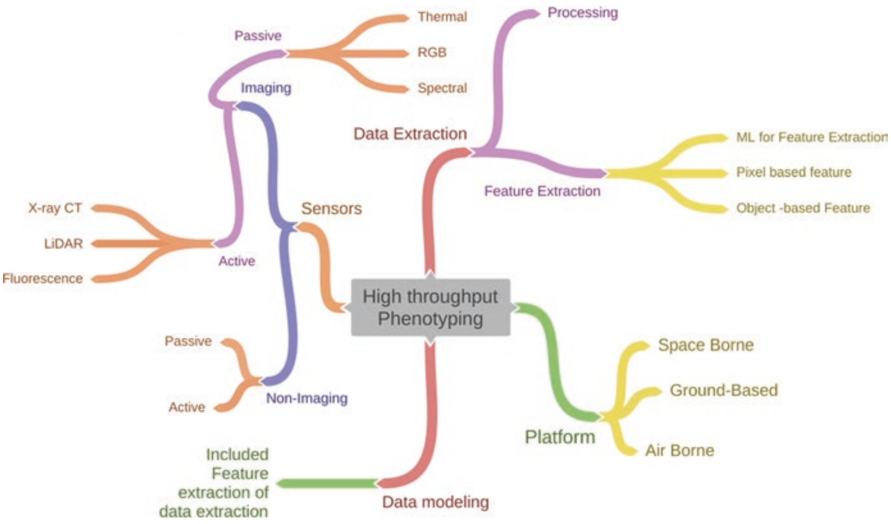

Fig. 6.2 Application of phenomics implemented in breeding program

significantly more quickly and efficiently than is now possible by connecting the genotype to the phenotype. Breeders can benefit from advances in technology such as next-generation DNA sequencing, which might potentially boost the rate of genetic improvement through molecular breeding (Jaradat, 2018). However, our capacity to unravel the genetics of quantitative variables relevant to growth, yield, and stress adaptability is limited because of a paucity of phenotyping skills. Long before the discovery of DNA and molecular markers, plant breeders and farmers made decisions based on phenotypes. The more crosses and habitats that are used for selection, the better the chance of finding a superior variety.

It is necessary to improve breeding efficiency to fulfill future demands. The establishment of huge mapping populations has been aided by high-throughput genotyping and phenotyping panels made up of hundreds of recombinant inbred lines and the creation of massive mapping populations and phenotyping diversity panels made up of hundreds of recombinant inbred lines. Although molecular breeding techniques place a greater focus on genotypic information, phenotypic data is still required. Phenotypes are used for selection and to train a prediction model in genomic selection. A single phenotyping cycle is utilized in maker-assisted recurrent selection phenotyping to develop markers for future selection through generations to find potential events in transgenic investigations (Chaerle & Straeten, 2001).

Breakthroughs in phenotyping are critical for capitalizing on advances in traditional, molecular, and transgenic breeding (Li et al., 2014). Plant phenomics is concerned with defining the plasticity of the plant phenome when subjected to a variety of environmental variables rather than just correlating a genotype with one phenotype in a specific state (e.g., in a controlled environment). In contrast to most animals, which maintain roughly the same structure regardless of their environment, plants can take on a variety of architectural forms depending on the circumstances. After being exposed to either short- or long-day circumstances, the same type of Arabidopsis thaliana can produce a huge 30-leaf plant or a small 8-leaf plant. Water deficiency, nitrogen deficiency, and poor light all have a significant impact on the quantity and size of plant organs. As a result, plant phenomics research concentrates on the study of variation in organism structure, whereas animal phenomics research is primarily concerned with metabolism (Tardieu et al., 2017).

Quantitative Plant Morphology Detection Through Phenomics

Analysis of plant development, production, and formation is called Phenomics. According to (Soulé, 1967), the word “phenome” implies an entire phenotype like; genome manifestation in a certain location; collection of expression in a body belongs to phenome. To get valuable characters from assembled germplasm, forward phenomics act as a tool. Complete analysis of traits exposes systematic understanding and permits the development of this mechanism in new methods.

Measurable and qualitative characteristics of a fused at a certain phase of ontogenesis in certain living conditions of a living system. At a considerable range, a superior proportion of phenotypic data find through phenomics. Skelly, Lobos, Orgogozo, and some other scientists proved that phenomics is usually considered parallel to genomics.

The procedure of development, transformation, and regulation of phenotypic expressions in living systems are examined in phenomics, then decreased to regularities (Skelly et al., 2013; Orgogozo et al., 2015; Lobos et al., 2017) though varies from genomics. Because of differences in phenotypic manifestation of characteristics upon the ecological circumstances, the entire classification of a genome is feasible in genomics, while the entire classification of phenome is not easy in phenomics, have been proved by Houle (Houle et al., 2010). Achievement of molecular genetics and breeding efforts particularly in field crops ever more defines through phenomics (Afonnikov et al., 2016). Plant phenotyping is considered an advanced and practically designed method of plant physiology (Furbank et al., 2011). Phenotypical modification that detect structural variation is quite easy to identify and examine. Stress response phenotypes depend on structural markers to compute stress responses in both ways. Phenotypes of numerous plants were recorded by Parent in 2015 because of the development of visual imagination and remote sensing skills and can easily be calculated at once mechanically and constantly (Parent et al., 2015).

Several sensors are utilized by extraordinary-data examining systems to access some structural characteristics like: plant height, canopy size, leaf area, green leaf pigment, shoot angle, virus spot size, and plant wilt degree. An individual can widely explain the significance of characters through this data like plant manner, nutritional value, drought acceptance, and virus resistance. A number of technologies are applied in various plants. By utilizing the Tomato Analyzer image, fruit shape traits were evaluated in 21 eggplant accessions from four varieties (Hurtado et al., 2013). A total of 23 fruit form parameters were calculated for agreement for fruit shape index, blockiness, homogeneity, proximal fruit end shape, asymmetry, internal eccentricity, and slenderness. (Hui et al., 2018). Three-dimensional (3D) canopy of cucumber, pepper, and eggplant based on multiview stereo (MVS) about plant canopy. By utilizing Crop Circle ACS-470 technique, Jaradat (2018) has isolated phenotypic information and some factors involving less heat tolerance during propagation, premature plant, etc. (Jaradat, 2018). Brassica napus verities that commonly grow in the Midwestern United States having extraordinary yields, and these can be measured through attributes. Tomato biomass and important linear association among expected shoot area, plant numeral biomass was analyzed by a scientist Laxman et al. (2018) using Scan analyzer 3D large scale imaging platform (Laxman et al., 2018). Bernotas et al. (2019) brief about photometer stereoscopic (PS) images, which consist of phenotype arrangement and its eudicot variety, including some vegetables like cabbage, tomato, and oilseed rapes (Bernotas et al., 2019).

Phenotyping of Roots in Plants Through Phenomics

Root system architecture (RSA) explains the spatial configuration of the root system rising from root morphology, topology, and distribution (Lynch, 1995). Root architecture, domestication environment, and techniques may be used to direct breeding programs to connect a root system with a life strategy and agroecology, increasing system adaptability (Bullock et al., 2017; Schmidt et al., 2016). Hypocotyl roots, as well as basal roots in some species, initiate epigeal germination between the radical and the cotyledons, which are elevated out of the soil. Above the basic root, there are three groups of epigeal germinators (Zobel, 2011). Basal roots of common beans can be divided into three types (Zobel & Waisel, 2010). Hypocotyl, main, and basal roots are among the types of roots. Basal roots emerge from the hypocotyl's base. Root morphology (Zhu et al., 2011), leaf features (Micol, 2009), biomass (Tackenberg, 2007; Golzarian et al., 2011), yield-related traits (Duan et al., 2011), photosynthetic proficiency (Clark et al., 2011), and abiotic stress response (Rellan-Alvarez et al., 2015) are the most widely considered phenotypic traits Here, we will go through some of the most important plant phenotyping instruments, as well as some of the most promising photonics-based technologies.

As a result, despite notable breakthroughs, there are relatively few publically available root phenotyping datasets. Laboratory investigations benefit from improved levels of control, and at least in a few cases, loci with fundamental RSA in early root development have been identified. Nonetheless, the growth flasks utilized in these experiments, which were filled with actual or artificial soil (Rellan-Alvarez et al., 2015), limited geographic and temporal explanations for small or immature root systems (Judd et al., 2015; Lobet et al., 2013). Individual tools offer varying degrees of computational automation, ranging from manual to semiautomatic to fully automatic, making this software assembly an exciting prospect. None of these, however, give a combined stage that can (a) combine secondary root images with environmental and phenotypic metadata, (b) provide nontechnical users with continuous access to supercomputing resources, and (c) communicate content within a cooperative team and with the general public.

We formed DIRT in order to speak about these issues. The DIRT stage includes several key features that enable researchers to: (a) manage root picture collections and metadata, (b) interactively standardize dimension pipelines, (c) calculate crop root traits on available high-throughput compute platforms; and (d) analyze computation outcomes. DIRT enables researchers to process thousands of root images, complete the pipeline with routine parameters, and display and analyze calculated RSA output connected to the raw images. As a result, our stage allows researchers with few practical capabilities to access high-throughput computational stages. Thus, automation, remote control, and data (image) investigation pipelines agreeable to HTP stages acceptable showing of large plant populations, germplasm collections (core collections), breeding material, and mapping populations with increased accuracy and precision in phenotypic trait achievement attached with decreased labor input attained by high-throughput (Junker et al., 2015).

More study is needed to fully utilize genomics and molecular breeding methods in crop improvement, which address the creation of phenotyping tools and technologies, phenomics for a specific trait, phenotyping requirements, ongoing initiatives, and obstacles (Furbank & Tester, 2011; Cobb et al., 2013; Lobet, 2017). This review study aims to: emphasize the importance of phenomics and phenotypic constraints in crop improvement in the genomics era, (i) review the current status of phenomics stages and accommodations worldwide, (ii) emphasize the use of high-throughput phenomics platforms for trait separation in different crop plants and detection of genes/QTLs for a variety of traits in different crop plants, and (iii) emphasize the need for phenomics files and phenotyping. Responsible root function in soil, as well as root structure and growth screening, has long been a fascinating area (Gregory et al., 2009). For cereal species growing on stored soil moisture, access to water at penetration is critical for drought tolerance, and a study using model species to identify genes relevant for root characteristics is now underway. Small, short-lifecycle crop models, which are better suitable for cereal species, have recently been produced and are great systems for phenomic display (Watt et al., 2009).

This topic denotes a few technologies ranging from imaging in thin layers of soil or reproduction media to MRI and X-ray CT-scanning (Faget et al., 2009; Nagel et al., 2009). Root crown phenotyping occurs at the apex of crop root systems and can be utilized for marker-assisted breeding, genetic mapping, and a more sympathetic understanding of how roots inspire soil resource acquisition. There are a number of imaging methodologies and picture series available, but none of them are optimized for high-throughput, reproducible, and vigorous root crown phenotyping. The RhizoVision Crown stage includes an imaging unit, picture detention software, and image analysis software that have been upgraded to remove measurements from huge numbers of root crowns in a uniform manner to identify that root crown shapes. The hardware platform uses a backlight and a monochrome machine vision camera. The RhizoVision Imager and RhizoVision Analyzer are free, open-source applications that improve picture capture and analysis by incorporating spontaneous graphical user boundaries.

Physical validation of the RhizoVision Analyzer was done using copper wire, and feature validation was done with 10,464 ground truth simulated images of dicot and monocot root systems. The soybean and wheat root crowns were then phenotyped using this platform. The researchers phenotyped 2799 soybean (Glycine max) root crowns from 187 lines and 1753 wheat (Triticum aestivum) root crowns from 186 lines in both species; principal component analysis revealed comparable connections between characteristics. The greatest heritability was 0.74 in soybean and 0.22 in wheat, demonstrating that species and population variations must be taken into account. The RhizoVision Crown platform enables HTP of crop root crowns and establishes a benchmark against which open plant phenotyping platforms can be measured.

The total volume of soil that roots can investigate is influenced by RSA, which is shaped by interactions between genetic and environmental components (Schmidt et al., 2016). The number, length, growth angle, elongation rate, diameter, and branching of axial and lateral root phenes (or elemental units of phenotypic) shape the final RSA. Weaver and colleagues (Weaver, 1925; Weaver & Bruner, 1926) pioneered root-digging, diagramming, and photography methods that have been widely utilized for almost half a century (Böhm, 2012). These classical methods were since changed by Stoeckeler and Kluender (1938) with the use of water to remove soil particles from the root systems on a large scale and the use of high-pressure air to enter soil pores while leaving roots complete (Kosola et al., 2007). Devised hydro pneumatic root elutriation to give a rapid and repeatable method for extracting roots from the soil of field-composed soil important samples with minimal harm (Smucker et al., 2009).

Traditional digging methods are best for trees and shrubs because the root systems of woody plants are often stronger and more resistant to breakage than grasses or annual crops. The existing inability to quantify root architecture in the field is a major hindrance to current "phenomic" technologies' claims of marker-assisted selection for better root system features. Traditional field approaches for root phenotyping, such as digging up soil cores and using standard digging techniques to control root depth, root branching density, and root angle, are still considered the best (Trachsel et al., 2011; Nielsen et al., 1997). Such approaches, however, do not reveal the finer aspects of root architecture, anatomy (for example, root hair densities), or function (e.g., nutrient uptake as a result, identifying crops with increased root architectural traits, as well as developing appropriate instruments for studying root growth in the soil, largely under field settings, remains a major challenge for current plant biology. Under drought conditions, root architecture changes dramatically, favoring the formation of more long lateral roots and root hairs to increase total surface area for better water absorption (Osmont et al., 2007). The increase in root quantity, mostly deeper in the soil, results in an enhanced plant water status, which is required to promote biomass production and yield when combined with techniques that limit water loss, such as stomatal closure, leaf systematic, and leaf abscission.

A new machine vision-based facility for the automated evaluation of yield-related characteristics in rice has been developed. This work resulted in the creation of an integrated facility for completely automated yield trait scoring. The facility can thresh rice panicles, evaluate rice production attributes, and pack loaded spikelets automatically. The accuracy (mean absolute percentage error is less than 5%) and efficiency of this unique machine vision-based facility were demonstrated in tests (1440 plants per continuous 24 h workday) (Table 6.2).

Future Perspective Phenotypic–genotypic integrated breeding as the sequencing technology of crops has advanced. With the emergence of phenomics, breeding has entered a new age. It allows breeders to accurately phenotype many samples. Breeders may be able to correlate a lot more traits with accordant genotypes if it is combined with NGS technology. In current years, even more innovative attempts in the phenomics field have been made; computational approaches like machine learning (ML), deep learning (DL), and artificial intelligence (AI) have been integrated with HTP analyses to anticipate the population of many crops.

Table 6.2 Advantages and disadvantages of HTP application in field crops

Sr. No.	Technology and tools	Advantages	Disadvantages
1	GROWSCREEN-Rhizo	In soil-filled rhizotrons, high-throughput methods for obtaining shoot and root traits were used	In 2D rhizotrons, root development is restricted (rhizobox)
2	PhenoBox	Affordably priced and simple to maintain	Large-scale screening requires a lot of work
3	Field Scanalyzer, a rail-based gantry phenotyping system	High picture resolution is achieved by the integration of many optical sensors	Expensive; small image area; fluctuating ambient light
4	MRI–PET; PET–CT; MRI–CT	3D root system topologies may be obtained in soil-filled tubes	Costly; time-consuming; no specialist prototype for agriculture research
5	TraitMill; Scanalyzer3D; PHENOARCH; HRP	For big populations, dynamic and automatic methods are used to acquire shoot growth, biomass, and a wealth of information	It is expensive to maintain and upgrade; it need the involvement of diverse professionals
6	CPRS, a fixed phenotyping tower	Simple to set up and maintain	There was only a limited amount of agricultural information available in fixed regions

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