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Genomic Clues and Phenotypic Views: A High-Throughput Perspective on Trait Discovery

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ABSTRACT

The use of molecular marker technologies has significantly advanced biological sciences and plant genetic analysis, particularly in revealing individual variations in DNA sequence. Molecular markers are useful tools in plants, particularly in marker-assisted selection, genome-wide association studies and QTL identification that impacts complicated hereditary traits. As the development of genomic tools in plant breeding and our knowledge of plant genomes increases, rapid and high-throughput phenotyping methods continue to be discussed as significant improvement applications in plant breeding programs. Since quantitative traits such as yield traits, quality traits, and resistance to abiotic/biotic stress factors in plants are an element that determines the indirect effects of both genetic and environmental factors and their interactions, phenotyping is a critical element in crop development. High-throughput phenotyping methods capture changes in environmental factors more sensitively compared to traditional applications, and thus selection efficiency is successfully increased. Correct and ethical use of genomic technologies with high-throughput phenotyping techniques is critical for long-term success and sustainability in the agricultural sector. In this review, the use of molecular marker technologies developed in integration with plant breeding in mapping studies and studies on the use of high-throughput phenotyping technologies in plant breeding are discussed.

INTRODUCTİON

Advancements in genomic and molecular research in plant breeding have led to the development of various molecular markers, including (Rafalski, 2002). Numerous studies on plants, including population genetics, genetic mapping, resource identification, and the creation of markers associated with significant traits, have been made possible by the advent of DNA-based molecular marker techniques (Kefayati, 2019). Furthermore, molecular markers find application in the following domains: genotype identification; variety registration; breeding line identification and registration tests; hybrid variety purity tests; assessment of genetic diversity; identification of the genetic source of gene resources; estimation of agricultural performance and adaptability; and so on (Eserkaya Güleç, 2010; Bianco *et al.*, 2011). The of primary importance application areas of molecular markers in plant breeding are the use of marker-assisted selection (MAS), genome-wide association study (GWAS), genotypic characterization and QTL mapping (Yirgu *et al.*, 2023). RFLP, RAPD, SSR, DArT and SNP markers are widely used in breeding (Khlestkina and Salina 2006). Some distinguishing features of these markers are given in Table 1. SNPs are differences in a single nucleotide occurring in the genome sequence. Compared to other types of markers, SNPs are a common type of variation in DNA and are discovered at a significantly higher rate in the genome (Tian *et al.,* 2021). They can appear in intergenic, coding and non-coding regions of the genome (Ren *et al.,* 2023). Considering their basic characteristics, they are among the codominant markers, which allows SNPs to distinguish between homozygous and heterozygous alleles. The rate of polymorphism is high. For this reason, it can be used as an significant tool for genetic mapping, GWAS, map-based on cloning and MAS (Amitiye, 2021). Additionally, they are used to find polymorphisms that other markers fail to identify. Due to their biallelic origin, SNPs are less polymorphic than SSR markers; however, this shortcoming is easily compensated by their prevalent distribution throughout the genome and their ability for high-throughput automation. SNP markers offer an advantage over SSRs due to their independence from gel technology and single base pair position differences in genomes (Manivannan *et al.,* 2021). Their high density increases the probability of detecting polymorphisms in target genes, making them popular in plant molecular genetics.

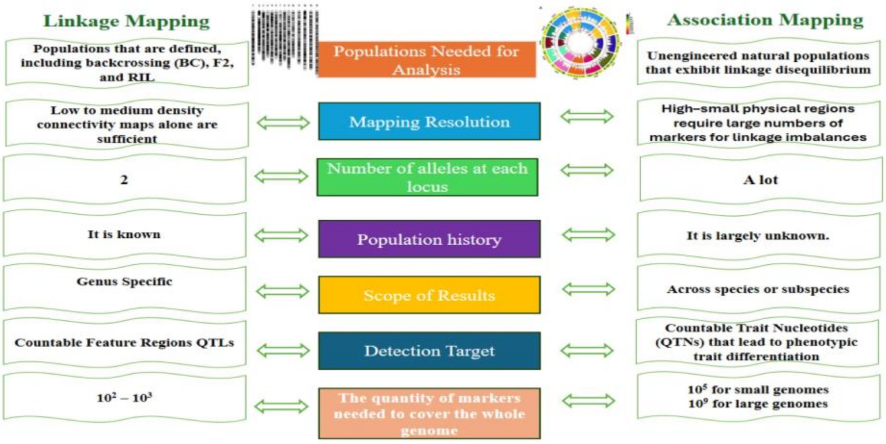
Tablo 1: Comparison of Properties of Different Molecular Marker Techniques

Molecular Marker Type	Being PCR Based	Inheritance Type	Polymorphısm Level
RFLP(Restriction Fragment Length Polymorphism)	Hybridization based	Co-dominant	Low/Medium
RAPD (Random Amplified Polymorphic DNA)	PCR	Dominant	Medium/High
SSR (Simple Sequence Repeats)	PCR	Co-dominant	High
SNP (Single Nucleotide Polymorphism)	PCR	Co-dominant	High
DArT (Diversity arrays technology)	Hybridization based	Dominant	Extremely High

Genomic technologies have recently provided high-quality and valuable information while also reducing the cost of acquiring large-scale genomic data (Gu *et al.,* 2022). However, collecting reliable phenotypic data for multiple traits from thousands of plots in a short time is one of the major challenges in scaling up plant breeding programs or incorporating selection for multiple traits simultaneously (Chawade *et al.,* 2019). Of late years, intensive work has been done on the investigation of genome-based associations (GWA) to identify new genomic associations associated with quantitative traits in plants (Sajjad *et al.,* 2012). A research method called a GWAS looks for correlations between genotypes and traits by screening a population's complete genome. Traditional breeding techniques might be difficult when environmental factors affect quantitative qualities. To overcome these obstacles, it is crucial to combine traditional and molecular approaches

(Arruda *et al.,* 2016). One of the foremost areas of use of molecular markers is genetic mapping studies (Singh, 2017). Linkage mapping (LD) and association mapping are two of the most common methods used to detect the relationship between molecular markers and phenotypic traits (Xu *et al.,* 2017). Both approaches have their own differences, advantages, disadvantages, challenges, costs, and requirements (Alqudah *et al.,* 2020). Genetic mapping studies aim to determine the locations of genes and markers on the chromosome, map QTL regions and determine their distances from each other. Linkage maps are used to identify these QTL regions, detect the relationship between markers and characters and determine their positions on the map (Madhusudhana, 2015). In the technique called Linkage Mapping, generally backcross, haploid, Recombinant inbreed lines (RIL) and F_2 populations obtained from the same mother and father are used. Since the stages of obtaining phenotypic data and developing special populations (F_2, GM, RIL) in Linkage Mapping are tedious and time consuming, association mapping has become a practical application. In addition, as a new alternative to traditional linkage mapping, association mapping has significant advantages such as greater map density, less study time on natural populations with high and distinct diversity, and greater allelic diversity (Yu and Buckler, 2006).

The method of genotyping molecular markers on a genome-wide scale has become possible thanks to recent advances in computational statistics and high-throughput genomic technologies that enable rapid and efficient discovery of these markers (Xiao *et al.,* 2022). This has made it easier to use GWAS to track and assess complicated traits and quantitative characteristics that segregate across populations. Association Mapping is a method that uses the relationship of genotype to phenotype to identify QTL regions associated with important target traits (Verdeprado *et al.,* 2018). Association mapping evaluates the correlation of character differences with molecular marker polymorphisms on a population basis. Since the population used in linkage mapping studies is obtained by crossing two parents, genetic variation is limited, while in relationship mapping, genetic variation is very high since a population consisting of many generations is used (Ashwath *et al.,* 2023). Association mapping establishes a connection between phenotype and genotype on the basis of LD, using the linkage between loci seen in the population or the non-random association of alleles located at different loci (marker locus and phenotypic trait locus), additionally known as gametic phase imbalance, gametic imbalance and allelic association (Ibrahim *et al.,* 2020; Ersoz *et al.,* 2007). The most obvious fundamental difference in association and linkage mapping studies is the answer to the question of whether recombinations occur in populations or in families. In fact, in practice, both of these mapping techniques identify molecular markers associated with QTL, so even though they have a common strategy, differences between them cannot be ignored (Figure 1). It is anticipated that in the future, when the era of worldwide genome sequencing begins, this difference in mapping techniques will also disappear (Myles, 2009).



Linkage Mapping		Association Mapping
Populations that are defined, including backcrossing (BC), F2, and RIL	Populations Needed for Analysis	Unengineered natural populations that exhibit linkage disequilibrium
Low to medium density connectivity maps alone are sufficient	Mapping Resolution	High–small physical regions require large numbers of markers for linkage imbalances
2	Number of alleles at each locus	A lot
It is known	Population history	It is largely unknown.
Genus Specific	Scope of Results	Across species or subspecies
Countable Feature Regions QTLs	Detection Target	Countable Trait Nucleotides (QTNs) that lead to phenotypic trait differentiation
$10^2 – 10^3$	The quantity of markers needed to cover the whole genome	10^5 for small genomes 10^9 for large genomes

Figure 1: Key differences in link mapping and association mapping techniques.

With molecular marker integrated into plant breeding; QTL mapping, GWAS, MAS and gene pyramiding studies have significantly improved plant breeding by selecting and improving desired traits such as adaptation, yield, stress tolerance, quality, disease and pest resistance (Karaağaç and Balkaya, 2017). At the same time, more effective and reliable phenotyping methods need to be developed in parallel to further improve modern plant breeding (Chawade *et al.*, 2019). Although the evaluation of desired traits in breeding programs is done with traditional methods, these techniques are time-consuming and can create bias due to different evaluation methods of different people. Phenomics, like genomics, has become an important research topic in plant breeding (Xie & Yang, 2020). Plant phenotyping aims to measure complex traits like resistance to biotic and abiotic stress agent, yield and quality at a certain level of organization from organs to canopies (Yang *et al.*, 2020). For this purpose, it is obvious that phenotyping requires interdisciplinary expertise, especially in biological and computer sciences, mathematics and engineering (White *et al.*, 2012). Of late years, thanks to developing technology, more effective phenotyping technologies have been developed. Compared to traditional phenotyping, the use of these effective technologies, using robotics, artificial intelligence and sensitive peripheral control imaging technologies, evaluates plant growth, performance and phenotypic responses to stress factors in field and greenhouse conditions (Li *et al.*, 2014). It is hoped that these studies will increase in the coming years and, just like molecular and genomic technologies, they will be further developed and integrated into modern plant breeding.

Quantitative Trait Loci Mapping with Molecular Markers in Plant Breeding

Many agriculturally important and desirable traits, especially the majority of quantitative characters as yield and yield related characteristics, quality or resistance to stress conditions, are controlled by various genes in plant breeding. However, it is unclear how many genes interact and how many genes control each other for these quantitative traits (Mohan *et al.,* 1997). Nowadays, with the use of genetic or marker technologies in plant breeding projects, it has become much easier to learn the genes and their roles related to phenotypic traits that are significant for agriculture. Quantitative trait loci (QTL) are identified by constructing a genetic map, which is one technique used to create markers linked to a characteristic studied in plants (Salazar *et al.,* 2014). To create an excellent high density genetic map, a reference genetic map created using markers is necessary. The idea of genetic mapping involves creating new genetic maps in various populations (Figure 3). These genetic maps allow QTL analysis to be used to place significant characters on linkage groups, find markers associated with significant characters, and aid in the characterization and cloning of significant genes. QTL mapping is defined in molecular breeding as the process of identifying genes using genetic markers that affect quantitative traits. Knowing the exact location of these genes in the genome is greatly benefited from in plant breeding studies (Ürün, 2023). Molecular markers are extensively employed in several crops to track genomic areas and loci for resistance qualities against different abiotic and biotic stressors (Phillips and Vasil, 2013; Gupta and Varshney, 2004). The development and use of marker technology in plants has enabled the control of genetic information underlying quantitative traits in particular.

In plant breeding, especially when it comes to developing new varieties with desired traits, it is necessary to know where these genes are located in the genome for both effective and rapid breeding applications because many genes affect quantitative aspects. A suitable population can be used to discover the positions of significant genes in a certain chromosome region by using the QTL analysis approach (Burçak, 2008). The target of QTL map investigations is to clone the genes that govern significant vegetative features based on these maps and create marker genes that can be identified from the vegetative trait of interest more successfully (Rafalski and Tingey, 1993). Nowadays, with the discovery of numerous QTL regions for desired traits in the chromosomes of hybrid populations formed by crossing 2 dissimilar parents and the deciphering of their nucleotide codes, some of the identified markers and important gene regions are still used successfully in MAS and backcrossing. Using DNA or molecular markers, it is possible to locate QTLs and map and map their distribution within the genome (Kushanov *et al.,* 2021). The identification of the location of these genes within the genome is of significant importance for the field of plant breeding studies. Locating QTLs for heritable traits of agricultural importance will enable future genetic manipulations (directional changes) and gene transfers between organisms. Lately, research on QTL have been conducted in many plant species and DNA markers associated with different traits that can be used in MAS have been developed (Diouf *et al.,* 2018). QTL mapping is essentially the process of determining a relationship between a genetic marker and a measured trait. For instance, if tall plants among 250 individual wheat plants of different plant heights all have a special allele of a moleculer marker, then a QTL for plant height is very likely to be associated with that marker in that plant population. The process of determining if a QTL is associated with a marker involves classifying the population by genotype and utilizing correlative statistics to evaluate significant differences (Dhingani *et al.,* 2015). The studies presented in Table 2 have mapped QTL regions controlling desirable traits in different plants and have been proposed for future use in plant breeding projects using MAS.

Table 2: QTL Mapping of Important Traits in Plants with Different Molecular Marker Techniques

Plant	**Mapped Traits**	**Number of QTL**	**Marker Technique**	**References**
*Wheat (*Triticum aestivum *L.)*	Yield and Physiological Traits (Drought Tolerance)	225 QTL	DArTs, SSRs and EST-SSRs	Xu *et al.,* (2017).
Soybeans *(*Glycine max (L.) Merrill*)*	Yield Related Traits	47 QTL	SNP	Liu *et al.,* (2017).
Triticale	Powdery Mildew Resistance	23 QTL	DArT, silicoDArT and SNP	Dyda *et al.,* (2022).
Sesame	Yield-Related Traits	46 QTL	Specific-Locus Amplified Fragment (SLAF)	Mei *et al.,* (2021).
Chickpea *(Cicer arietinum)*	Heat stress-related traits (canopy-closure and early flowering)	14 QTL	DArT	Jeffrey *et al.,* (2024).
Rape *(Brassica napus)*	Crude Fiber and Quality Traits' Genetic Variation	6 QTL	15K SNP	Holzenkamp *et al.,* (2025)
Rye *(Secale cereale L.)*	QTL linked to resistance to leaf rust are identified.	129 and 140 SNP-DArTs and 767 and 776 silico-DArTs	SNP-DArT and silico-DArT	Matuszkiewicz *et al.,* (2024).
Sorghum *(*Sorghum bicolor)	Salt Tolerance	53 QTL	SSR	Wang *et al.,* (2020).
Wheat *(Triticum aestivum L.)*	Resistance to Stripe Rust	7 QTL	SNP	Tehseen *et al.,* (2022).

Genotype and Phenotype Association Approaches in Plant Breeding: Genome-Wide Association

Of late years, the development of technology has led to the emergence of new techniques, as Next Generation Sequencing (NGS) and genotyping at high resolution, which are now widely used by researchers. The common point of these technologies can be described as revealing the differences on the genome as single nucleotide differences (SNP), which is the final point reached by molecular markers (Deokar and Tar'an, 2017). Association mapping provides useful information about the genetic architecture underlying quantitative traits in the genotype that are often unrelated to each other. The GWAS technique is a statistical method used to determine the genotype-phenotype relationship (Figure 2). It combines SNPs found in the genotype and phenotypic diversity in a genome-wide context, with the aim of deciphering the loci underlying a particular trait (Alsaleh, 2016). This technique is based on the examination of molecular markers distributed throughout the genome and their relationship with the trait under study. It utilises genotypes that contain recombination events from past to present in the genome of individuals in a population consisting of different individuals (Bajaj *et al.,* 2015). This advantage of GWAS provides the opportunity to evaluate multiple alleles simultaneously while providing higher resolution in the genome, compared to QTL mapping studies that are based on recombination events in only a few recent generations (Saini *et al.*, 2022). GWAS technique is an effective approach to associate phenotypes of interest with genotypes and find causal genes/loci with higher precision (Hussain *et al.*, 2022). It has a higher optical mapping resolution compared to standard genetic and linkage mapping techniques to identify candidate alleles/genes specifically related to the trait of interest (Kole *et al.*, 2015). A large relationship panel of trading varieties and breeding lines/clones helps breeders discover superior alleles in their gene pool (Dwivedi *et al.*, 2020).

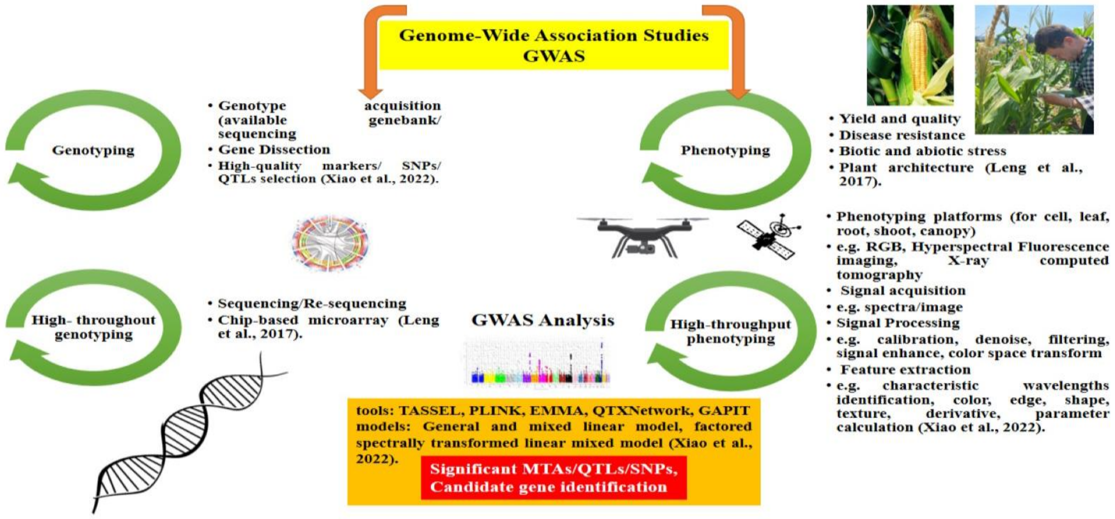


Figure 2: Combining High-Throughput Genotyping and Phenotyping in Plants: Example Schematic Illustration of the GWAS Technique

GWAS significantly improves the study of genetic architectures associated with complex phenotypes for cultivar development in plant breeding and plays an effective and improving role in plant breeding by deeply investigating the genetic basis of plant phenotype variability (Li *et al.*, 2023). The most important advantage of the GWAS approach over other genetic mapping techniques is the use of natural populations as plant material for the traits under investigation (Korte and Farlow, 2013). This is because, unlike hybrid populations created by crossing two plants, natural populations have a high level of genetic diversity (Huang and Han, 2014). The utilisation of germplasm materials and genetic information derived from a single natural population in GWAS studies permits the investigation of the association between numerous traits and genotype, as well as the impact of genetic information derived from the genome on the phenotype (Alseekh *et al.*, 2021; Sukumaran and Yu, 2014). Thus, it eliminates the need for repeated population creation for use in traditional linkage and genetic mapping studies and significantly reduces the costs required to identify candidate alleles/genes for and gene sequencing, while also saving time (Rawat *et al.*, 2014). The genetic mechanisms of important quantitative agricultural traits such as yield, quality, tolerance to abiotic and biotic stress factors in plants are generally affected by the genotype×environment from the relatıonshıp with the effect of constantly changing environmental terms and are regulated by more than one gene (Gonzalez Guzman *et al.*, 2022; Jakutis and Stainier, 2021). These traits have a more complex genetic structure than a trait regulated by a single gene. Therefore, the use of GWAS to investigate the genetic mechanisms of plant traits has received great attention. By now, the majority of GWAS research in plants has focused on staple crops with economic value. In 2017, 49,769 unique SNP-trait correlations were discovered in the GWAS database compiled from analyzes covering at least 3092 articles and 100,000 SNPs (Mohammadi *et al.*, 2020). As a result, examples of research conducted with high-throughput genotyping GWAS technique approaches are given in (Table 3).

Table 3: Abstracts of Research Using the GWAS Technique in Plant Molecular Breeding

Plant	**Sample Size**	**Traits**	**Markers**	**Marker Trait Associations İdentified**	**References**
Barley *(Hordeum vulgare L.)*	148	Morphological traits related to drought stress tolerance	407 Polymorphic marker (AFLP and SSR)	167 significant marker trait associations divided into 65 QTLs.	(Jabbari *et al.*, 2018).
Sorghum *(Sorghum bicolor L.)*	96	Agronomic Traits and Phenolic Content	192.040 SNP	40 significant SNP.	(Lee *et al.*, 2023).
Canola *(Brassica napus L.)*	399	Freezing Tolerance Traits	251.576 SNPs	13 significant SNP and 25 candidate genes.	(Chao *et al.*, 2021).
Cotton *(G. Hirsutum)*	231	Fiber Quality Traits and Yield Components	122 SSR and 4729 SNP	134 QTL for fiber quality traits and 122 QTL for yield components and 35 common candidate genes.	(Liu *et al.*, 2018).
Rapeseed *(Brassica napus)*	119	Under drought stress, agronomic and yield-related characteristics	52,157 SNPs	1,281 SNPs related to agronomic and yield traits and 215 candidate genes.	(Salami *et al.*, 2024).
Potato *(Solanum tuberosum)*	237	Floral traits	12.720 SNP	15 important SNPs related to flower characteristics.	(Zia *et al.*, 2022).
Wheat *(Triticum aestivum L.)*	600	Resistance to PstS2 and Warrior Races of Stripe (Yellow) Rust in Bread Wheat Landraces	25,169 SNP	Across 19 genomic areas, 47 significant SNP markers were developed.	(Tehseen *et al.*, 2020).

High-Throughput Phenotyping Approaches in Plant Breeding: A Technological Revolution

Genomic technologies have recently reduced the cost of acquiring large-scale genomic data while providing high-quality and valuable information (Bhat *et al.*, 2016). However, collecting reliable phenotypic data for multiple traits from thousands of plots in a short period of time is one of the major challenges in scaling up plant breeding programs or incorporating selection for multiple traits simultaneously (Uyaner, 2020). In plants, phenotyping is carried out at many organizational levels, including field, canopy, whole plant, organ, tissue, and cellular levels (Großkinsky *et al.*, 2015). The data gathered are then classified as either physiological, structural, or performance-based. Predicting how plants will react to various environmental conditions is made possible by accurate phenotyping. Researchers employed manual procedures in the traditional methods used for this aim. Especially during studies on phenotyping plants, examination of the plant during its life cycle is restricted due to damage to the plants (Karaşahin and Samancı, 2018). These problems, which caused low efficiency and inconsistent results, showed that there was a need to switch to automation systems. Recent advances in sensor and information technologies have enabled plant breeders to increase phenotyping accuracy and speed while minimizing labor and cost using high-throughput phenotyping (HTP) approaches (Shakoor *et al.,* 2017). Studies in the field of precision agriculture applications have gained momentum over the last twenty years (Saiz-Rubio *et al.,* 2020), and developments in detection and image processing technologies in particular have paved the way for studies to be carried out with high precision in this field (Shi *et al.,* 2016). With the development of biotechnology, new breakthroughs in the field of DNA sequencing and molecular biotechnology in plant breeding have significantly enriched and deepened our knowledge of plant genomes (Mir *et al.,* 2019; Haghighattalab *et al.,* 2016). Despite the rapid development of plant genomic tools, current traditional methods used in phenotyping and selection are still slow, laborious and costly, creating an imbalance between genomic and phenomic data (Bhat *et al.,* 2016).

In plant molecular breeding, the essential requirement for successful variety development programs is to reveal a strong relationship between genotypic and phenotypic data and to make successful predictions about variety performance. The disproportionality of data related to high-throughput phenotyping studies poses an obstacle to both genetic selection and gene mapping studies (Crain, 2016). Being able to establish a linkage between genotype and phenotype relationships will lead to success in the selection of varieties that are resistant to abiotic and biotic stress factors, can adapt to regional environmental conditions and are also high-yielding (Villalobos-López *et al.,* 2022). High-throughput phenotyping and remote sensing offer the advantage of providing real-time data and capturing a comprehensive view of crop health and growth, allowing policy makers and farmers to make informed decisions and optimize agricultural practices for higher yields and sustainable resource management (Na *et al.,* 2024). In this context, in recent years, many measurement methods such as spectroscopy, light detection and ranging (LIDAR), visible and far infrared rays, hyperspectral measurements, thermal imaging, three-dimensional laser scanning and red, green, blue (RGB) imaging have been used with automatic remote sensing systems (satellites, automatic field robot systems, unmanned aerial vehicles, etc.) (Fu & Jiang, 2022; Tardieu *et al.*, 2017; Singh *et al.*, 2016). Large data sets obtained in a short time with these technologies, when used with machine learning algorithms such as Random Forest, PLSR, KNN, CNN, are successfully evaluated for purposes such as disease detection (Hernandez-Rabadan, 2014), measurement of morphological features (Prado *et al.*, 2018), classification (Kruse et al, 2014) and even yield estimation (Gonzalez-Sanchez, 2014) (Table 4). Thus, by increasing plant production, the food demands of the increasing world population can be met. Thus, the obstacles experienced in determining super genotype characteristics in variety development and breeding studies can be eliminated (Sankaran *et al.,* 2015). Some studies using high-throughput phenotyping in various plant species using different technologies are given in Table 4.

Table 4: High-throughput phenotyping platform examples

Technology Used	Subject of Research	Plant Type	Observed Measurements	Referances
A Land-Based Platform and Unmanned Aerial Vehicle (UAV)	Examine Drought Adaptive Traits	*Triticum turgidum* L.	Dry biomass, Leaf Curl, and Chlorophyll Content	Condorelli *et al.,* (2018).
Camera and Sensor (BlueBox)	Root Phenotyping	*Triticum aestivum* L.	Root Number-Root Length	Wasson *et al.,* (2016).
UAV-Based Imaging Hyperspectral	Tracking Crop Growth and Managing Fertilizer	*Triticum aestivum* L.	Leaf Area Index (LAI)	Zhang *et al.,* (2021).
PhenoArch Phenotyping Platform	Well-watered and Water Stress Conditions	*Zea mays* L.	Fresh Biomass, Transpiration Rate and Plant Leaf Area	Prado *et al.,* (2018).
Spectrometer (HR2000)	Drought Resistance	*Triticum aestivum* L.	Chlorophyll (ChlRI), Light diffusion by the leaf, Photochemical reflection, Flavonoids	Rusakov & Kanash, (2022).
Spectroscopy	Metabolic Response to Drought Stress	*C.annuum and C. pepo*	Proline and Abscisic Acid	Burnett *et al.,* (2021).

Conclusion and Recommendations

This article provides an overview of the use of QTL and GWAS, high-throughput phenotyping approaches in plants. Gene maps derived from molecular markers have made it possible to genetically control quantitative traits, as these markers have become a fundamental component of plant breeding. Most agricultural traits of economic importance are polygenic and quantitative in nature and are controlled by many genes on the same or different chromosomes. QTL mapping is a method that uses molecular markers to find genes affecting traits of interest. With the discovery of QTLs for heritable traits important for agriculture, future genetic modifications (directional changes) and gene transfers between organisms have become possible. Analysis of the locations of relevant genes on chromosomes, the magnitude of their effects and whether the gene effect is dominant or additive, and the use of a suitable population for analysis can now be performed, especially by applying GWAS and QTL analysis methods. Genotyping and phenotyping in plants is a critical element in crop improvement through genetics because quantitative traits as yield traits, quality traits, and resistance to abiotic/biotic stress factors in plants are an important determinant of the indirect effects of both genetic and environmental factors and their interactions. High-throughput phenotyping provides high-quality phenotypic data for GWAS and QTL by offering contactless and more efficient measurements, unlike traditional methods. This improves the understanding of the genetic structure of complicated plant traits. Integration high-throughput phenotyping with genetic and association mapping approaches has broad applications, including investigating more phenotypes and genotypes. As genomic tools for plant breeding are developed and our knowledge of plant genomes increases, rapid and high-throughput phenotyping methods have been discussed as important advances in plant breeding programs since 2010. High-throughput phenotyping methods capture changes in environmental factors more sensitively than traditional practices, thereby successfully increasing selection efficiency. Breeders are particularly interested in continuing to explore and use these new technologies to meet the primary goals of their plant breeding projects due to the short data collection time and the need to phenotype hundreds of plots.

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