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Chapter

New Age of Common Bean

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Abstract

Common bean (*Phaseolus vulgaris* L.) is a plant with high nutritional value that occupies an important place in human nutrition worldwide. Its yields vary widely and are often below the genetic potential of the species, given the diversity of cropping systems and climatic changes. Common bean landraces are a source of great genetic variability and provide excellent material for the selection and improvement of numerous agronomic traits and the creation of modern cultivars. It is also important to use high quality seed of high-yielding cultivars in production, because in common bean, in addition to yield and resistance to abiotic and biotic stress factors, traits such as nutritional value and digestibility are also the focus of interest. The success of common bean production depends to a large extent on the quality of the seed, the production approach and new breeding programs.

Keywords: breeding, common bean production, climate changes, genetic variability, landraces

1. Introduction

Grain legumes production have been neglected regardless of their potential to provide nutrition and food security [1]. They are at the crossroads of many societal challenges affecting agriculture, such as climate change, sustainability and food security [2]. Due to their high content of proteins, fibers, carbohydrates, vitamins and minerals, they play a crucial role in the development of a plant-based diet and are important nutritional components to eliminate hunger and malnutrition [1, 2]. In addition, they improve soil fertility, for example by fixing nitrogen through symbiosis with rhizobia, and at the same time keep crop yields high [3]. Nowadays, however, the trend is changing and many consumers are demanding local food for economic reasons (increasing farmers' income, adding more value to local stakeholders, etc.), social reasons (i.e. maintaining the population in the area), environmental reasons (reducing traffic and gas emissions, landscape conservation and biodiversity, etc.) and because local products are perceived to be fresher or of better quality [4]. The COVID-19 pandemic and the Russian-Ukrainian war have led to drastic fluctuations in energy prices and disruptions in energy and food supply chains, access to fertilizers is limited, and future harvests are uncertain [5–8]. As a result, the availability and supply of an extensive range of food commodities and end products are under threat, with notable implications for sourcing, production, processing and logistics, and world markets have recently experienced

an increase in food prices [6]. Both crises initially seemed to be an opportunity for a low-carbon energy transition: the pandemic because it accelerated the transition from carbon-intensive energy to modern renewables (such as solar and wind) and illustrated the scale of changes in lifestyle and behavior in a short period of time, and the war because it highlighted the need for greater diversification of energy supply and reliance on local, renewable energy sources [6, 7]. However, early indications suggest that policymakers around the world are focusing on short-term, seemingly quicker solutions, such as supporting the established energy industry in the post-pandemic period to save the economy and finding new fossil fuel supply routes to increase energy security after the war [7]. Accordingly, interest in the use of grain legumes and their components in food is growing in many developed countries. Factors contributing to this trend include the fact that legumes are grown in almost all climatic conditions, as well as their nutritional and health benefits [9].

The aim of this chapter is therefore to highlight the importance of common bean as one of the most important legumes in the world and to point out the possibility of creating new cultivars with desirable traits using new technologies (GWAS and high-throughput phenotyping).

2. Common bean importance

Although its Latin and English names (*Phaseolus vulgaris* L.; common bean) suggest that it is an ordinary plant species, considering the nutritional properties and genetic structure of the common bean, it can be concluded that, on the contrary, it is an exceptional species that represents a potential crop for future food and nutrient security [10, 11]. It originated in Mexico and, through later diversification and spread throughout the Americas and the world, has become the most ecologically adapted species of the genus *Phaseolus*, quickly becoming popular for its nutritional qualities [12]. The common bean is the most widely cultivated legume in the world for direct human consumption and a staple food that does not require industrial processing [2, 13]. It is mainly grown as a grain (i.e. dried beans) and as a fresh vegetable (i.e. snap beans, green beans) [2]. In 2021, global production of dry common bean is estimated at more than 27 million tons on more than 34 million ha [14], feeding more than 300 million people linked to the global agricultural economy [15]. An outstanding feature of the germplasm of common bean is its particularly high diversity [16]. It is grown all over the world in different local environments and climates, with extremely diverse cultivation methods, uses and range of environments to which it is adapted, which has contributed to the great diversity of common bean in terms of growth type, seed characteristics and maturity period [16, 17], but unfavorable environmental conditions, especially drought and salinity in soils, affect its overall performance and reduce productivity and harvest but also consequently the nutritional value [10, 18]. As a food source, it can help reduce global food shortages in the coming years [11]. Common bean is a food with high nutritional value, but also with medicinal properties, which is why it plays an important role in human nutrition and is valued as a functional food [19, 20]. It contains all amino acids but is low in sulfur-containing amino acids such as methionine, cysteine and tryptophan, and is an excellent substitute for meat when combined with cereals, which contain plenty of them [21]. Although the nutrient composition of common bean seeds depends on factors such as origin, genotype and environmental conditions [22], it has the highest content of minerals in its seeds of all legumes [23]. In fact, the common bean is among the most nutrient-dense foods available and is often referred to as the “poor man’s meat”;

“the near-perfect food” and “the grain of hope” for poor communities [11, 24–26]. It is considered a potential food to address malnutrition [27]. In addition, the common bean properties are also recognized in other areas. For example, the use of common bean protein as a fish meal substitute and the production of functional fermented beverages from germinated bean seeds have recently been demonstrated [23, 28]. In addition, the N₂-fixing capacity of this crop is well known to minimize the need for synthetic N fertilizer to increase yield and quality [29].

3. Common bean breeding

It is of great importance to make synergistic efforts to advance the efficiency and accuracy of common bean breeding and to develop genetic gain opportunities by integrating common bean genetic and genomic resources and improved phenotyping methods into breeding activities [11, 30].

Breeding of common beans is often done locally and focuses on improving response to biotic and abiotic stresses, which are particularly challenging in certain locations [30]. Among abiotic stressors, drought is the number one environmental stress because of temperature dynamics, lighting intensity and lack of rain, affecting 60% of total crop production worldwide [31, 32]. Farmers' preferences in seed selection and seed lot management had a significant role in the evolutionary development of domesticated beans, their genetic diversity, population structure and chemical composition, which change over time and also depend on agroecological growing conditions [9]. In this context, various researchers around the world use local populations or samples of common bean landraces as reference sets to study their genetic diversity and population structure [9]. Although conventional plant breeding and a collection of global germplasm were the primary sources of improvements in common bean to produce cultivars with greater yield potential [30, 33], in the cases where the study samples come from gene banks, this diversity has remained static over the years [9]. Conventional plant breeding is also designed to address limited requirements and the specific needs of farmers and certain growing environments [30].

In common beans, in addition to yield and resistance to abiotic and biotic stress factors, traits such as nutritional value and digestibility are also the focus of interest [13, 30, 34]. For years, a variety of breeding activities have been carried out to improve several key traits [11] but researchers recognize that current breeding projects would not be sufficient to meet expected future food needs under current climatic conditions [35]. However, to improve the efficiency and accuracy of bean breeding and increase genetic gain, there are tremendous opportunities such as the use of genomic tools and improved phenotyping methods [30]. Thus, common bean variability and a large number of local populations can be used for breeding purposes to create new cultivars with desirable traits (high yielding, adapted to abiotic stresses and with increased nutritional value), and new technologies such as genome-wide association studies (GWAS) and high-throughput phenotyping (HTP) can help to quickly select for these desirable traits.

4. GWAS for biofortification

Hidden hunger is generally a nutritional deficiency that occurs when the quality of food is inadequate for normal growth and development, i.e. as a result of an

energy-rich but nutrient-poor diet [36]. It is estimated that more than two billion people worldwide are affected, with young children and women of reproductive age living in low-income countries most at risk [36, 37].

Biofortification is a multidisciplinary strategy to improve staple foods in terms of mineral or vitamin content as a means to combat malnutrition in developing countries [24]. It can be achieved through a variety of approaches such as fertilizer application to the soil or foliage, conventional plant breeding or genetic engineering with genetic modification and transgenesis, using expertise from different fields [34]. Biofortification of common bean is an important strategy to reduce mineral deficiencies, especially in regions of the world where this crop plays a key role in nutrition [38]. Since iron, phosphorus and zinc deficiencies are among the most important nutrient deficiencies in the human diet, research on the genetic control of seed composition focuses mainly on the study of these minerals [10, 39–42]. Iron is essential for the prevention of anemia and for the proper functioning of many metabolic processes, while zinc is essential for proper growth and resistance to gastrointestinal and respiratory infections, especially in children [24]. In recent years, many efforts have been made to achieve Fe biofortification of common beans with two main objectives: to increase the Fe concentration in common bean seeds and to reduce the content of phytic acid (PA), which is known to reduce the absorption of dietary iron [24, 38, 43]. Finally, research on Fe nutrition has shown that biofortified Fe in common beans can improve the nutritional status of the target population [44].

Recent advances in molecular markers, sequencing technologies and the finishing of the common bean genome sequence have opened up numerous opportunities for fine mapping and characterization of genes [9, 45–47]. The application of marker-assisted selection (MAS) for more complex traits, such as yield, has recently shifted to genomic selection approaches that are based on genome-wide association studies (GWAS) [33]. Genome-wide association studies (GWAS) have become a widely accepted strategy for studying traits of importance to agriculture, thanks to the introduction of NGS-based SNP markers to decipher genotype–phenotype associations in many species [48]. Recently, a number of GWAS studies on diseases [49–52], abiotic stress [53, 54], agronomic traits [55–57], cooking time and culinary quality traits [58] and root traits [59, 60] have been conducted on common beans. In addition, the GWAS results can serve as a basis for understanding the genetic architecture of the nutritional properties of bean seeds, with the aim of increasing the macro- and micronutrient content in the bean breeding program [61].

4.1 Case study: Croatian common bean landraces

Although the common bean is an important food crop in Croatia, production is almost exclusively based on landraces, as there are no current breeding programs that would create new varieties [62]. On the other hand, in the course of the long tradition of bean cultivation in Croatia, many landraces with great genetic and morphological diversity have developed (**Figure 1**), known by their vernacular names, which are mainly based on the morphological characteristics of the seeds, i.e. the color and mosaic of the seed coat [62–64]. Landraces are an important source of genes for adaptation to local growing conditions and disease resistance [60, 65]. Furthermore, compared to modern cultivars, landraces are essential sources of key nutritional components for food security and a healthy food supply [66]. However, due to complex socio-economic changes in rural communities in recent decades, such as the low profitability of smaller farms and the aging of farmers who grow modern common bean cultivars and/or other



Figure 1.
Diversity of Croatian common bean landraces.

more profitable crops instead of landraces, there is a risk of genetic erosion of landraces [67]. In addition, current abiotic and biotic stress factors are also affecting Croatia, with a focus on drought, reducing agricultural production [68].

Accordingly, the aim of our studies was first to collect landraces of common bean throughout Croatia, in such a way as to include the most cultivated landraces that could be clearly distinguished based on seed morphological characteristics and accordingly divided into 10 morphotypes [62]. Subsequently, by combining phaseolin genotyping, analysis of SSR and SNP markers and morphological traits, 174 accessions of Croatian common bean landraces were evaluated for their origin, genetic diversity, population structure and morphological diversity, and a set of true-type morphogenetic groups was created. The 122 accessions were classified into 14 morphogenetic groups: (1) Mesoamerican (H1A) ('Biser', 'Kukuruzar', 'Tetovac', 'Trešnjevac'), (2) Andean indeterminate type (H2B1) ('Dan noć', 'Sivi', 'Puter', 'Sivi prošarani', 'Trešnjevac') and (3) Andean determinate type (H3B2) ('Bijeli', 'Dan noć', 'Puter', 'Trešnjevac', 'Zelenčec'). Fifty-two accessions are putative hybrids between morphogenetic groups [69]. As published in Carović-Stanko et al. [62], the STRUCTURE analysis based on 26 SSRs identified $K = 2$ as the most likely number of clusters ($\Delta K = 20,533, 24$) and assigned the accessions of Mesoamerican origin (phaseolin type 'S') to cluster A, while the accessions of Andean origin (phaseolin type 'H'/'C' or 'T') formed cluster B, which split into two clusters (B1 and B2) at $K = 3$ ($\Delta K = 1935.93$) and separated the vast majority of phaseolin type 'H'/'C' accessions from those with phaseolin type 'T'. Thus, at $K = 3$, 48 (27.59%) accessions were assigned to cluster A, 29 (16.67%) to cluster B1 and 80 (45.96%) to cluster B2. For 17 accessions (9.77%), the membership probabilities $Q < 75\%$ for any of the clusters and they were therefore considered as "mixed origin". The Q values of each accession obtained at $K = 3$ were used to control for genetic background in the GWAS.

The created panel of accessions was then used for GWAS based on DArTseq-derived SNP markers with the aim of identifying quantitative trait nucleotides (QTNs) associated with variation in seed nutrient content (N, P, K, Ca, Mg, Fe, Zn and Mn) for which phenotypic data on nutrient content were collected from a broader panel of 226 accessions in the research of Palčić et al. [70].

DArTseq analysis was carried out by Diversity Arrays Technology Pty Ltd., Bruce, Australia (<https://www.diversityarrays.com/>). The quality of the SNP markers derived from DArTseq was determined using the parameters 'reproducibility' (percentage of technical replicate pairs that score identically for a given marker), 'call-rate' (percentage of samples for which a given marker was scored) and 'MAF' (minor-allele frequency) [71]. The marker sequences were aligned against the reference genome of *P. vulgaris* [46] using BLASTN [72]. By excluding all SNPs with MAF < 0.05 and all SNPs with >0.05 heterozygotes, a final quality control of the SNP data was performed, resulting in the final set of 6311 high-quality DArTseq-derived SNPs. The missing SNP data were imputed using the Beagle 5.1 genotype imputation method [73]. The imputed dataset was then used to construct a kinship matrix using four methods implemented in the software TASSEL 5 [74]: (1) centered IBS [75], (2) normalized IBS [76], (3) dominance-centered IBS [77] and (4) dominance-normalized IBS [78]. In addition, as suggested by Diniz et al. [79], we have used the corrected kinship matrix.

Linkage disequilibrium, the random association between alleles at different loci was measured by the squared value of the coefficient of determination (r^2). Bias caused by relatedness and/or population structure was removed by correcting r^2 : (a) for relatedness using different relatedness matrices (r_v^2), (b) for population structure using Q values obtained with STRUCTURE (r_s^2), or (c) for both (r_{vs}^2) [80]. The Hill and Weir model [81] was used to represent the decline of LD as a function of distance between loci. According to the uncorrected r^2 estimate, the strength of LD did not decrease at all even at a distance of 10 Mbp, and the value of r^2 remained above 0.3, even for pairs of loci at opposite ends of the chromosome. The bias caused by consanguinity is stronger than the bias caused by population structure. There was almost no difference between the correction for consanguinity alone and for consanguinity and population structure, in both cases the r^2 value fell below 0.1 at about 1 Mbp. Although the differences between the curves for the different kinship matrices were not so pronounced, the centralized IBS matrix was used for GWAS as it gave a slightly better result.

Before performing GWAS, missing phenotypic data were imputed with the method PHENIX which was implemented in the R package of the same name [82]. Before imputation, outliers with the option "trim" in "phenix" were removed (trim.sds = 1.96). GWAS was performed using single-locus models fitted in TASSEL 5 [83] and multi-locus models used in the R package MLM [84]. In both cases, mixed linear models were fitted with corrections for population structure and genetic relatedness (Q and K matrices). TASSEL "raw" p-values were subjected to adjustment for multiple testing using the "qvalue" package for R [85], with a q-value of 0.2 chosen as the significance threshold. The distribution of TASSEL "raw" p-values was visualized using Manhattan plots created with the "CMplot" package for R [86]. In creating the Manhattan plots, an approximate threshold was calculated for each trait as the p-value of a hypothetical SNP that would have a q-value of 0.2. A similar approximate significance threshold was calculated for MLM, by using zero-step p-values to estimate the p-value of a hypothetical SNP that would have a q-value of approximately 0.2. Violin plots were created to visualize the distribution of alleles across subpopulations for each QTN.

On chromosomes Pv01, Pv02, Pv03, Pv05, Pv07, Pv08 and Pv10 were detected 22 QTNs which were associated with nitrogen content of the seeds (**Figure 2**). A total of five QTNs were associated with seed phosphorus content, four on chromosome Pv07 and one on Pv08. On chromosome Pv09, one QTN was found for seed calcium content and on chromosome Pv08 one for seed magnesium content. On chromosome Pv06, two QTNs were found for the zinc content of the seeds.

As expected, fitting the multilocus model to the MLM resulted in significantly fewer discoveries of marker-trait associations. Of the 22 QTNs found by TASSEL for N, the MLM confirmed only two: one of four on chromosome Pv01 and the first of two QTNs on Pv10. Similarly, only one of the four QTNs found by TASSEL for P was on chromosome Pv07. An additional discovery was a QTN found by MLM for N on chromosome Pv05.

Regarding the relationship between the sizes of the different variance component estimates by MLM, the comparison of the residual sum of squares (RSS) plots for N and P can be summarized in two key points: (1) population structure explained 40% of the total variability for N and 0% of the total variability for P; (2) the error variability was similar to the genetic variability for N and twice as large for

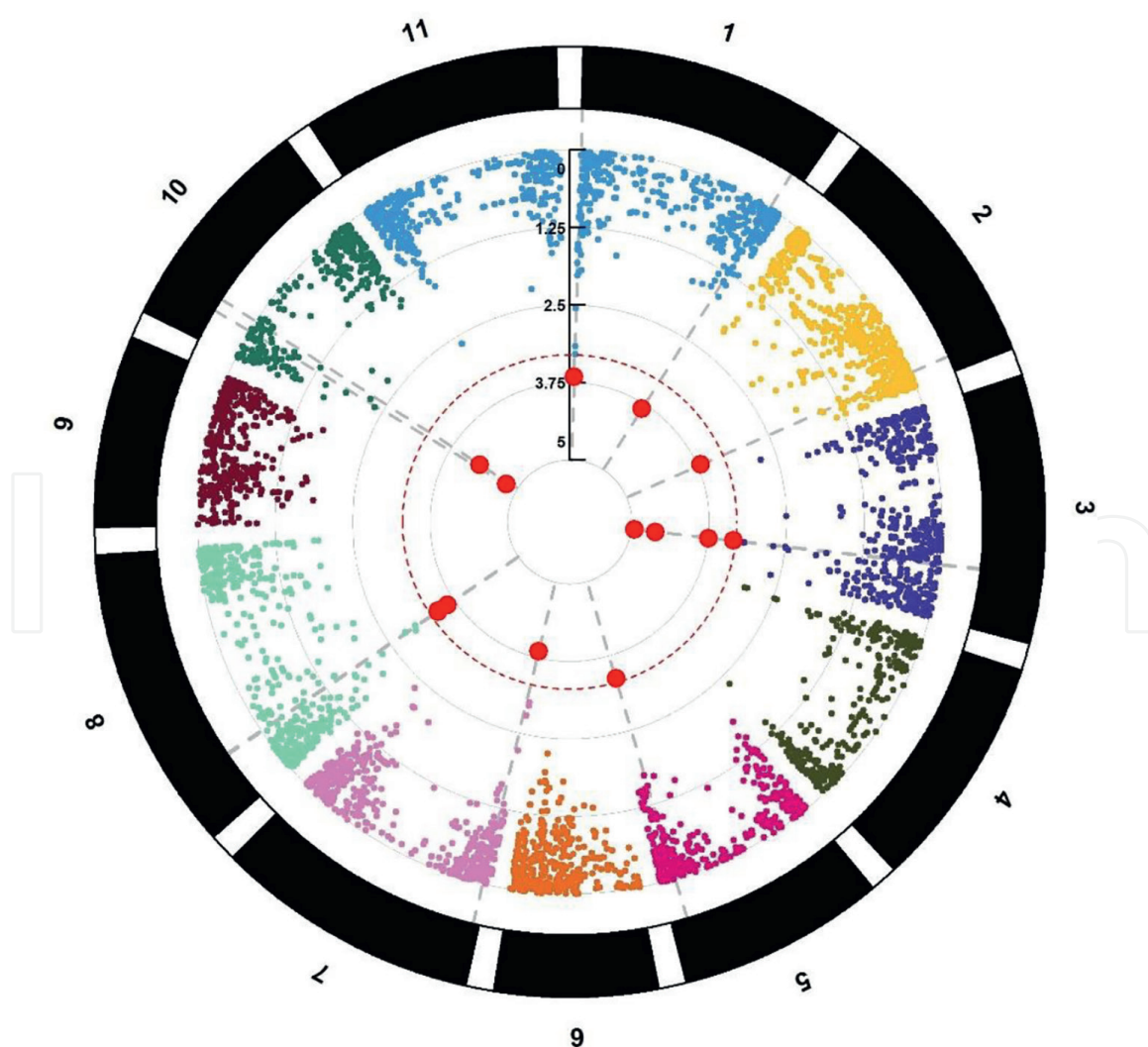


Figure 2.
Circular Manhattan plot for significant markers detected by TASSEL for N.

P. Consequently, MLM discovered three QTNs with p-values below the threshold for N and only one for P despite the similar relative size of genetic variability for N and P.

The largest proportion of total phenotypic variability is explained by QTN Mg_8, which explains 13% of the total phenotypic variability for Mg. Associated markers were distributed throughout the genome, except on chromosomes Pv04 and Pv11, where none were found. N is the trait associated with the greatest number of markers, but individual marker effects were smaller than for other traits. Most markers were located closer to the ends of the chromosomes and only a few were closer to the centromeric region.

The strong effect of population structure on N may be related to the effect of allelic substitution at the QTN loci. In all subpopulations, the reference allele was always present for all QTNs, and the mean N content of individuals carrying the reference allele in subpopulation A (Mesoamerican origin) always lies somewhere between the mean values of subpopulations B1 and B2 (Andean origin). There are three possible scenarios for the distribution of the SNP alleles. They could be present only in the subpopulations of Andean origin, but their positive effect, which is visible in B1 and B2, has almost disappeared at the level of the total population hidden by the effect of population structure. In the second scenario, the SNP allele is only present in subpopulation A (Mesoamerican origin) and has an obvious negative effect that is attenuated by the effect of population structure. Finally, if an SNP allele is present in all subpopulations, its effect varies from one subpopulation to another and becomes almost invisible at the population level. The same scenarios occur with other elements, e.g., with P (**Figure 3**).

This result will serve as a basis for breeding and improving common beans for nutrient content.

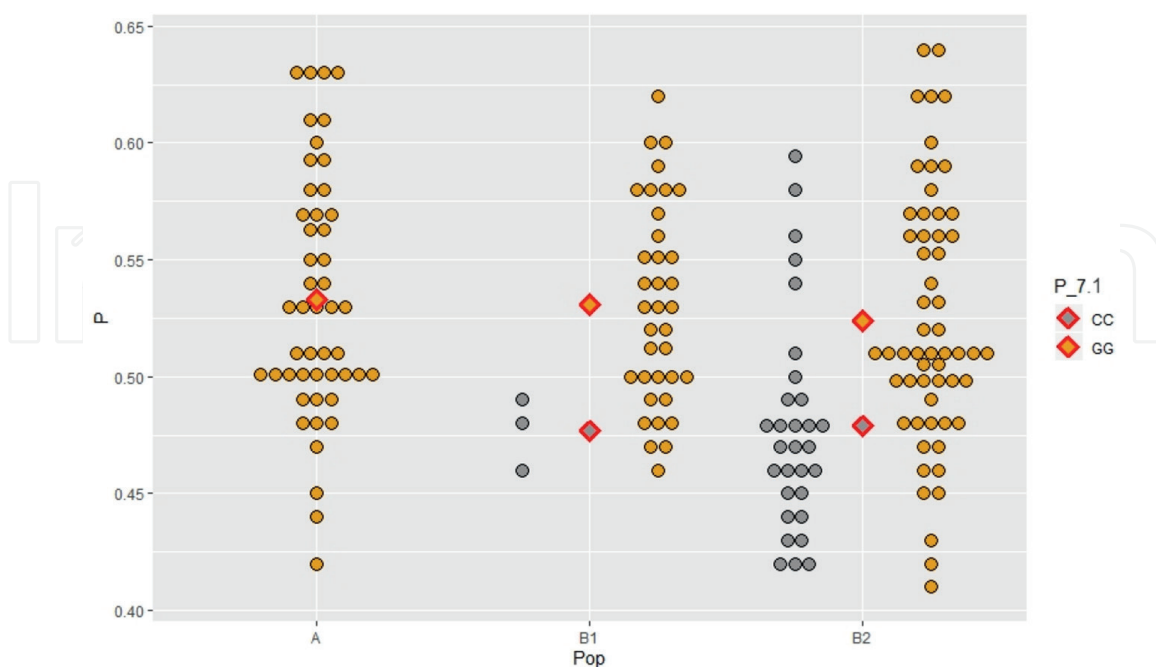


Figure 3. P seed content distribution for different allele classes within subpopulations (A Mesoamerican; B1 Andean; B2 Andean). Diamonds designate subpopulation means for reference allele homozygotes (gray) and SNP homozygotes (yellow).

5. Phenotyping

Climate change and growing populations have led to the need to develop integrated biotechnological approaches to increase agricultural production while coping with environmental threats. This has led to the concept of developing “climate-proof crop varieties” [31]. In plant breeding and quantitative genetics, a large number of measurements are usually made to select superior individuals or identify regions in the genome that control a trait, which requires high-throughput phenotyping [87]. The tools and applied methods of phenotyping differ in the various -omics disciplines, but basically, they are all used to assess and measure complex traits related to growth, yield, quality and adaptation to various biotic and abiotic stress factors [88]. Therefore, it is necessary to monitor the plant during its growth and development for the early detection of plant responses to stress in each growing season (because each season is different) [89]. This can be done by using new non-destructive automated phenotyping techniques with integrative and simultaneous quantification of multiple morphological and physiological traits, allowing early detection and quantification of different stress factors on a whole-plant basis, i.e. timely identification of how certain stress factors such as drought or e.g. nutrient deficiencies affect the plant [90]. That is, high-throughput phenotyping (HTP) technology plays a crucial role in developing new or better crops through traditional or molecular breeding using marker-assisted selection or genetic selection [35]. The most widely used methods for the non-destructive investigation of phenotypic traits of plants under stress conditions, combining different techniques for measuring gas exchange and techniques for imaging and analyzing the images obtained, are multispectral imaging and multispectral 3D scanning, and chlorophyll fluorescence imaging [90]. These methods provide precise insight into the physiological state of plants under specific environmental conditions, excellently detect morphological and biochemical changes such as light utilization by the photosystem II (PSII) and the underlying biochemical processes, leaf pigment content, chemical composition of leaves, morphological and architectural features of leaves and shoots, etc., and enable rapid data collection and processing [90, 91]. HTP enables objective, fast and precise quantification of morphological, anatomical, physiological and biochemical properties of plants and modeling of ideotypes of agricultural crops adapted to growing in specific agroecological conditions [92]. By growing plants in controlled conditions of growth chambers that enable the management and control of environmental factors such as temperature, duration, spectral composition and intensity of light, availability of nutrients and water, in combination with the latest available methods of spectral analysis (VIS, NIR, IR), chlorophyll fluorescence and measurements of gas exchange, the phenotypic properties of plants, i.e. the complex interaction of genotypes with their environment, are analyzed in an innovative way [88].

In recent years, HTP technology has revolutionized phenotyping and accelerated plant breeding in screening large numbers of plants at different phenological stages [35]. To increase the accuracy and efficiency of plant trait evaluation non-destructive and high-throughput methods have been developed [93]. By using advanced sensors and data acquisition systems, HTP platforms can take full advantage of monitoring, quantifying and evaluating specific phenotypes for large-scale agricultural experiments [94]. Platforms can be used in the laboratory and in the field under controlled and natural conditions and are not necessary to wait for the plants to mature in the field, as the desired traits can be studied quickly in the early stages [35]. This is a

crucial step in breeding to select better performing cultivars in terms of yield, abiotic and biotic stress tolerance to accelerate crop improvement programs [35].

To improve the production and quality of common beans, it is necessary to possess in-depth knowledge of its genetic diversity, the genome and the functions of the genes, but also to be familiar with the new phenotyping techniques [35, 95].

As drought is one of the significant environmental stressors due to its significant detrimental effects, there is an increasing need to create tolerant genotypes of agricultural crops [32]. The analysis of gas exchange is based on the fact that drought stress causes rapid closure of stomata [96]. By closing the leaves, the plant saves water, but also reduces the diffusion of CO₂ needed for photosynthesis from the atmosphere into the leaf. By measuring stomatal conductance (gas exchange) it is possible to quantify drought stress and select tolerant genotypes [97]. The analysis of chlorophyll fluorescence is based on the fact that the light energy absorbed by the chlorophyll molecules in the photosystems can undergo one of three processes: It can be used to initiate photosynthesis (photochemical reactions), it can be released as heat or it can be re-emitted as long-wave light radiation, i.e., fluorescence. These three processes are interdependent, i.e., any increase in one process leads to a decrease in the value of the other two. Photosystem two (PSII), located in the thylakoid membranes of chloroplasts, is responsible for the uptake of light energy and the initiation of photosynthesis, and at the same time is very sensitive to abiotic stress. Therefore, the measurement of chlorophyll fluorescence, which provides information on changes in the efficiency of photosynthesis, is one of the most commonly used methods for stress assessment in plants [98]. Multispectral analyses are based on the reflection of light of different wavelengths. Many physiological and chemical properties of plants affect the way their tissues absorb and reflect light. When a plant is exposed to stress, these properties can change and thus the intensity of the light reflected by the leaves also changes [99]. The spectral reflectance data of the leaves are used to calculate vegetation indices. Some of the commonly used vegetation indices to assess abiotic stress are the normalized differential vegetation index (NDVI), anthocyanin index (ARI) and chlorophyll index (CHI) [100, 101]. Since drought stress leads to physical and biochemical changes (reduction of leaf area, wilting of the plant, closure of stomata, closure of PSII, disruption of gas exchange, decrease in the intensity of photosynthesis, changes in the composition of pigments, etc.), these parameters can be used to assess the tolerance of genotypes to drought.

Also, for the successful production of beans and obtaining a high yield, a good supply of nutrients to the plant is necessary [102]. Their level can be determined by analyzing the soil, but the nutritional status of beans can be determined by analyzing plant material (leaves). Nutrient deficiency in plants leads to specific symptoms that can be easily detected, for example, by 3D scans with PlantEye F500 multispectral 3D scanner (**Figure 4**) and chlorophyll fluorescence measurements with CropReporter™ (PhenoVation B.V., Wageningen, The Netherlands) (**Figure 5**) [103].

Current ground-based phenotyping platforms are likely to be replaced by new and specialized UAVs (drones) and will facilitate next-generation breeding programs to develop improved varieties [35].

The combination of HTP methods with advanced high-throughput genotyping techniques in genome-wide association studies (GWAS) will allow the identification of gene regions and genes associated with specific phenotypic traits (such as drought resistance, increased efficiency of nutrient utilization or disease resistance). The implementation of the results of this research into breeding programs through

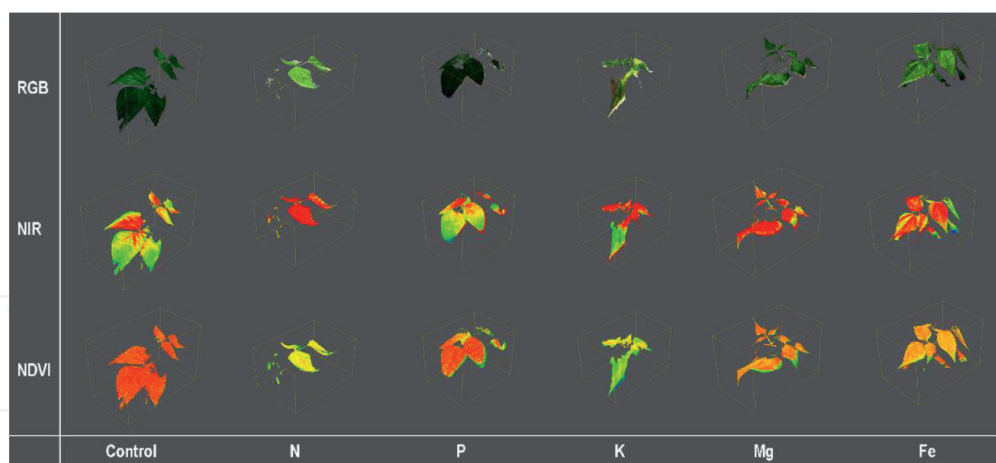


Figure 4. Color [red, green, and blue (RGB)] and pseudo-color [near infra-red (NIR) and normalized differential vegetation index (NDVI)] images of 3D common bean plants grown for 9 days (MT3) in treatment solutions [12 modified Hoagland's solution (control), and solutions without nitrogen (N), phosphorus (P), potassium (K), magnesium (Mg), and iron (Fe)] [103].

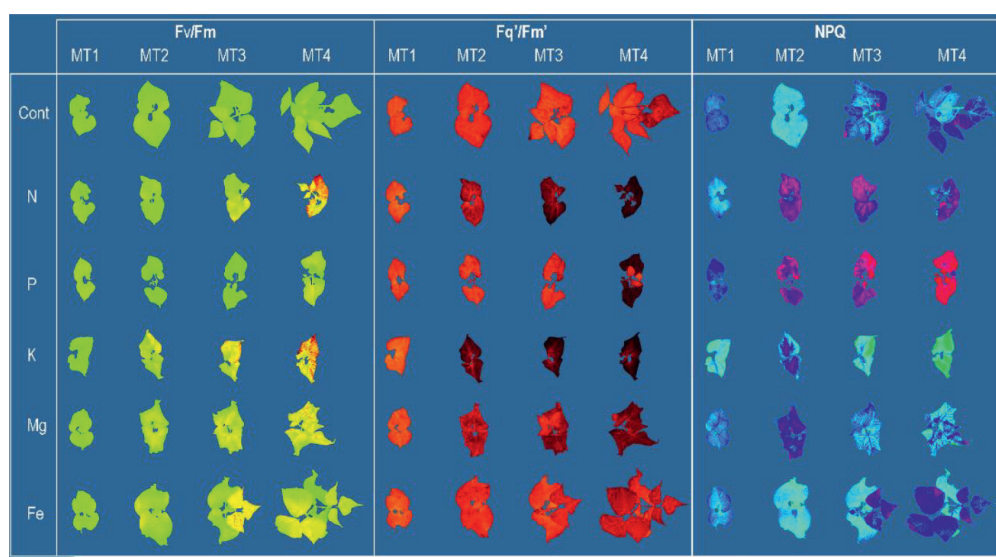


Figure 5. Color and pseudo-color images of common bean plants with maximum quantum yield of PSII (F_v/F_m), effective quantum yield of PSII (F_q'/F_m') and non-photochemical quenching (NPQ) taken during four measurements (MT1-MT4), for 12 days every 3 days of growth in the control [12 modified Hoagland solution (Cont)] and solutions without nitrogen (N), phosphorus (P), potassium (K), magnesium (Mg) and iron (Fe) [103].

marker-assisted breeding will enable a faster and more efficient breeding process that will produce new, more efficient and more productive crop genotypes.

6. Conclusion and future perspectives

In these challenging times (climate change, sustainability and food security), the success of common bean production depends not only on seed quality and production approach, but also to a large extent on breeding programs. The implementation of the results of GWAS and phenotyping research into breeding programs through

marker-assisted breeding will enable a faster and more efficient breeding process that will produce new, more efficient and more productive common bean genotypes. The combination of advanced high-throughput genotyping techniques in genome-wide association studies (GWAS) will enable the identification of gene regions and genes associated with specific phenotypic traits (e.g. mineral content, drought resistance, increased nutrient utilization or disease resistance).

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Conflict of interest


The authors declare no conflict of interest.

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