Legume Genomics and Genetics 2024, Vol.15, No.5, 244-256
http://cropscipublisher.com/index.php/lgg

Research Insight **Open Access**

Translational Genomics in Legumes: Enhancing Crop Resilience and Yield

Xiaomei Wang, Chunmei Zong, Yuxin Qi, Guohong Sun, Changyuan Liu, Yanping Wang
Mudanjiang Branch, Heilongjiang Academy of Agricultural Sciences, Mudanjiang, 157000, Heilongjiang, China
Corresponding email: wyping1981@126.com

Legume Genomics and Genetics, 2024 Vol.15, No.5 doi: 10.5376/lgg.2024.15.0024
Received: 08 Sep., 2024
Accepted: 09 Oct., 2024
Published: 20 Oct., 2024

Preferred citation for this article:
Wang X.M., Zong C.M., Qi Y.X., Sun G.H., Liu C.Y., and Wang Y.P., 2024, Translational genomics in legumes: enhancing crop resilience and yield, Legume Genomics and Genetics, 15(5): 244-256 (doi: 10.5376/lgg.2024.15.0024)

Abstract Legume crops play a crucial role in global food security, yet their cultivation faces significant challenges from biotic and abiotic stresses. This study explores the potential of translational genomics as a vital tool for enhancing legume crop resilience and yield. We provide an overview of recent advances in legume genomics, highlighting the impact of sequencing technologies and key genome projects. By examining model legumes like *Medicago truncatula* and *Lotus japonicus*, we illustrate how discoveries can be translated into crop legumes to address critical issues such as drought tolerance and nitrogen fixation. We discuss genomic approaches to improve stress resistance, yield-related traits, and the integration of emerging technologies like CRISPR/Cas9. Our findings underscore the importance of an integrative approach, combining omics technologies and participatory breeding, to develop climate-resilient legume varieties. This study emphasizes the need for collaborative efforts in policy and funding to further advance translational genomics in legume improvement, ensuring sustainable agricultural practices for the future.

Keywords Legume crops; Translational genomics; Stress resilience; Nitrogen fixation; Crop improvement

1 Introduction

Legume crops, belonging to the Fabaceae family, are a cornerstone of global agriculture and nutrition. They are cultivated extensively for their seeds, which are rich in proteins, dietary fibers, vitamins, and minerals, making them a vital component of human and livestock diets (Broughton et al., 2004; Roy et al., 2010; Bulut et al., 2023). Legumes such as common beans, chickpeas, lentils, and lupins are particularly significant due to their ability to fix atmospheric nitrogen, thereby enhancing soil fertility and reducing the need for synthetic fertilizers (Smýkal et al., 2015). This unique trait not only supports sustainable agricultural practices but also contributes to the nutritional security of millions of people worldwide, especially in developing regions (Thudi et al., 2020).

Despite their importance, legume crops face numerous challenges that hinder their productivity and quality. Biotic stresses, including diseases caused by fungi, bacteria, and viruses, as well as pest infestations, significantly impact legume yields (Varshney, 2016; Koul et al., 2022). Abiotic stresses such as drought, salinity, and extreme temperatures further exacerbate these challenges, particularly in marginal environments where many legumes are grown (Varshney et al., 2018). Climate change has intensified these stresses, making it imperative to develop legume varieties that are resilient to both biotic and abiotic factors (Thudi et al., 2020). Traditional breeding methods have had limited success in overcoming these challenges, necessitating the integration of advanced genomic tools and techniques.

Translational genomics refers to the application of genomic information and technologies to develop improved crop varieties with enhanced traits such as yield, nutritional quality, and stress resistance. This approach involves the use of high-throughput sequencing, genome-wide association studies (GWAS), and marker-assisted selection to identify and incorporate beneficial genetic traits into breeding programs. In legumes, translational genomics has led to significant advancements, including the development of drought-tolerant chickpeas, disease-resistant groundnuts, and high-yielding common beans. By bridging the gap between genomic research and practical breeding, translational genomics holds the promise of accelerating genetic gains and ensuring food security in the face of growing environmental challenges (Varshney, 2016; Thudi et al., 2020).

This study evaluates the successes and challenges of translational genomics in legume breeding and proposes strategies for integrating genomic technologies into legume breeding programs to address biotic and abiotic stresses. It further emphasizes the potential socio-economic impacts of improving legume varieties for smallholder farmers and global food security. The aim is to understand the current state of legume genomics, its application in crop improvement, and to identify key genomic resources and tools that can be used to enhance the stress resistance and yield of legume crops.

2 Advances in Legume Genomics

2.1 Overview of genomic resources in legumes

Recent advancements in genomics have significantly contributed to the development of extensive genomic resources for legume crops. These resources include large-scale sequence data, genome-wide molecular markers, genetic linkage maps, and trait mapping tools. Such developments have been pivotal in understanding genome architecture and dynamics, facilitating gene discovery, and enhancing crop productivity (Varshney et al., 2015; Afzal et al., 2019; Jha et al., 2022). The establishment of comprehensive transcriptome assemblies and genome sequences for major legume crops like chickpea, pigeonpea, and groundnut has transformed these species from 'orphan' crops to 'genomic resources rich' crops (Varshney et al., 2013).

2.2 Sequencing technologies and their impact on legume genomics

The advent of next-generation sequencing (NGS) technologies has revolutionized legume genomics by enabling high-throughput genotyping and phenotyping. NGS has facilitated the sequencing and re-sequencing of important legume species, making structural variation and functional genomics studies feasible (Afzal et al., 2019; Salgotra and Stewart, 2022). These technologies have allowed for the accurate and accelerated delivery of genomic information, which is crucial for breeding programs aimed at improving legume crop yield and resilience (O’Rourke et al., 2014). The application of RNA sequencing (RNA-Seq) has provided considerable insights into gene characterization and expression profiling, especially in species with limited genomic information.

2.3 Key legume genome projects and achievements

Several key genome projects have been undertaken to enhance our understanding of legume genomics. For instance, the genome sequencing of model legumes like *Medicago truncatula* has provided valuable insights into gene families of practical importance and facilitated marker development and gene discovery in related crop species (Young and Udvardi, 2009). The translational genomics approach has been successfully applied to place thousands of unigenes on the pea functional map, identifying candidate genes for important traits (Bordat et al., 2011). Additionally, comprehensive genome assemblies and resequencing efforts have been completed for various legume crops, aiding in the identification of genes underlying traits of breeding importance (Figure 1) (Jha et al., 2022).

2.4 Functional genomics approaches: gene annotation, expression profiling, and mutant libraries

Functional genomics in legumes encompasses a range of approaches, including RNA transcription, protein expression, and metabolomics. The development of resources such as transcriptomes, proteomes, metabolomes, and mutant libraries has been instrumental in identifying genes that play essential roles in plant resistance to biotic and abiotic stresses, protein and oil accumulation in seeds, and beneficial plant-microbe symbiosis (Libault and Dickstein, 2014). Techniques like TILLING (Targeting Induced Local Lesions IN Genomes) have been employed to create mutant libraries, providing powerful tools for functional genomics studies. These approaches have already yielded valuable information for enhancing legume productivity and hold promise for future advancements.

3 Translational Genomics: From Model Legumes to Crops

3.1 Definition and scope of translational genomics

Translational genomics involves the application of genomic insights and technologies from model organisms to improve and enhance the traits of crop species. This field bridges the gap between basic genomic research and practical agricultural applications, aiming to transfer knowledge gained from model species to economically important crops. The scope of translational genomics encompasses gene discovery, functional genomics, and the development of genetic markers, all of which contribute to crop improvement in terms of yield, resilience, and stress tolerance (Huang, 2024).

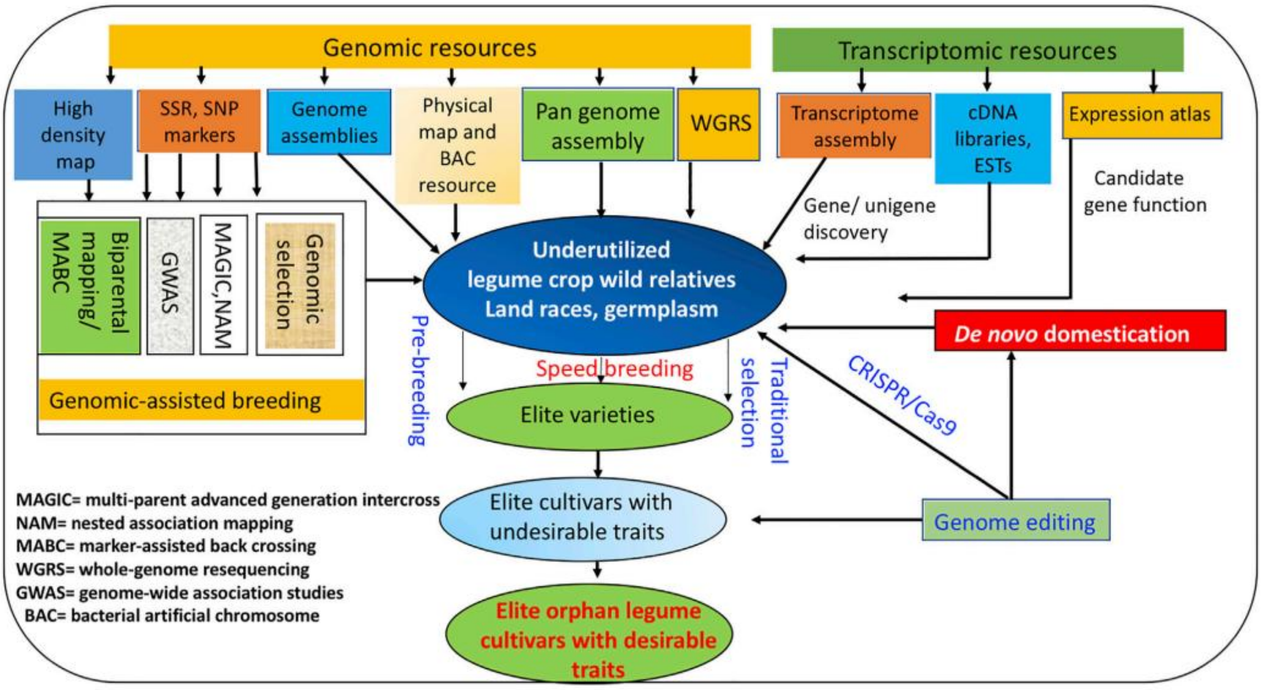

Figure 1 “Omics” and emerging novel breeding approaches for improving genetic gain in underutilized legumes (Adopted from Jha et al., 2022)

3.2 Model legumes as genomic tools: *Medicago truncatula* and *Lotus japonicus*

Medicago truncatula and *Lotus japonicus* have been established as model legumes due to their favorable genetic attributes, such as small genome sizes, diploid nature, and ease of transformation. These species have been instrumental in advancing our understanding of legume-specific processes like nitrogen fixation, nodulation, and secondary metabolite biosynthesis. The availability of comprehensive genomic resources, including genome sequences and functional genomics tools, has made these model legumes invaluable for studying plant development, stress responses, and plant-microbe interactions (Thoquet et al., 2002; Rose et al., 2008; Cañas and Beltrán, 2018).

3.3 Translating discoveries from models to crop legumes

The genomic resources developed in *Medicago truncatula* and *Lotus japonicus* have significant potential for application in crop legumes. For instance, the synteny between the genomes of *M. truncatula* and economically important legumes facilitates the transfer of genomic information, aiding in marker development, gene discovery, and positional cloning in crops like alfalfa and pea. This translational approach accelerates the identification of candidate genes and the development of genetic markers, which are crucial for breeding programs aimed at improving crop traits (Young and Udvardi, 2009; Bordat et al., 2011).

3.4 Case study: translational genomics from arabidopsis to soybean for drought tolerance

A notable example of translational genomics is the application of knowledge from *Arabidopsis thaliana* to soybean for enhancing drought tolerance. Arabidopsis, a well-studied model plant, has provided insights into the genetic and molecular mechanisms underlying drought response. By identifying and characterizing drought-responsive genes in Arabidopsis, researchers have been able to pinpoint homologous genes in soybean. Functional validation and genetic manipulation of these genes in soybean have led to the development of drought-tolerant varieties, demonstrating the power of translational genomics in addressing critical agricultural challenges (Roy et al., 2019).

4 Enhancing Crop Resilience through Translational Genomics

4.1 Genomic basis of abiotic stress tolerance

Drought and heat stress are significant challenges for legume crops, impacting their productivity and yield. Genomic approaches, including sequencing of genomes and transcriptomes, have been instrumental in identifying genes associated with drought and heat tolerance. For instance, proteomic analyses have revealed that stress-responsive proteins involved in photosynthesis, carbohydrate metabolism, and signal transduction play crucial roles in stress adaptation (Jan et al., 2022). Additionally, transcriptomic studies have identified novel stress-responsive genes and signaling pathways that contribute to enhanced resilience against these stresses (Kamali and Singh, 2023). The integration of these genomic tools has facilitated the development of legume varieties with improved tolerance to drought and heat, thereby enhancing crop resilience (Kudapa et al., 2013; Dwivedi et al., 2017).

Salinity and cold stress are other critical abiotic factors that adversely affect legume production. Epigenetic mechanisms, such as DNA methylation and histone modification, have been shown to regulate gene expression in response to these stresses (Yung et al., 2022). Proteomic approaches have identified proteins involved in stress adaptation, including those related to metabolic adjustments and defense mechanisms (Jan et al., 2022). Furthermore, genomic and transcriptomic studies have highlighted the importance of genetic diversity in breeding programs aimed at improving salinity and cold tolerance in legumes (Abdelrahman et al., 2018). These insights are crucial for developing legume cultivars that can withstand adverse environmental conditions (Rane et al., 2021).

4.2 Genomic approaches to biotic stress resistance

Biotic stresses, including fungal, bacterial, and viral diseases, pose significant threats to legume crops. Genomic tools such as marker-assisted breeding and genetic transformation have been employed to enhance disease resistance in legumes. The identification of quantitative trait loci (QTLs) and single nucleotide polymorphisms (SNPs) associated with disease resistance traits has been pivotal in breeding programs (Dwivedi et al., 2017). Additionally, functional genomics approaches have facilitated the discovery of candidate genes involved in disease resistance, providing valuable resources for developing resistant legume varieties (Kudapa et al., 2013; Ramalingam et al., 2015).

Pest resistance is another critical aspect of biotic stress management in legumes. Genomic and transcriptomic studies have identified key genes and regulatory networks involved in pest resistance (Kamali and Singh, 2023). Proteomic analyses have further elucidated the role of stress-responsive proteins in defense mechanisms against pests (Jan et al., 2022). These findings have been integrated into breeding programs to develop legume varieties with enhanced pest resistance, thereby reducing yield losses and improving crop productivity.

4.3 Integrating genomic tools for multi-stress resilience

The integration of genomic tools, including genomics, transcriptomics, proteomics, and metabolomics, is essential for developing legume varieties with multi-stress resilience. By combining data from various omics approaches, researchers can gain a comprehensive understanding of the molecular mechanisms underlying stress tolerance (Ramalingam et al., 2015). This integrated approach enables the precise manipulation of crop genomes to enhance resilience against multiple abiotic and biotic stresses, ultimately leading to the development of robust legume cultivars (Abdelrahman et al., 2018; Kamali and Singh, 2023).

4.4 Emerging technologies: CRISPR/Cas9 and RNA interference (RNAi)

Emerging technologies such as CRISPR/Cas9 and RNA interference (RNAi) offer promising avenues for enhancing stress resilience in legumes. CRISPR/Cas9 has been successfully used to edit genes associated with stress tolerance, providing a powerful tool for crop improvement (Kamali and Singh, 2023). RNAi technology has also been employed to silence specific genes involved in stress responses, thereby enhancing tolerance to various stresses. These advanced genetic engineering techniques hold significant potential for developing legume varieties with improved resilience and yield under adverse environmental conditions (Kudapa et al., 2013; Ramalingam et al., 2015).

5 Case Study: Translational Genomics for Nitrogen Fixation Improvement

5.1 Importance of biological nitrogen fixation in legumes

Biological nitrogen fixation (BNF) is a critical process for legumes, allowing them to convert atmospheric nitrogen into a form usable by plants, thus reducing the need for synthetic nitrogen fertilizers. This process not only enhances soil fertility but also contributes to sustainable agricultural practices by reducing greenhouse gas emissions and improving crop resilience (Rodriguez et al., 2020; Karavidas et al., 2022; Ma et al., 2022). Legumes such as common bean and cowpea are particularly valuable in cropping systems due to their ability to fix nitrogen through symbiotic relationships with rhizobia, which significantly boosts soil nitrogen levels and benefits subsequent crops (Kebede, 2021).

5.2 Genomic approaches to enhance symbiotic nitrogen fixation

Recent advances in genomics have provided new insights into the genetic mechanisms underlying symbiotic nitrogen fixation (SNF) in legumes. Studies have identified nearly 200 genes involved in SNF, which are crucial for various processes such as nodule formation, microbial infection, and nitrogen assimilation. Genomic tools like transcriptomics, proteomics, and metabolomics have been employed to understand the complex interactions between legumes and rhizobia, leading to the identification of key genes and pathways that can be targeted for improving SNF efficiency (Ramalingam et al., 2015; López et al., 2023). These approaches have been particularly useful in model legumes like *Medicago truncatula* and *Lotus japonicus*, as well as in crop species such as soybean and common bean (Figure 2) (Roy et al., 2020).

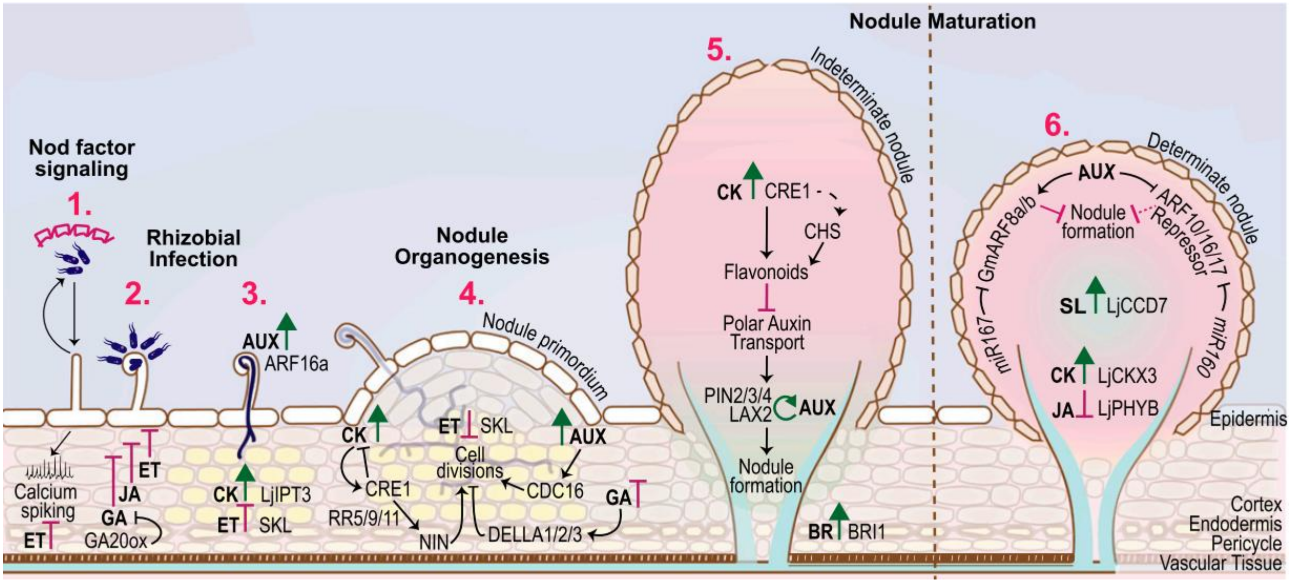

Figure 2 Hormonal control of symbiotic nitrogen fixation (Adopted from Roy et al., 2020)

Image caption: Ethylene (ET) represses calcium spiking induced upon recognition of a compatible Nod factor (1). Rhizobial infection is countered by the hormones ET, jasmonic acid (JA), and gibberellic acid (GA). By contrast, the hormone cytokinin (CK; whose biosynthesis is mediated by IPT3) and auxin (AUX) signaling (via ARF16a) positively regulate IT development (2 and 3). Multiple hormones control cell divisions at the site of infection that lead to the formation of the nodule primordium (4). As the primordium develops into a mature nodule, hormone requirements differ between indeterminate and determinate nodules (5 and 6). Positive and negative roles are shown in green and magenta, respectively. Medicago gene names are shown unless otherwise indicated (Adopted from Roy et al., 2020)

5.3 Translational research from model systems to cowpea and common bean

Translational research aims to apply findings from model systems to improve SNF in crop legumes like cowpea and common bean. For instance, the genetic discoveries in model legumes have paved the way for engineering enhanced SNF capabilities in these crops (Roy et al., 2020). Proteomic and metabolomic studies have revealed that common bean plants grown under nitrogen fixation conditions exhibit better drought resistance and overall stress tolerance compared to those fertilized with synthetic nitrogen (López et al., 2023; Zhu et al., 2024). This highlights the potential of leveraging genomic insights to develop legume varieties with improved SNF and resilience to environmental stresses.

5.4 Future perspectives and challenges in nitrogen fixation improvement

Despite significant progress, several challenges remain in enhancing SNF in legumes. One major challenge is the complexity of the genetic and environmental factors influencing SNF, which requires a multidisciplinary approach involving synthetic biology, plant breeding, and agronomy (Santi et al., 2013; Pankievicz et al., 2019). Additionally, translating genomic discoveries from model systems to diverse legume crops necessitates extensive field trials and the development of robust biotechnological tools. Future research should focus on integrating advanced genomic techniques with traditional breeding practices to create legume varieties that can maximize BNF and contribute to sustainable agricultural systems (Kebede et al., 2021).

6 Enhancing Yield through Translational Genomics

6.1 Yield-related traits and genomic interventions

Yield-related traits in legumes, such as maturity, plant height, and seed weight, are critical for improving overall crop productivity. Advances in next-generation sequencing and genotyping technologies have enabled the development of dense genetic maps and QTL maps, which are essential for identifying genomic regions associated with these traits. For instance, in soybean, significant SNPs associated with yield and related traits have been identified, facilitating the use of these markers in breeding programs to enhance yield (Ravelombola et al., 2021). Additionally, the integration of genomic resources and breeding approaches, such as marker-assisted selection (MAS) and marker-assisted backcrossing (MABC), has shown promise in improving yield-related traits in legumes like chickpea, pigeonpea, and groundnut (Varshney et al., 2013).

6.2 Genomic selection (GS) and genome-wide association studies (GWAS) for yield improvement

Genomic selection (GS) and genome-wide association studies (GWAS) are powerful tools for yield improvement in legumes. GWAS allows for the identification of marker-trait associations (MTAs) by examining the linkage disequilibrium (LD) between SNPs and phenotypic traits across the genome. This approach has been successfully applied in legumes to dissect complex traits and identify significant SNPs associated with yield (Susmitha et al., 2023). GS, on the other hand, uses genome-wide markers to predict the breeding values of individuals, thereby accelerating the selection process and improving the accuracy of breeding programs. Studies have shown that GS can significantly enhance the efficiency of breeding programs by reducing cycle time and increasing genetic gains (Spindel et al., 2015; Wang et al., 2018; Budhlakoti et al., 2022).

6.3 Molecular breeding and marker-assisted selection (MAS)

Molecular breeding techniques, including marker-assisted selection (MAS), have revolutionized legume breeding by enabling the precise selection of desirable traits. MAS involves the use of molecular markers linked to specific traits to select individuals with the desired genetic makeup. This approach has been effectively used to improve traits such as drought tolerance, disease resistance, and yield in legumes. For example, MAS has been employed to introgress QTL regions for drought tolerance and disease resistance in chickpea and groundnut, leading to the development of superior cultivars with enhanced resilience and productivity (Figure 3) (Varshney et al., 2013; Thudi et al., 2020).

6.4 Combining yield with quality traits: protein content, oil composition, and anti-nutritional factors

Combining yield improvement with quality traits such as protein content, oil composition, and the reduction of anti-nutritional factors is essential for enhancing the nutritional value of legumes. Legumes are valued for their high protein content and other nutritional components, making it crucial to maintain and improve these traits alongside yield. GWAS and GS have been instrumental in identifying and selecting for these quality traits. For instance, GWAS has been used to identify SNPs associated with protein content and oil composition in legumes, enabling the development of high-protein and nutritionally superior varieties (Ravelombola et al., 2021; Susmitha et al., 2023). Additionally, integrating genomic selection with traditional breeding methods can help achieve a balance between yield and quality traits, ensuring the development of legumes that meet both productivity and nutritional requirements (Jannink et al., 2010; Varshney et al., 2017).

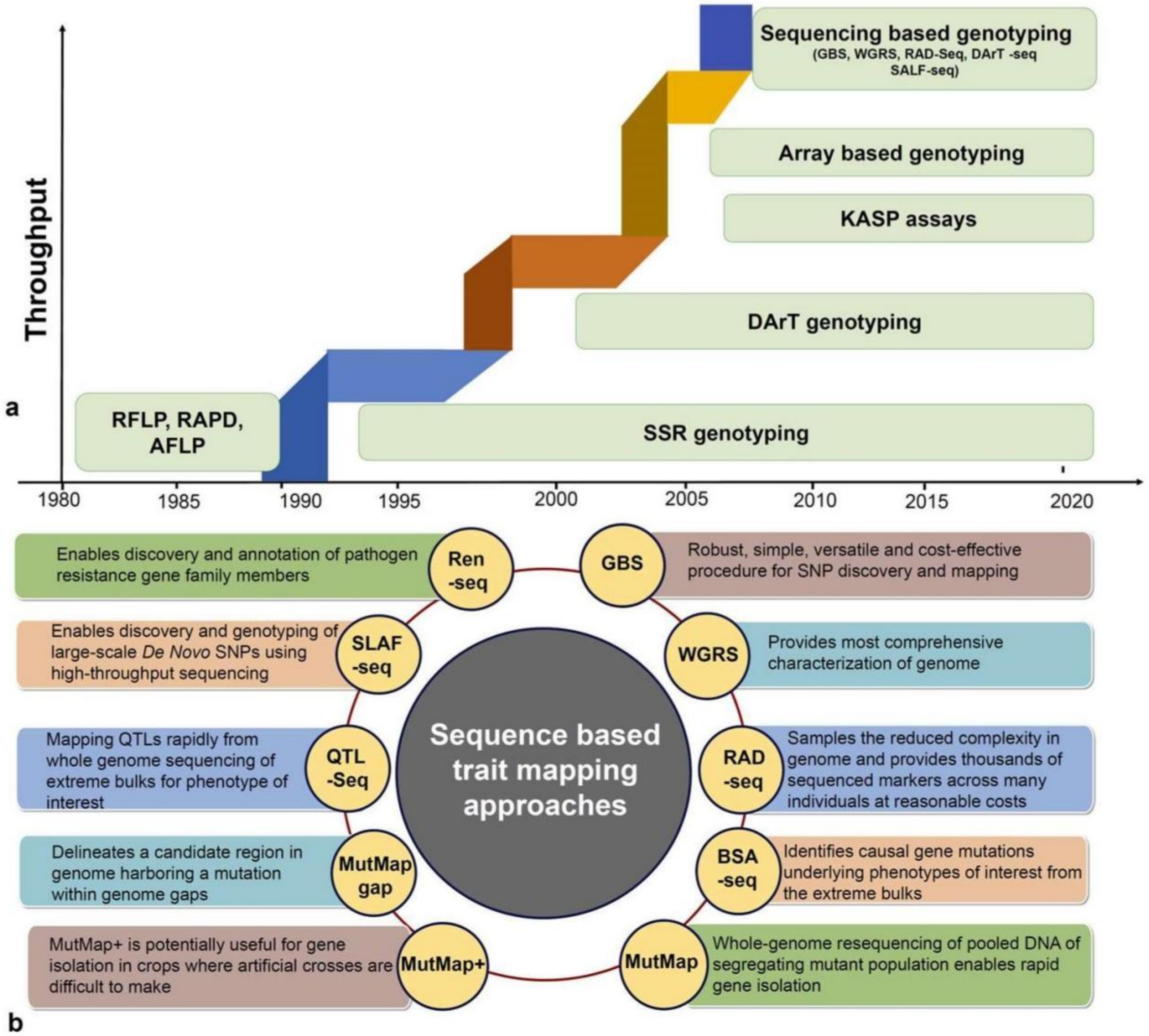

Figure 3 Genotyping platforms and key sequencing-based trait mapping approaches (Adopted from Thudi et al., 2020)

Image caption: (a)Molecular markers and genotyping platforms, during the last there decades, have evolved significantly. While throughput has been increasing and cost-per-marker datapoint has been decreasing over the years. (b) Availability of reference genome sequences, the costeffective genotyping platforms, and a range of genetic populations have provided new faster sequencing-based trait mapping approaches [like geotyping by sequencing (GBS), whole genome resequencing (WGRS), restriction site associated DNA Seq (RAD-seq), bulked segregant analysis-sequencing (BSA-seq) MutMap, MutMap+, MutMap-Gap, QTL-seq, Specific locus amplified fragment sequencing (SLAFseq), resistance gene enrichment sequencing (RenSeq)]. With these platforms and trait mapping approaches, it has been possible to map target traits for breeding programmes in time- and cost- effective manner in recent years (Adopted from Thudi et al., 2020)

7 Integrative Approaches for Legume Improvement

7.1 Integrating omics technologies: genomics, transcriptomics, proteomics, and metabolomics

The integration of various omics technologies, including genomics, transcriptomics, proteomics, and metabolomics, has revolutionized legume improvement by providing comprehensive insights into the molecular mechanisms underlying important agronomic traits. Advances in next-generation sequencing (NGS) have facilitated the development of genomic resources, such as linkage maps and the identification of quantitative trait loci (QTLs) and candidate genes associated with stress tolerance and yield (Varshney et al., 2018; Yang et al., 2021). Transcriptomics has enabled the identification of differentially expressed genes under various stress conditions, while proteomics and metabolomics have revealed key proteins and metabolites involved in stress responses and plant development (Ramalingam et al., 2015; Zenda et al., 2021; Tiwari et al., 2022). The integration of these omics approaches allows for a systems biology perspective, enhancing our understanding of complex traits and enabling the development of high-yielding, multi-stress-tolerant legume varieties (Pazhamala et al., 2021; Ali et al., 2022).

7.2 Bioinformatics and computational biology in legume research

Bioinformatics and computational biology play a crucial role in managing and analyzing the vast amounts of data generated by omics technologies. These disciplines facilitate the integration of multi-omics data, enabling the modeling and prediction of cellular functions and biological networks (Pazhamala et al., 2021). The development of genomic databases and bioinformatics tools has accelerated the identification of gene-trait associations and the discovery of novel genes involved in stress tolerance and other important traits (Ali et al., 2022; Salgotra and Stewart, 2022). By leveraging bioinformatics, researchers can efficiently translate genomic information into practical applications, such as marker-assisted selection and genomic selection, to enhance legume breeding programs (Varshney et al., 2015).

7.3 High-throughput phenotyping platforms

High-throughput phenotyping (HTP) platforms have emerged as essential tools for legume improvement, allowing for the rapid and precise measurement of phenotypic traits under various environmental conditions. These platforms utilize advanced imaging technologies and automated data analysis to assess traits such as root architecture, drought tolerance, and nutrient uptake (Kumar et al., 2020; Tiwari et al., 2022). The integration of HTP with omics data enables the identification of marker-trait associations and the development of superior legume varieties with enhanced stress tolerance and yield potential (Varshney et al., 2018; Zenda et al., 2021). HTP platforms are particularly valuable for screening large germplasm collections and accelerating the breeding process (Pazhamala et al., 2021).

7.4 Participatory breeding and farmer-centric genomic research

Participatory breeding and farmer-centric genomic research involve the active involvement of farmers in the breeding process, ensuring that the developed varieties meet their needs and preferences. This approach enhances the adoption of new varieties and ensures that breeding programs address the specific challenges faced by farmers (Varshney et al., 2018). By integrating modern genomics approaches with traditional breeding methods, researchers can develop legume varieties that are not only high-yielding and stress-tolerant but also tailored to local agronomic practices and market demands (Varshney et al., 2015). Participatory breeding fosters collaboration between scientists and farmers, leading to more sustainable and impactful legume improvement efforts.

8 Future Directions in Translational Genomics

8.1 Developing climate-resilient legume varieties

The development of climate-resilient legume varieties is crucial to address the challenges posed by climate change, which has increased the frequency and intensity of drought stress, particularly in rainfed regions where most legumes are produced. Genomic approaches provide an exceptional opportunity to identify genetic variations that can be employed in crop improvement programs to enhance resilience to environmental stresses (Mousavi-Derazmahalleh et al., 2018). Recent advances in genomics, transcriptomics, and small RNA studies have led to the identification of novel genes for various agronomic traits, which can be utilized to develop transgenic and gene-edited legume plants resilient to emerging pests, pathogens, and abiotic stresses (Sindhu et al., 2019). Additionally, the integration of modern genomics approaches, high throughput phenomics, and simulation modeling can support crop improvement, leading to improved varieties that perform well under climate stress conditions (Varshney et al., 2018).

8.2 Genomics-guided crop diversification strategies

Genomics-guided crop diversification strategies can enhance the sustainability of agriculture by increasing the use of nitrogen sources and reducing external inputs of nitrogen fertilizers. Intercropping, an agroecological practice where two or more crop species are grown simultaneously, has been shown to maximize resource use and enhance yields in low-input systems. This practice can stimulate complementary nitrogen use between legumes and cereals, increasing nitrogen fixation by grain legumes and soil nitrogen acquisition in cereals (Rodriguez et al., 2020). Furthermore, the development of genomic resources, such as genome-wide molecular markers and genetic linkage maps, can facilitate yield improvement in underutilized legumes, contributing to crop diversification and resilience (Jha et al., 2022).

8.3 Policy, collaboration, and funding for translational genomics research

Effective policy, collaboration, and funding are essential to advance translational genomics research in legumes. The integration of genomics, phenotyping, systems modeling, and agronomy requires substantial investment and coordinated efforts among researchers, policymakers, and funding agencies (Varshney et al., 2018). Collaborative efforts can accelerate the development and dissemination of improved legume varieties, ensuring that smallholder farmers in developing countries benefit from these advancements (Varshney et al., 2015). Additionally, policies that support the adoption of genomic technologies and provide incentives for research and development can drive progress in this field (Thudi et al., 2020).

8.4 Ethical and biosafety considerations in genomics applications

Ethical and biosafety considerations are paramount in the application of genomics in legume crop improvement. The development and deployment of genetically modified organisms (GMOs) and gene-edited plants must adhere to stringent biosafety regulations to prevent unintended environmental and health impacts (Sindhu et al., 2019). Public acceptance of GMOs and gene-edited crops is also a critical factor, necessitating transparent communication and engagement with stakeholders to address concerns and build trust (Choudhury and Rajam, 2021). Ethical considerations, such as equitable access to genomic technologies and the fair distribution of benefits, must be addressed to ensure that advancements in translational genomics contribute to global food security and sustainability (Jha et al., 2022). By focusing on these future directions, translational genomics can play a pivotal role in enhancing the resilience and yield of legume crops, contributing to sustainable agriculture and food security in the face of climate change.

9 Concluding Remarks

The research on translational genomics in legumes has highlighted significant advancements and potential applications in enhancing crop resilience and yield. Recent developments in genomics and associated disciplines, such as bioinformatics, have facilitated the creation of extensive genomic resources for legume crops. These resources have been instrumental in understanding genome architecture and dynamics, as well as in gene discovery. The integration of modern genomics approaches, high-throughput phenomics, and simulation modeling has been proposed to achieve faster genetic gains in legumes, particularly in rainfed conditions. Advances in next-generation sequencing (NGS) technologies, high-throughput genotyping (HTG), and high-throughput phenotyping (HTP) have enabled more precise and efficient legume breeding. Additionally, the translation of genomic data from model legumes like *Medicago truncatula* has shown promise in accelerating practical advances in crop legumes.

Translational genomics plays a crucial role in enhancing the resilience and yield of legume crops. Legumes are vital for human nutrition, livestock feed, and soil fertility through biological nitrogen fixation. However, their productivity is often hampered by biotic and abiotic stresses, particularly in marginal environments. The application of genomic resources and molecular breeding approaches has led to the development of superior legume lines with enhanced traits such as drought tolerance, disease resistance, and improved nutritional quality.

The integration of genomics with conventional breeding methods has the potential to break the yield plateau and achieve higher genetic gains in legumes. Furthermore, the development of genomic resources for underutilized legumes can contribute to global food security and the achievement of sustainable development goals.

The future of legume crop improvement lies in the continued integration of advanced genomic technologies with traditional breeding methods. The progress made in the last decade in genomics-assisted breeding has set a strong foundation for future research and development. The use of genomic resources, such as whole-genome arrays and tagged mutant populations, will enable detailed studies on gene expression and function, leading to the discovery of novel genes for important agronomic traits. Additionally, the application of novel breeding technologies, such as speed breeding, genomic selection, and genome editing, will further accelerate the development of climate-resilient and high-yielding legume cultivars. By harnessing the genetic diversity of wild relatives and underutilized legumes, researchers can broaden the genetic base of legume crops and enhance their adaptability to changing environmental conditions. Overall, the future of legume crop improvement looks promising, with translational genomics playing a pivotal role in ensuring food security and sustainable agriculture.

Acknowledgments

CropSci Publisher sincerely thanks the two anonymous peer reviewers for their suggestions.

Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

References

Abdelrahman M., Jogaiah S., Burritt D., and Tran L., 2018, Legume genetic resources and transcriptome dynamics under abiotic stress conditions, Plant, Cell and Environment, 41(9): 1972-1983.
https://doi.org/10.1111/pce.13123

Afzal M., Alghamdi S., Migdadi H., Khan M.N., Mirza S., Mirza S., and El-Harty E., 2019, Legume genomics and transcriptomics: from classic breeding to modern technologies, Saudi Journal of Biological Sciences, 27: 543-555.
https://doi.org/10.1016/j.sjbs.2019.11.018

Ali A., Altaf M., Nadeem M., Karaköy T., Shah A., Azeem H., Baloch F., Baran N., Hussain T., Duangpan S., Aasim M., Boo K., AbdelVarshney R., Kudapa H., Pazhamala L., Chitikineni A., Thudi M., Bohra A., Gaur P., Janila P., Fikre A., Kimurto P., and Ellis N., 2015, Translational genomics in agriculture: some examples in grain legumes, Critical Reviews in Plant Sciences, 34: 169-194.
https://doi.org/10.1080/07352689.2014.897909

Bordat A., Savois V., Nicolas M., Salse J., Chauveau A., Bourgeois M., Potier J., Houtin H., Rond C., Murat F., Marget P., Aubert G., and Burstin J., 2011, Translational genomics in legumes allowed placing in silico 5460 unigenes on the pea functional map and identified candidate genes in *Pisum sativum* L., Genes Genomes Genetics, 1: 93-103.
https://doi.org/10.1534/g3.111.000349

Broughton W., Hernández G., Blair M., Beebe S., Gepts P., and Vanderleyden J., 2004, Beans (*Phaseolus* spp.)-model food legumes, Plant and Soil, 252: 55-128.
https://doi.org/10.1023/A:1024146710611

Budhlakoti N., Kushwaha A., Rai A., Chaturvedi K., Kumar A., Pradhan A., Kumar U., Kumar R., Juliana P., Mishra D., and Kumar S., 2022, Genomic selection: a tool for accelerating the efficiency of molecular breeding for development of climate-resilient crops, Frontiers in Genetics, 13: 832153.
https://doi.org/10.3389/fgene.2022.832153

Bulut M., Wendenburg R., Bitocchi E., Bellucci E., Kroc M., Gioia T., Susek K., Papa R., Fernie A., and Alseekh S., 2023, A comprehensive metabolomics and lipidomics atlas for the legumes common bean, chickpea, lentil and lupin, The Plant Journal, 116(4): 1152-1171.
https://doi.org/10.1111/tpj.16329

Cañas L., and Beltrán J., 2018, Model legumes: functional genomics tools in *Medicago truncatula*, Methods in Molecular Biology, 1822: 11-37.
https://doi.org/10.1007/978-1-4939-8633-0_2

Choudhury A., and Rajam M., 2021, Genetic transformation of legumes: an update, Plant Cell Reports, 40: 1813-1830.
https://doi.org/10.1007/s00299-021-02749-7

Dwivedi S., Scheben A., Edwards D., Spillane C., and Ortiz R., 2017, Assessing and exploiting functional diversity in germplasm pools to enhance abiotic stress adaptation and yield in cereals and food legumes, Frontiers in Plant Science, 8: 1461.
https://doi.org/10.3389/fpls.2017.01461

Huang W.Z., 2024, The current situation and future of using GWAS strategies to accelerate the improvement of crop stress resistance traits, Molecular Plant Breeding, 15(2): 52-62.
https://doi.org/10.5376/mpb.2024.15.0007

Jan N., Rather A., John R., Chaturvedi P., Ghatak A., Weckwerth W., Zargar S., Mir R., Khan M., and Mir R., 2022, Proteomics for abiotic stresses in legumes: present status and future directions, Critical Reviews in Biotechnology, 43: 171-190.
https://doi.org/10.1080/07388551.2021.2025033

Jannink J., Lorenz A., and Iwata H., 2010, Genomic selection in plant breeding: from theory to practice, Briefings in functional genomics, 9(2): 166-177.
https://doi.org/10.1093/bfgp/elq001

Jha U., Nayyar H., Parida S., Bakır M., Wettberg E., and Siddique K., 2022, Progress of genomics-driven approaches for sustaining underutilized legume crops in the post-genomic era, Frontiers in Genetics, 13: 831656.
https://doi.org/10.3389/fgene.2022.831656

Kamali S., and Singh A., 2023, Genomic and transcriptomic approaches to developing abiotic stress-resilient crops, Agronomy, 13(12): 2903.
https://doi.org/10.3390/agronomy13122903

Karavidas I., Ntatsi G., Vougeleka V., Karkanis A., Ntanasi T., Saitanis C., Agathokleous E., Ropokis A., Sabatino L., Tran F., Iannetta P., and Savvas D., 2022, Agronomic practices to increase the yield and quality of common bean (*Phaseolus vulgaris* L.): a systematic review, Agronomy, 12(2): 271.
https://doi.org/10.3390/agronomy12020271

Kebede E., 2021, Contribution, utilization, and improvement of legumes-driven biological nitrogen fixation in agricultural systems, 5: 767998.
https://doi.org/10.3389/fsufs.2021.767998

Koul B., Sharma K., Sehgal V., Yadav D., Mishra M., and Bharadwaj C., 2022, Chickpea (*Cicer arietinum* L.) biology and biotechnology: from domestication to biofortification and biopharming, Plants, 11(21): 2926.
https://doi.org/10.3390/plants11212926

Kudapa H., Ramalingam A., Nayakoti S., Chen X., Zhuang W., Liang X., Kahl G., Edwards D., and Varshney R., 2013, Functional genomics to study stress responses in crop legumes: progress and prospects, Functional Plant Biology, 40(12): 1221-1233.
https://doi.org/10.1071/FP13191

Kumar J., Gupta D., Djalović I., Kumar S., and Siddique K., 2020, Root-omics for drought tolerance in cool-season grain legumes, Physiologia Plantarum, 172(2): 629-644.
https://doi.org/10.1111/ppl.13313

Libault M., and Dickstein R., 2014, Advances in functional genomics in legume, Legumes in the Omic Era, 2014: 15-39.
https://doi.org/10.1007/978-1-4614-8370-0_2

López C., Alseekh S., Torralbo F., Rivas F., Fernie A., Amil-Ruiz F., and Alamillo J., 2023, Transcriptomic and metabolomic analysis reveals that symbiotic nitrogen fixation enhances drought resistance in common bean, Journal of Experimental Botany, 74(10): 3203-3219.
https://doi.org/10.1093/jxb/erad083

Ma J., Olin S., Anthoni P., Rabin S., Bayer A., Nyawira S., and Arneth A., 2022, Modeling symbiotic biological nitrogen fixation in grain legumes globally with LPJ-GUESS (v4.0, r10285), Geoscientific Model Development, 15(2): 815-839.
https://doi.org/10.5194/gmd-15-815-2022

Mousavi-Derazmahalleh M., Bayer P., Hane J., Valliyodan B., Nguyen H., Nelson M., Erskine W., Varshney R., Papa R., and Edwards D., 2018, Adapting legume crops to climate change using genomic approaches, Plant, Cell and Environment, 42: 6-19.
https://doi.org/10.1111/pce.13203

O'Rourke J., Bolon Y., Bucciarelli B., and Vance C., 2014, Legume genomics: understanding biology through DNA and RNA sequencing, Annals of Botany, 113(7): 1107-1120.
https://doi.org/10.1093/aob/mcu072

Pankievicz V., Irving T., Maia L., and Ané J., 2019, Are we there yet? The long walk towards the development of efficient symbiotic associations between nitrogen-fixing bacteria and non-leguminous crops, BMC Biology, 17(1): 99.
https://doi.org/10.1186/s12915-019-0710-0

Pazhamala L., Kudapa H., Weckwerth W., Millar A., and Varshney R., 2021, Systems biology for crop improvement, The Plant Genome, 14(2): e20098.
https://doi.org/10.1002/tpg2.20098

Ramalingam A., Kudapa H., Pazhamala L., Weckwerth W., and Varshney R., 2015, Proteomics and metabolomics: two emerging areas for legume improvement, Frontiers in Plant Science, 6: 1116.
https://doi.org/10.3389/fpls.2015.01116

Rane J., Singh A., Kumar M., Boraiah K., Meena K., Pradhan A., and Prasad P., 2021, The adaptation and tolerance of major cereals and legumes to important abiotic stresses, International Journal of Molecular Sciences, 22(23): 12970.
https://doi.org/10.3390/ijms222312970

Ravelombola W., Qin J., Shi A., Song Q., Yuan J., Wang F., Chen P., Yan L., Feng Y., Zhao T., Meng Y., Guan K., Yang C., and Zhang M., 2021, Genome-wide association study and genomic selection for yield and related traits in soybean, PLoS One, 16(8): e0255761.
https://doi.org/10.1371/journal.pone.0255761

Rodriguez C., Carlsson G., Englund J., Flöhr A., Pelzer E., Jeuffroy M., Makowski D., and Jensen E., 2020, Grain legume-cereal intercropping enhances the use of soil-derived and biologically fixed nitrogen in temperate agroecosystems, a meta-analysis, European Journal of Agronomy, 118: 126077.
https://doi.org/10.1016/j.eja.2020.126077

Rose R., 2008, *Medicago truncatula* as a model for understanding plant interactions with other organisms, plant development and stress biology: past, present and future, Functional Plant Biology, 35(4): 253-264.
https://doi.org/10.1071/FP07297

Roy F., Boye J., and Simpson B., 2010, Bioactive proteins and peptides in pulse crops: pea, chickpea and lentil, Food Research International, 43: 432-442.
https://doi.org/10.1016/J.FOODRES.2009.09.002

Roy S., Liu W., Nandety R., Crook A., Mysore K., Pislariu C., Frugoli J., Dickstein R., and Udvardi M., 2020, Celebrating 20 years of genetic discoveries in legume nodulation and symbiotic nitrogen fixation, Plant Cell, 32: 15-41.
https://doi.org/10.1105/tpc.19.00279

Salgotra R., and Stewart C., 2022, Genetic augmentation of legume crops using genomic resources and genotyping platforms for nutritional food security, Plants, 11(14): 1866.
https://doi.org/10.3390/plants11141866

Santi C., Bogusz D., and Franche C., 2013, Biological nitrogen fixation in non-legume plants, Annals of Botany, 111(5): 743-767.
https://doi.org/10.1093/aob/mct048

Sindhu M., Kumar A., Yadav H., Chaudhary D., Jaiwal R., and Jaiwal P., 2019, Current advances and future directions in genetic enhancement of a climate resilient food legume crop, cowpea (*Vigna unguiculata* L. Walp.), Plant Cell, Tissue and Organ Culture, 139: 429-453.
https://doi.org/10.1007/s11240-019-01695-3

Smýkal P., Coyne C., Ambrose M., Maxted N., Schaefer H., Blair M., Berger J., Greene S., Nelson M., Besharat N., Vymyslický T., Toker C., Saxena R., Roorkiwal M., Pandey M., Hu J., Li Y., Wang L., Guo Y., Qiu L., Redden R., and Varshney R., 2015, Legume crops phylogeny and genetic diversity for science and breeding, Critical Reviews in Plant Sciences, 34: 104-143.
https://doi.org/10.1080/07352689.2014.897904

Spindel J., Begum H., Akdemir D., Virk P., Collard B., Redoña E., Atlin G., Jannink J., and McCouch S., 2015, Genomic selection and association mapping in rice (*Oryza sativa*): effect of trait genetic architecture, training population composition, marker number and statistical model on accuracy of rice genomic selection in elite, tropical rice breeding lines, PLoS Genetics, 11(2): e1004982.
https://doi.org/10.1371/journal.pgen.1004982

Susmitha P., Kumar P., Yadav P., Sahoo S., Kaur G., Pandey M., Singh V., Tseng T., and Gangurde S., 2023, Genome-wide association study as a powerful tool for dissecting competitive traits in legumes, Frontiers in Plant Science, 14: 1123631.
https://doi.org/10.3389/fpls.2023.1123631

Thoquet P., Ghérardi M., Journet E., Kereszt A., Ané J., Prosperi J., and Huguet T., 2002, The molecular genetic linkage map of the model legume *Medicago truncatula*: an essential tool for comparative legume genomics and the isolation of agronomically important genes, BMC Plant Biology, 2: 1-13.
https://doi.org/10.1186/1471-2229-2-1

Thudi M., Palakurthi R., Schnable J., Chitikineni A., Dreisigacker S., Mace E., Srivastava R., Satyavathi C., Odeny, D., Tiwari V., Lam H., Hong Y., Singh V., Li G., Xu Y., Chen X., Kaila S., Nguyen H., Sivasankar S., Jackson S., Close T., Shubo W., and Varshney R., 2020, Genomic resources in plant breeding for sustainable agriculture, Journal of Plant Physiology, 257: 153351.
https://doi.org/10.1016/j.jplph.2020.153351

Tiwari M., Singh B., Min D., and Jagadish S., 2022, Omics path to increasing productivity in less-studied crops under changing climate-lentil a case study, Frontiers in Plant Science, 13: 813985.
https://doi.org/10.3389/fpls.2022.813985

Varshney R., 2016, Exciting journey of 10 years from genomes to fields and markets: Some success stories of genomics-assisted breeding in chickpea, pigeonpea and groundnut, Plant Science, 242: 98-107.
https://doi.org/10.1016/j.plantsci.2015.09.009

Varshney R., Kudapa H., Pazhamala L., Chitikineni A., Thudi M., Bohra A., Gaur P., Janila P., Fikre A., Kimurto P., and Ellis N., 2015, Translational genomics in agriculture: some examples in grain legumes, Critical Reviews in Plant Sciences, 34: 169-194.
https://doi.org/10.1080/07352689.2014.897909

Varshney R., Mohan S., Gaur P., Gangarao N., Pandey M., Pandey M., Bohra A., Sawargaonkar S., Chitikineni A., Kimurto P., Janila P., Saxena K., Fikre A., Sharma M., Rathore A., Pratap A., Tripathi S., Datta S., Chaturvedi S., Mallikarjuna N., Anuradha G., Babbar A., Choudhary A., Mhase M., Bharadwaj C., Mannur D., Harer P., Guo B., Liang X., Nadarajan N., and Gowda C., 2013, Achievements and prospects of genomics-assisted breeding in three legume crops of the semi-arid tropics, Biotechnology Advances, 31(8): 1120-1134.
https://doi.org/10.1016/j.biotechadv.2013.01.001

Varshney R., Roorkiwal M., and Sorrells M., 2017, Genomic selection for crop improvement, Crop Science, 49: 1-12.
https://doi.org/10.1007/978-3-319-63170-7

Varshney R., Thudi M., Pandey M., Tardieu F., Ojiewo C., Vadez V., Whitbread A., Siddique K., Nguyen H., Carberry P., and Bergvinson D., 2018, Accelerating genetic gains in legumes for the development of prosperous smallholder agriculture: integrating genomics, phenotyping, systems modelling and agronomy, Journal of Experimental Botany, 69(13): 3293-3312.
https://doi.org/10.1093/jxb/ery088

Wang X., Wang X., Xu Y., Hu Z., and Xu C., 2018, Genomic selection methods for crop improvement: current status and prospects, The Crop Journal, 6(4): 330-340.
https://doi.org/10.1016/J.CJ.2018.03.001

Yang Y., Saand M., Huang L., Abdelaal W., Zhang J., Wu Y., Li J., Sirohi M., and Wang F., 2021, Applications of multi-omics technologies for crop improvement, Frontiers in Plant Science, 12: 563953.
https://doi.org/10.3389/fpls.2021.563953

Young N., and Udvardi M., 2009, Translating *Medicago truncatula* genomics to crop legumes, Current Opinion in Plant Biology, 12(2): 193-201.
https://doi.org/10.1016/j.pbi.2008.11.005

Yung W., Huang C., Li M., and Lam H., 2022, Changes in epigenetic features in legumes under abiotic stresses, The Plant Genome, 16(4): e20237.
https://doi.org/10.1002/tpg2.20237

Zenda T., Liu S., Dong A., Li J., Wang Y., Liu X., Wang N., and Duan H., 2021, Omics-facilitated crop improvement for climate resilience and superior nutritive value, Frontiers in Plant Science, 12: 774994.
https://doi.org/10.3389/fpls.2021.774994

Zhu Z.Y., An X., Luo X.H., Chen C.L., Liu T.T., Zou L.N., and Zhu G.L., 2024, Research progress of NAC transcription factor family in plant stress resistance, Molecular Plant Breeding, 15(3): 90-99.
https://doi.org/10.5376/mpb.2024.15.0011