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Genetic Diversity of Legume Germplasm Resources and Their Application in High-Yield Breeding

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Abstract As an important food and feed resource, legume crops play an important role in ensuring food security, improving soil fertility and promoting sustainable agricultural development. Rich germplasm resources provide a key genetic basis for high-yield breeding of legumes. This study systematically sorted out the diversity characteristics of the current main germplasm resources of legumes, covering their geographical distribution, phenotypic variation and genetic background, and focused on analyzing important agronomic traits related to high yield, such as pod number, grain weight, stress resistance and nitrogen fixation ability. It further explored the specific application paths of diversity resources in modern breeding, including the introduction of excellent alleles, the development of pre-breeding materials, and the integration of marker-assisted selection and genomic selection technology. At the same time, the actual value of diversity germplasm in improving breeding efficiency and yield performance was explained through typical high-yield breeding cases. Fully exploring and accurately utilizing the genetic diversity of legumes is one of the core strategies to promote high-yield, stable yield and green development of legumes. This study hopes to provide theoretical support and practical reference for the construction of efficient breeding systems and the creation of new germplasm in the future.

Keywords Germplasm diversity; Legume crops; High-yield breeding; Trait improvement; Molecular breeding techniques

1 Introduction

Legumes are very important in global agriculture. They contribute about 27% of global food production (Coyne et al., 2020). A large part of the protein people eat comes from legumes. Legumes are also a component of many animal feeds. Legumes also have a very practical function. They can "move" nitrogen from the air into the soil. This ability makes the soil more fertile and is very helpful for agriculture. This is especially important in areas where fertilizers are scarce, resources are scarce, or people are malnourished (Smýkal et al., 2015).

There are many germplasm resources of legumes, including excellent varieties, local varieties and wild relatives. These resources contain a large number of different genes. They can provide "good genes" required for important traits such as drought resistance, disease resistance and high yield. These genes are particularly helpful for breeding new varieties with strong stress resistance and high yield (Sharma et al., 2013; Coyne et al., 2020; Rajpal et al., 2023). Now, scientists use these valuable genes in breeding through gene introgression, pre-breeding, and genomic technology. This will enable the breeding of leguminous crops with greater adaptability and better traits (Dwivedi et al., 2017; Pratap et al., 2021).

This study will systematically analyze legume germplasm diversity to identify and utilize genetic resources that can drive high-yield breeding. This includes evaluating and utilizing functional diversity, discovering new alleles and quantitative trait loci (QTLs) associated with yield and stress resistance, and integrating them into breeding programs using modern genomics and phenotyping tools. By leveraging the full range of genetic variation, this study hopes to optimize breeding strategies and breed legume varieties that meet the needs of the global food system, address climate change challenges, and promote sustainable agricultural productivity.

2 Diversity of Legume Germplasm Resources

2.1 Geographic distribution and species diversity in legumes

Leguminous plants are distributed all over the world. Their diversity is mainly concentrated in East Asia, the Near East, Africa and the Americas. There are more than 800 genera and more than 20 000 species of legumes recorded so far, making it the third largest flowering plant family in the world. They are also a very important type of plant in global food production (Smýkal et al., 2015). For example, wild soybeans (*Glycine soja*) are mainly distributed in East Asia, especially the Korean Peninsula, where wild resources are very rich and are also important for the domestication process of soybeans. For example, white lupins (*Lupinus albus*) and beans (*Phaseolus vulgaris*) have adapted to a variety of climates and soil conditions. Their germplasm resources are spread across multiple continents and show rich genetic and trait differences (Tanwar et al., 2024).

2.2 Wild relatives and landraces as reservoirs of rare alleles

Wild relatives and local varieties preserve many valuable genes. These genes are often lost during crop domestication, but they are useful for breeding, helping to increase yields, and improving adaptability such as disease and pest resistance and drought and salt resistance (Nawaz et al., 2020). For example, wild soybeans and wild peas (such as *P. fulvum* and *P. sativum* subsp. *elatius*) retain more genetic variation than cultivated varieties. These variations can provide some unique genetic resources for breeding programs (Smýkal et al., 2017). The same is true for local varieties. After long-term selection and adaptation by farmers, varieties in different places have different characteristics. For example, common beans in Portugal and the Himalayas contain many new genetic combinations, including some hybrids and hybrids (Jan et al., 2021).

2.3 Agro-morphological variation among accessions

Leguminous germplasm resources differ in many agronomic traits. These differences are critical for selecting good varieties. Studies have found that crops such as beans, rice beans, adzuki beans, and cowpeas (*Vigna stipulacea*) show wide variation in growth patterns, leaf shape, flower color, pod and seed appearance, and nutritional content (Gore et al., 2022; Divakara et al., 2024). For example, beans from the Himalayas and Portugal vary greatly in seed size, shape, and nutritional content. Rice beans and adzuki beans from Asia also vary in flowering time, number of pods, and yield. If these trait data are analyzed together with molecular markers, useful materials can be found more quickly. This not only allows targeted breeding, but also establishes a core germplasm bank with strong representativeness and genetic diversity (Leitão et al., 2017).

3 High-Yield Related Traits in Legumes

3.1 Major yield components: pods per plant, seed size, biomass

The yield of legumes is mainly related to several aspects, such as the number of pods per plant, the size of the seeds, and the biomass of the whole plant. Taking mung beans and broad beans as examples, studies have found that the number of effective pods per plant, the total number of seeds, and the weight of each seed will directly affect the final yield. Moreover, there are obvious differences in these traits between different varieties, which is a genetic difference. Some studies have also used meta-QTL analysis to find gene regions related to yield. These regions can affect traits such as the number of pods and seed weight. This kind of information is particularly useful for breeding work and can help breed new varieties with higher yields (Arriagada et al., 2022). In addition to these, researchers often use biomass and total seed production to judge whether the variety is good or not. Different varieties perform differently in different environments. Some varieties can grow more plants and seeds, while others are less so (Papastylianou et al., 2021).

3.2 Stress-resilient traits linked to yield stability

The stress resistance of leguminous plants, such as drought resistance and heat resistance, is very important for maintaining stable yields. There are several physiological indicators related to these abilities, such as high chlorophyll content, strong leaf cooling ability, and good cell membrane stability, which are all related to high yields under harsh conditions (Sofi et al., 2021; Jha et al., 2025). For example, in drought resistance research, the "stress resistance index" is often used to measure, that is, to consider the yield performance of crops under normal and water-deficient conditions. For example, the number of seeds per plant and the number of pods per plant are often used as key indicators for variety selection (Balko et al., 2023). Now, scientists have also found many stress-related genes through transcriptome and physiological experiments. These genes are important for breeding varieties that are resistant to harsh environments and can also have high yields (Araújo et al., 2015; Abdelrahman et al., 2018).

3.3 Physiological efficiencies: nitrogen fixation and source-sink relationships

In order for leguminous plants to have high yields, they must not only grow fast, but also have "high internal efficiency". A key point is that they can coexist with rhizobia to fix nitrogen in the air, which not only helps their own growth, but also improves the soil and reduces the use of chemical fertilizers. After producing nutrients, plants need to transport these "goods" reasonably to leaves, roots, seeds and other places. Whether this distribution is efficient is directly related to whether more biomass and seeds can be produced. The structure of the roots, water use efficiency, and photosynthesis ability are also very important (Duc et al., 2015; Sofi et al., 2021). Current breeding work is also paying more and more attention to these "invisible" physiological traits. Scientists hope to select new leguminous varieties that are both high-yielding and use fewer resources by integrating these characteristics (Dutta et al., 2022).

4 Utilization of Germplasm in Breeding Programs

4.1 Trait introgression from exotic or wild donors

In breeding, scientists often introduce wild relatives, local varieties or exotic species into excellent legume crops. This practice is called gene introgression breeding. Doing so can bring new genetic variation, help us improve varieties, improve disease resistance, drought tolerance, and yield. There are many successful examples, such as hybridization with wild or exotic species to breed better chickpeas, pigeon peas, peanuts, lentils, mung beans, urdu beans and kidney beans. These varieties not only grow better, but are also more disease-resistant and stress-resistant. In order to transfer these complex traits faster, many people now use some "specially designed" breeding populations in combination with new tools such as molecular markers. These methods can reduce the problem of unwanted traits being transferred in together. Now, gene introgression breeding has become a common method for improving legume crops (Sharma et al., 2013; Pratap et al., 2021; Gore et al., 2022).

4.2 Development of pre-breeding lines and core collections

In the early stages of breeding, researchers will first introduce excellent genes from wild species or local varieties, and then introduce them into those strains that are more suitable for breeding. This step can solve the problem of incompatibility during hybridization and avoid bringing in some unwanted traits. They will first collect a lot of germplasm materials, then evaluate and screen them one by one, and finally establish a core germplasm bank. This germplasm bank retains many useful genes and alleles for subsequent breeding. Taking cowpea breeding as an example, the core germplasm has helped us find a lot of good materials with potential. These resources are also critical because they can support subsequent improvement work and help varieties better adapt to different environments (Egan et al., 2021; Gayacharan et al., 2023; Chaudhary et al., 2025).

4.3 Marker-assisted and genomic selection approaches

Now many breeding projects have begun to use some modern methods, such as marker-assisted selection (MAS), marker-assisted backcrossing, and genomic selection. These methods can speed up the process of finding good traits and breed new high-yield and disease-resistant varieties more quickly. With high-density genetic maps, complete genomic information and molecular markers, we can more accurately find the genetic locations (QTLs) related to yield, disease resistance and stress tolerance, and then transfer them to the target varieties. GWAS (genome-wide association analysis) and next-generation sequencing can also enable us to improve the entire population faster and achieve continuous genetic progress. Now we can also combine omics technology and artificial intelligence to more efficiently explore traits and assist decision-making, thereby supporting the breeding of high-yield and stress-resistant legume varieties (Varshney et al., 2018; Singh et al., 2021; Jha et al., 2022; Biswas et al., 2023).

5 Case Studies in High-Yield Legume Breeding

5.1 Soybean: Chinese landraces for elite yield traits

China has a wide variety of soybean local varieties and rich genetic diversity. These varieties contain some unique and excellent genes that are very helpful in increasing yields. Introducing them into breeding projects can find and utilize these useful traits, while also expanding the source of genes for breeding. Studies have found that if local varieties and wild soybeans can be used for pre-breeding, combined with genomic tools, it can help soybeans break through the yield bottleneck and further improve breeding results (Figure 1) (Singh et al., 2022; Rubiales, 2023).

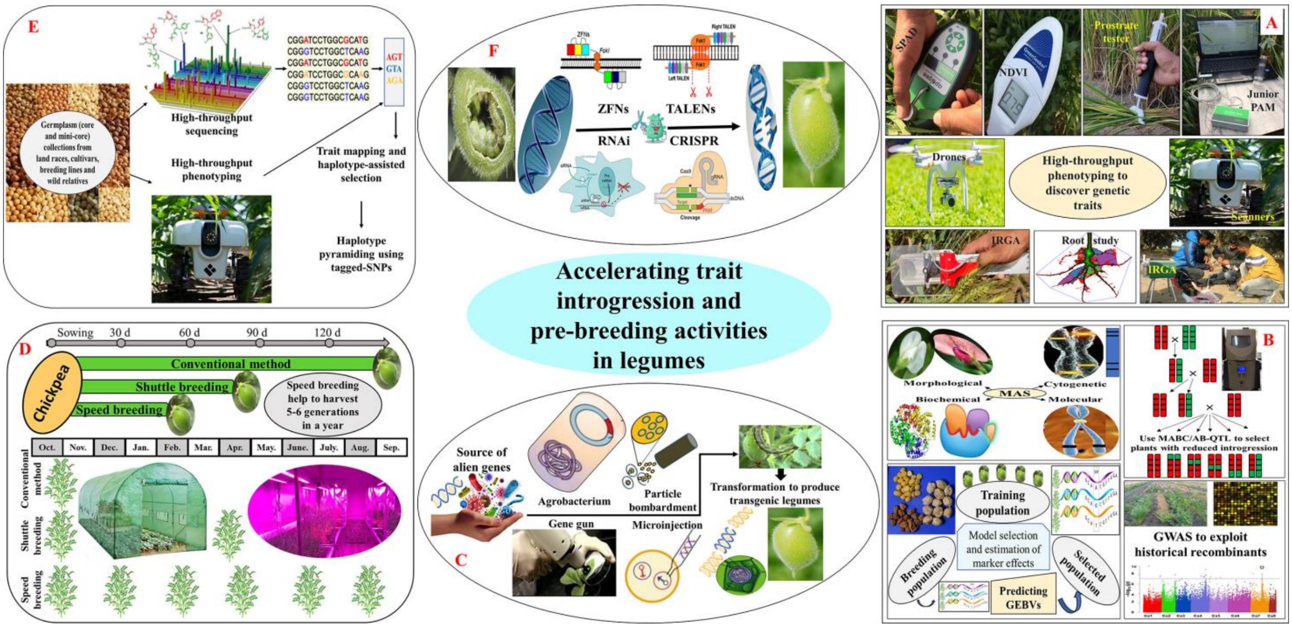

Figure 1 Integrated approaches for accelerating trait introgression and achieving higher genetic gain in legumes (Adopted from Singh et al., 2022)

Image caption: (A) high-throughput phenotyping (SPAD-meter, green seeker, prostrate tester, junior PAM, drones, scanners, IRGA, etc.) to take full advantage of large-scale genomic data sets built by next-generation sequencing (NGS) tools; (B) bringing genomic tools like, marker-assisted selection (MAS), marker-assisted backcrossing (MABC), advanced backcross quantitative trait loci mapping (AB-QTL), marker-assisted recurrent selection (MARS), genomic selection (GS), and genome wide association studies (GWAS) to identify and introgress desirable genes or QTLs into legumes with high efficacy; (C) biotechnology (gene gun, particle bombardment, microinjection, and Agrobacterium) mediated transformation of alien genes to produce pest, disease and herbicide resilient transgenic crops; (D) dialling physiology of plants with protracted photoperiod, elevated temperature and CO2 coupled with immature seed harvest to accelerate generation advancement; (E) developing tailor-made crop varieties by using haplotype-based breeding; (F) targeted genome editing using meganucleases, zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and clustered Regularly Interspaced Short Palindromic Repeats (CRISPRs) to produce non-transgenic, genome edited crops (Adopted from Singh et al., 2022)

5.2 Cowpea: enhancing productivity under drought-prone regions

In cowpea breeding, scientists used the genetic differences between wild relatives and local varieties to improve cowpea yield and adaptability in arid areas. They first did pre-breeding and slowly introduced drought-tolerant traits. Gradually, they selected varieties that could maintain stable yields even in water-scarce environments. This breeding method is particularly useful in areas with a lot of climate change and common droughts. Now, new technologies such as genomics, phenomics, and rapid breeding have also been added. These methods make breeding faster and the selected varieties more reliable (Varshney et al., 2018; Singh et al., 2022).

5.3 Faba bean: cold-adaptive lines improving yield in temperate zones

In broad bean breeding, breeders selected cold-resistant strains so that broad beans can produce high yields in areas with lower temperatures. These cold-resistant and variable maturity genetic resources not only increase yields, but also allow broad beans to be planted in places that could not be planted before. In order to make broad beans more adaptable to abiotic stresses such as cold, breeding work needs to pay special attention to selecting strains with strong resistance. This is critical to improving the planting effect in temperate regions (Duc et al., 2015; Rubiales, 2023).

6 Integration of Multi-Omics for Trait Mining

6.1 Use of transcriptomics and GWAS to identify yield QTLs

Transcriptome and GWAS are commonly used methods to study yield and other complex traits in legumes. Combining these two types of data can find genes related to yield, seed composition, stress resistance, and quantitative trait loci (QTL). These methods have been used in soybeans and other crops. The results are also good. Not only have many important genes been found, but some useful molecular markers have also been developed (Chaudhary et al., 2015; Yang et al., 2021). Now, with multi-omics databases and platforms, it has become more convenient to find these candidate genes and understand their regulatory mechanisms. These tools have greatly improved the efficiency of identifying traits (Yang et al., 2023).

6.2 Genomic prediction models for complex traits

If only one type of data is used for prediction, the effect is usually not ideal. But if several different data are put together, such as genome, transcriptome and methylation group data, the prediction results will be more accurate. This approach can help us understand more clearly which genes are affecting trait changes, how they interact and how they are regulated. Studies have also found that this multi-omics approach performs better than traditional methods in various environments (Wang et al., 2024). Now, many breeding projects have also begun to use machine learning and statistical methods to process these data. Methods such as random forests and multi-kernel learning can make predictions more stable and reliable (Acharjee et al., 2016; Briscik et al., 2024).

6.3 Combining metabolomic and phenomic data for precision breeding

If we use metabolome and phenotypic data together with other omics data, we can see more clearly which molecules and physiological mechanisms affect yield and quality. In this way, a predictive model from genes to traits can be established to help us identify important metabolic pathways and biomarkers (Hu et al., 2021). This information can help us improve target traits faster, shorten breeding time, and make it easier to breed legumes with good performance.

7 Concluding Remarks

Legumes have rich genetic diversity, which is the basis for their improvement. These genetic differences can help us increase yields, enhance disease resistance, and improve nutritional quality. In particular, wild species and local varieties carry many unique genes. These genes are very helpful for breeding. Using these variations, we can cultivate legumes that can adapt to climate change, resist pests and diseases, and adapt to different environments. This diversity also affects some important traits, such as some varieties have well-developed root systems and strong drought resistance; some can coexist with rhizobia to help plants fix nitrogen. These characteristics not only increase yields, but also protect soil and the environment.

In the future, breeding should combine traditional methods with modern technologies. For example, genomic tools, phenotyping, and rapid breeding can be used to make breeding more efficient. Introducing good genes from wild species, that is, pre-breeding, can help increase genetic diversity. This can solve the problem of stagnant yield growth. There are many advanced tools now, such as high-throughput phenotyping, modeling software, gene editing, etc., which can help us find good traits faster and improve breeding efficiency. Breeders, agricultural experts and farmers also need to work together. They have to jointly decide the breeding goals, considering both yield and sustainable development.

In terms of technology, digitizing germplasm resources is an important step. If combined with multi-omics data, artificial intelligence and some intelligent analysis tools, we can greatly change the way of breeding. Through these databases and models, we can find useful traits and excellent genes faster and make more scientific choices.

These new methods are expected to help us breed new legume varieties that are high-yielding, resistant to stress, and adaptable to climate change, ensuring food and nutrition security for humans in the future.

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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.

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