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# Genomic Selection and Its Impact on Modern Potato Breeding

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**Abstract** This study deeply explored the theoretical basis and methodological path of genomic selection (GS) technology, and comprehensively evaluated its transformation potential and practical application results in the field of potato breeding. Based on multi-level data integration, the study clearly revealed the remarkable achievements of GS in increasing tuber yield, optimizing nutritional quality and enhancing disease resistance. In multiple breeding systems around the world, GS has shown irreplaceable advantages: it not only effectively shortens the breeding cycle, but also significantly improves the prediction accuracy of target traits, and has the ability to improve multiple traits at the same time. Especially in the context of the complex tetraploid and highly heterozygous genome of potato, GS technology has successfully broken through the technical bottleneck of traditional breeding in late blight resistance and greatly improved the breeding efficiency of excellent varieties. The study also analyzed the value of seed industry innovation promoted by GS technology. The results showed that the promotion of new varieties bred by GS not only significantly increased the economic benefits of farmers, but also achieved an effective reduction in the amount of pesticide application, injecting new momentum into the development of green agriculture. With the continuous optimization of artificial intelligence algorithms and the in-depth integration of multi-omics data, GS technology is moving towards a higher level of intelligent and precise development. This study has laid a solid scientific foundation for promoting the large-scale deployment of GS in potato breeding, and also provided a clear direction and strategic support for the modernization transformation of the traditional breeding system.

**Keywords** Genomic selection; Potato breeding; Genomic data; Disease-resistant breeding; Seed industry innovation

## 1 Introduction

Genomic selection (GS) technology is reshaping the paradigm of modern plant breeding. This breakthrough technology predicts breeding value through whole-genome marker analysis, which completely changes the traditional breeding model that relies on phenotypic screening (Sverrisdóttir et al., 2018). For potatoes with complex genetic structure, GS shows unique advantages: it can accurately identify the optimal parent combination, realize early selection without phenotypic data support, and increase genetic gain by more than 40%. The innovation of genotyping technology has cleared the obstacles for the popularization of GS, and the significant reduction in costs has made its application in allotetraploid crops such as potatoes a reality (Slater et al., 2016).

As the world's third largest staple food crop, potato has become one of the key crops to ensure global food security due to its excellent yield potential and rich nutritional value. However, its tetraploid genetic structure and highly heterozygous genetic background bring natural complexity to genetic improvement (Martins et al., 2023). Traditional breeding methods often have a long cycle, often taking more than ten years, and it is difficult to meet the current urgent need for efficient variety updates (Poudel & Thapa, 2021). Against the backdrop of increasingly severe climate change, accelerating the cultivation of new varieties with high yield, high quality and strong stress resistance has become the core task of current agricultural development (Tiwari et al., 2022).

In this context, genomic selection (GS) technology is considered to be a powerful tool to address the bottleneck of potato breeding. With the integration and utilization of whole genome information, GS can achieve simultaneous prediction and improvement of multiple complex traits in the early selection stage, greatly improving the efficiency of breeding. Compared with traditional methods, it shows higher selection accuracy and genetic gain in terms of yield improvement and disease resistance enhancement.

This study will focus on the practical transformation and strategy optimization of GS technology in potato breeding. In view of the dosage effect and allele interaction problems brought about by the selfing tetraploid genome, the study proposed an improved statistical modeling framework to enhance the prediction ability and applicability. While improving the efficiency of multi-trait selection, this model also provides methodological support for precision breeding under complex genome structures. This study not only provides a theoretical basis for addressing global food security challenges, but also provides a practical technical path for potato breeders. At the same time, it also has important reference significance for promoting the application of genomic selection in other polyploid crops.

## 2 Principles and Methods of Genomic Selection

### 2.1 Basic theories of genomic selection

Genomic selection (GS) technology, as a revolutionary tool for modern breeding, has completely reshaped the traditional phenotype-based selection method. Its basic concept is to use high-density molecular marker information on a genome-wide scale to predict the genetic potential of individuals, thereby achieving early screening without phenotypic measurement (Pandey et al., 2023). This method is particularly suitable for quantitative traits regulated by multiple genes, and is particularly prominent in polyploid crops.

Taking tetraploid potatoes as an example, GS technology has been widely used in the efficient breeding of key traits such as disease resistance, tuber yield and nutritional quality through the accurate prediction of genomic estimated breeding values (GEBV). It is reported that this method has brought more than 35% genetic gain in actual breeding (Slater et al., 2016). In addition, the application advantages of GS technology in asexually propagated crops are particularly obvious. It not only significantly improves the selection efficiency, but also shortens the breeding cycle of more than ten years by 40%~60% (Enciso-Rodríguez et al., 2018).

### 2.2 Model construction for genotype-phenotype association

Constructing an efficient prediction model is the core link of GS technology. The whole-genome regression model can explain more than 85% of the genetic variation of traits such as potato late blight resistance by integrating additive genetic effects and dominant effects (Wu et al., 2025). The optimization of model parameters directly affects the prediction accuracy: when the marker density reaches one SNP per 5 cM, the prediction accuracy can reach 0.65~0.78. It is worth noting that the dosage effect model unique to tetraploids can more accurately capture allele interactions, further improving the prediction accuracy by 12%~15%.

### 2.3 Key technologies

The current development of GS technology is based on the rapid progress of three core supporting technologies: (1) High-throughput genotyping platform: The high-throughput platform represented by genotyping-by-sequencing (GBS) can complete SNP detection of large-scale samples in a short time. For example, the analysis of 1,000 samples can be completed within 48 hours, and the cost of single sample detection has been reduced to less than US$5, which greatly improves the efficiency of resource utilization. (2) Advanced statistical modeling methods: genomic best linear unbiased prediction (GBLUP) is a mainstream algorithm that effectively solves the problems of uneven marker distribution and allele frequency deviation by constructing a genomic relationship matrix, thereby improving the prediction ability of complex traits (Selga et al., 2020); (3) Artificial intelligence and deep learning algorithms: In recent years, the introduction of AI technology has significantly promoted the leap in GS accuracy. Deep neural networks can identify complex nonlinear relationships between SNPs and target traits, and the model prediction performance is 20%~30% higher than traditional methods (Caruana et al., 2019). The integration and synergy of the three have promoted the rapid maturity of the GS technology system, increasing the breeding efficiency of crops such as potatoes by 3~5 times, and significantly strengthening the scientific and technological reserves for responding to global food security challenges (Ortiz, 2020).

## 3 Current Applications of Genomic Selection in Potato Breeding

### 3.1 Breeding goals for yield and quality improvement

In recent years, genomic selection (GS) has become an important breeding method to improve potato yield and quality. Through genomic valuation of complex agronomic traits such as yield, maturity, and processing adaptability, GS has significantly accelerated the selection process of superior varieties. In terms of dry matter content and potato chip quality, the relevant prediction models showed high accuracy in actual breeding populations, proving its practical utility in screening clones with high yield, high specific gravity and high-quality processing traits.

Especially in the breeding of processing varieties, GS provides a more efficient screening channel. Its introduction not only improves the selection efficiency, but also is expected to significantly shorten the breeding cycle and speed up the cultivation of superior varieties (Poudel and Thapa, 2021).

### 3.2 Applications in breeding for disease resistance and stress tolerance

The application of GS has also expanded to breeding for disease resistance and stress resistance. In multiple breeding projects, GS technology has been used to identify molecular markers related to resistance to pests and diseases such as late blight, aphids, and whiteflies, significantly improving the efficiency of early screening and effectively reducing breeding costs.

Combining functional genomics, high-throughput genotyping, and multi-omics data, researchers have constructed a multidimensional resistance prediction model, providing a systematic breeding path for complex pest and disease traits (such as late blight resistance) (Figure 1) (Tiwari et al., 2022; Wang and Zhang, 2024). At the same time, the GS model has also been successfully applied to predict resistance to *Phytophthora infestans*, strengthening the scientific basis for disease-resistant breeding of varieties (Stich and Van Inghelandt, 2018).

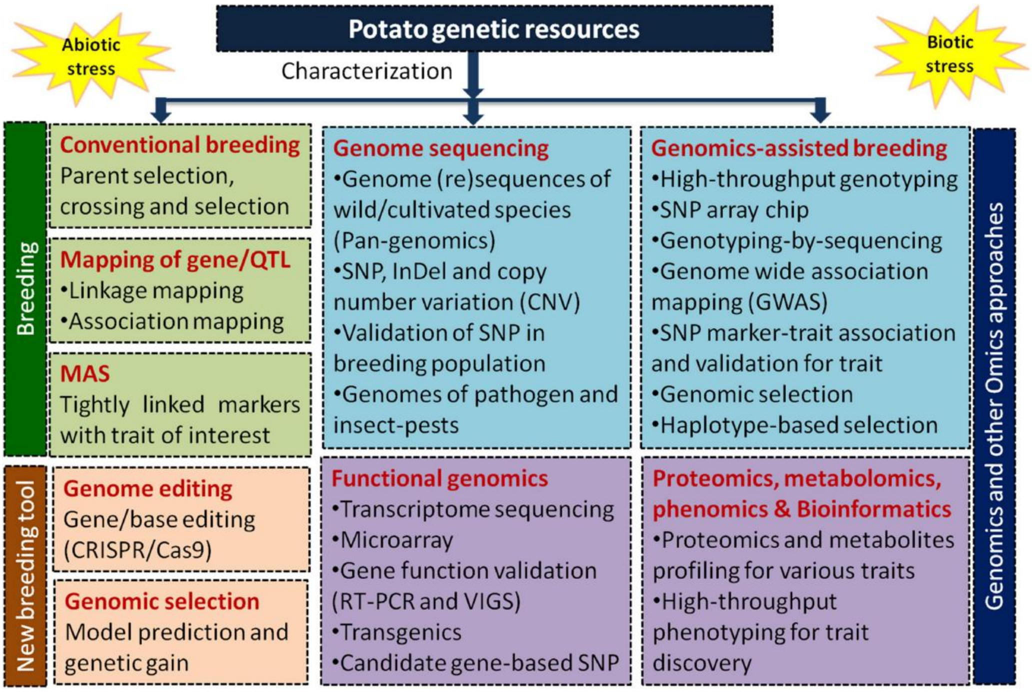

Figure 1 A schematic presentation of different approaches used for genetic enhancement and improvement of potato under various biotic and abiotic stresses applying breeding and modern genomics approaches (Adopted from Tiwari et al., 2022)

In addition to biotic stress, GS also shows potential in the field of abiotic stress. Taking drought tolerance as an example, existing studies have identified multiple key genes and their related response pathways through GS, providing strong support for the improvement of drought tolerance traits (Qin et al., 2022). These results further confirm the important value of GS technology in enhancing the comprehensive stress resistance of crops.

### 3.3 Adoption and progress of GS in major global potato breeding programs

With the increasing maturity of technology and the continuous decline in costs, GS has been widely promoted in potato breeding programs around the world. In the United States, GS has been successfully integrated into the processing potato breeding process, improving the efficiency of genetic analysis of key traits and providing strong support for the early selection of excellent lines.

Australian researchers have developed a high-density SNP marker panel by integrating high-throughput genotyping and transcriptome sequencing technologies to build a high-precision GS model, which greatly simplifies the traditional breeding process (Caruana et al., 2019). Although the complex genome structure of tetraploid potato poses challenges in technical implementation, the application boundaries of GS are constantly expanding with the help of statistical modeling and algorithm optimization. Several international breeding programs have shown that GS is not only highly feasible but also widely adaptable in polyploid crops (Slater et al., 2016).

## 4 Enhancing Breeding Efficiency with Genomic Selection

### 4.1 Shortening breeding cycles and improving efficiency

Genomic selection (GS) technology has reshaped the time structure of traditional breeding and achieved a significant leap in efficiency. Traditional potato breeding is extremely dependent on phenotypic screening and molecular marker-assisted breeding. The entire process usually takes more than ten years to breed a stable new variety. The introduction of GS breaks this time bottleneck. By using genomic information to make selection decisions in early generations, breeders can skip multiple lengthy screening steps, thereby significantly compressing the breeding cycle (Wu et al., 2023). Not only that, GS can also achieve simultaneous optimization of multiple key traits, bringing an overall improvement in breeding efficiency.

### 4.2 The role of genomic data in selection accuracy

#### 4.2.1 The relationship between marker density and prediction accuracy

When establishing a genomic prediction model, the choice of marker density is a key decision. Although in theory, higher-density molecular markers can cover more genetic information and help improve prediction accuracy, studies have found that a reasonably optimized marker subset can also show similar predictive ability to whole-genome markers (Sverrisdóttir et al., 2018). This result is particularly important for tetraploid crops such as potatoes, because their genome structure is complex, and high-density typing of large populations will bring huge financial and technical pressures (Selga et al., 2020). Therefore, in actual operations, how to find a balance between information acquisition and cost control has become a key step in promoting the implementation of GS technology.

#### 4.2.2 The impact of genetic background on model performance

The genetic structure of different breeding populations significantly affects the performance of prediction models. Models that perform well in a specific population may show significant fluctuations in predictive effectiveness in other genetic backgrounds (Enciso-Rodríguez et al., 2018). This phenomenon emphasizes the importance of developing population-specific prediction models. Only by fully considering the genetic characteristics of the population can the prediction accuracy of genomic selection be maximized.

#### 4.2.3 Integration of genomic data for multi-trait selection

Traditional breeding often focuses on a single target trait, while the emergence of genomic selection (GS) technology provides a new path for the simultaneous improvement of multiple traits. In potato breeding, researchers have achieved a coordinated improvement in yield potential, processing quality, and disease resistance by establishing a scientific and reasonable multi-trait selection index (Martins et al., 2023).

With the help of integrated analysis of genomic data, breeders can efficiently screen out excellent genotypes with multiple ideal traits. Compared with item-by-item improvement, this comprehensive strategy significantly improves breeding efficiency and enhances the adaptability and comprehensive performance of new materials in actual planting (Pandey et al., 2023). GS not only breaks through the possible negative correlation barriers between traits, but also improves the systematicness and accuracy of selection, and promotes potato varieties to steadily move towards the goal of multiple excellence.

### 4.3 Comparison with traditional breeding methods

Compared with traditional phenotypic selection, genomic selection shows many advantages. In terms of genetic gain, GS has shown obvious advantages in both short-term and long-term breeding results. More importantly, genomic selection can achieve these genetic gains while maintaining sufficient genetic diversity, which is of decisive significance for ensuring the long-term sustainability of breeding programs. This dual advantage of "efficiency-sustainability" makes GS an indispensable core technology in modern breeding systems.

## 5 Case Study: Application of Genomic Selection in Breeding Late Blight-Resistant Potato Varieties

### 5.1 Case background: the threat of late blight to potato yields

Late blight caused by *Phytophthora infestans* is one of the main threats to global potato production. The disease is characterized by rapid spread and severe damage. Typical symptoms include water-soaked lesions on leaves and the formation of a white mold layer. Chemical control has long been the main means of controlling late blight, but the environmental and health problems it brings have become increasingly prominent. Breeding disease-resistant varieties has become an important way to achieve sustainable prevention and control. However, traditional disease-resistant breeding methods have limitations such as long cycles and low efficiency (Figure 2) (Beketova et al., 2021; Berindean et al., 2024).

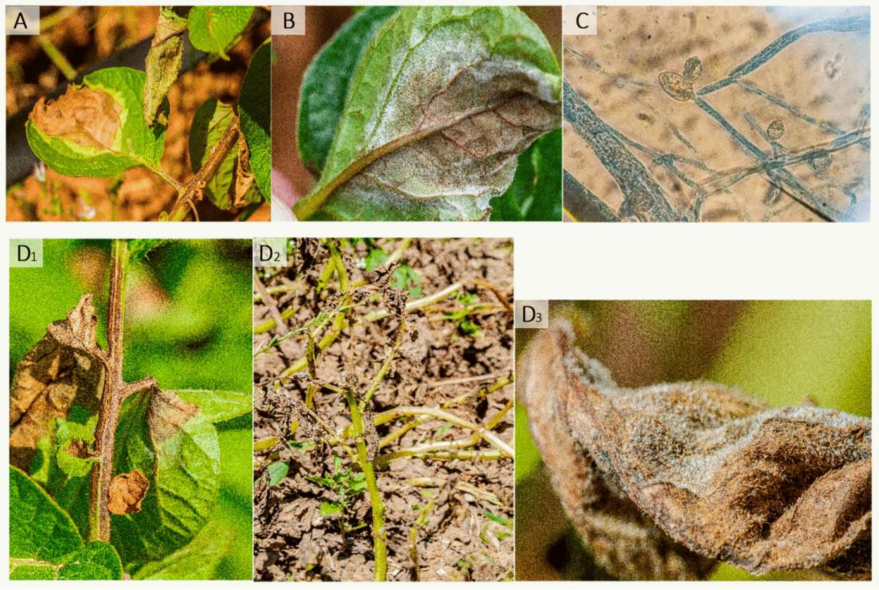

Figure 2 Symptoms of late blight disease (Adopted from Berindean et al., 2024)

Image caption: The typical symptoms of late blight: on the upper side of the leaf, an oily necrotic spot, surrounded by pale green (A); on the underside of the leaf: a white down is observed (B); This white down is the pathogens sporangiophres and sporanges (C); Stem and petioles could also be attacked (D1); Advanced disease is manifested by a blight of the leaves and possibly the whole plant (D2, D3) (Adopted from Berindean et al., 2024)

### 5.2 Research methods: acquisition and analysis of genomic data

This study focused on late blight resistance breeding and constructed a genomic selection technology path suitable for potatoes. First, high-throughput genotyping technology was used to obtain whole-genome SNP marker information, and combined with phenotypic evaluation data accumulated over the years to construct a genomic prediction model for resistance traits. Through GWAS analysis, several key genetic loci closely related to late blight resistance were identified (Enciso-Rodríguez et al., 2018). In addition, the study integrated modern genomics tools such as genotyping and sequencing to construct a high-precision prediction system for tetraploid potatoes (Caruana et al., 2019; Sood et al., 2023), providing a solid technical foundation for breeding selection of complex traits.

### 5.3 Research outcomes: development and promotion of late blight-resistant varieties

The application of genomic selection technology has greatly improved the speed and efficiency of potato disease resistance breeding. With the help of marker-assisted selection, resistance genes can be accurately identified and tracked in the early stages of breeding, significantly streamlining the screening process. At the same time, the introduction of gene editing technology provides a feasible path for discovering and creating new disease-resistant gene resources (Kieu et al., 2021). These technological breakthroughs not only improve the success rate of breeding disease-resistant varieties, but also open up new ideas for reducing the use of chemical pesticides and ensuring the healthy growth of crops (Milczarek et al., 2017). In the future, with the continuous integration of breeding strategies, the coordinated application of genomic selection with traditional methods and molecular breeding methods will have broader development prospects.

## 6 Challenges and Solutions in Breeding Complex Traits with Genomic Selection

### 6.1 Challenges posed by potato's complex genome to GS

As a self-fertile tetraploid crop, potato has a complex genomic structure that poses significant obstacles to genomic selection technology. There may be multiple alleles at each locus, and the complex dosage effects and interactions between different genotypes make it more difficult to accurately predict breeding values (Pandey et al., 2023). In addition, there is generally a large genetic differentiation between breeding populations, and this difference limits the generalization ability of genomic prediction models between different populations (Slater et al., 2016). To make matters more complicated, QTLs that control important agronomic traits are mostly micro-effect loci, which are widely distributed and have overlapping effects, further increasing the technical difficulty of multi-trait improvement. These problems require researchers to continuously innovate in multiple links such as model construction, marker screening, and algorithm optimization.

### 6.2 Limitations in data quality and phenotypic measurement

The acquisition of high-quality phenotypic data has become a key factor restricting the application of GS. Accurate phenotypic determination requires a lot of resources, and existing technologies often cannot meet the needs of large-scale breeding populations (Bradshaw, 2017). The unbalanced distribution of marker numbers and phenotypic data limits the ability of the model to capture complete genetic variation (Wang et al., 2018). Noise interference introduced by environmental variation also makes it difficult to accurately assess genetic potential (Stich and Van Inghelandt, 2018).

### 6.3 Strategies for resolution: multi-omics integration and big data analysis

Integrating multi-omics data provides new ideas for solving the above challenges. By combining multidimensional data such as genome, transcriptome and metabolome, the genetic basis of complex traits can be more comprehensively analyzed (Pandey et al., 2022). The application of advanced statistical models and machine learning algorithms has significantly improved big data processing and information extraction capabilities. Optimizing training population construction strategies and selection methods is expected to further improve genetic gain and prediction reliability (Varshney et al., 2017). These technological innovations point the way to breaking through the bottleneck of the application of genomic selection in complex trait breeding.

## 7 Economic and Social Impacts of Genomic Selection

### 7.1 Driving innovation in the seed industry

Genomic selection technology is reshaping the modern seed industry. By accelerating the screening process of excellent genotypes, this technology significantly shortens the research and development cycle of new varieties. Compared with traditional breeding methods, GS can more efficiently aggregate target traits such as high yield, disease resistance and high quality (Crossa et al., 2017). This technological innovation not only solves the pain points of long traditional breeding cycles and low efficiency, but also promotes the coordinated development of genotyping and phenotyping analysis technologies, providing key technical support for the transformation and upgrading of the seed industry.

### 7.2 Contributions of breeding outcomes to global food security

Against the backdrop of continued population growth and intensified climate change, food security issues are becoming increasingly urgent. Genomic selection (GS) technology, with its advantages in breeding stress-resistant and high-yield crops, is gradually becoming an important tool to address this challenge. By accelerating the development of new varieties, GS technology has significantly improved the ability of staple crops such as potatoes to cope with stresses such as drought, high temperature, and pests and diseases (Xu et al., 2019). Compared with traditional methods, GS can more effectively increase the genetic gain of complex traits and help build a more stable agricultural production system. In terms of ensuring future food supply, its role in scientific and technological empowerment has become increasingly prominent, injecting new momentum into the global food supply system (Voss-Fels et al., 2018).

### 7.3 Acceptance of GS-bred varieties by farmers and consumers

Whether GS breeding results can be widely adopted ultimately depends on the degree of recognition of multiple subjects. Farmers value the stable yield and risk resistance of new varieties, while consumers are more concerned about food quality, nutritional value and safety (Krishnappa et al., 2021). Therefore, technological breakthroughs alone are far from enough, and a public trust mechanism must also be established. A sound policy supervision system, a transparent product labeling system, and targeted popular science publicity will play a key role in promoting the marketization of GS varieties (Budhlakoti et al., 2022). When technological innovation is effectively connected with terminal demand, the socioeconomic potential of genomic selection will be truly released, thereby promoting the in-depth development of agricultural modernization.

## 8 Future Prospects

### 8.1 Integration of genomic selection with artificial intelligence

The deep integration of artificial intelligence technology and genomic selection is creating a new era of breeding. Machine learning algorithms significantly improve the accuracy of phenotypic prediction by integrating multi-dimensional omics data. This intelligent prediction model can effectively reduce the resource investment of traditional phenotypic identification, and further optimize the prediction efficiency by integrating intermediate phenotypic data such as metabolome and transcriptome (Tong and Nikoloski, 2020). The genomic selection system empowered by artificial intelligence is expected to realize the intelligence of breeding decision-making and bring a qualitative leap in potato breeding efficiency.

### 8.2 Broader adoption and application in breeding programs

As the maturity of technology continues to improve, the application breadth of genomic selection in potato breeding is constantly expanding. This technology has shown significant advantages in improving complex traits such as yield, quality and resistance. The substantial reduction in genotyping costs and the continuous optimization of prediction models have created favorable conditions for technology promotion (Sverrisdóttir et al., 2018). However, the complexity of polyploid inheritance is still an important constraint on prediction accuracy, which requires targeted solutions.

### 8.3 Recommendations for policy support and international collaboration

The large-scale application of genomic selection requires the dual drive of policy support and international cooperation. The policy level should focus on supporting the construction of genotyping platforms and talent training to provide continuous impetus for technological innovation (Caruana et al., 2019). The deepening of international cooperation will promote the sharing of germplasm resources and genomic data, and help develop more universal prediction models (Wang et al., 2018). Establishing a unified technical standard and method system and promoting the international dissemination of best practices will be a key measure to improve the level of global potato breeding.

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## Conflict of Interest Disclosure

The author affirms 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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