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Plant Genetics and Breeding in Kazakhstan: Current Status, Crop-Specific Advances, and Strategic Priorities for 2025-2030

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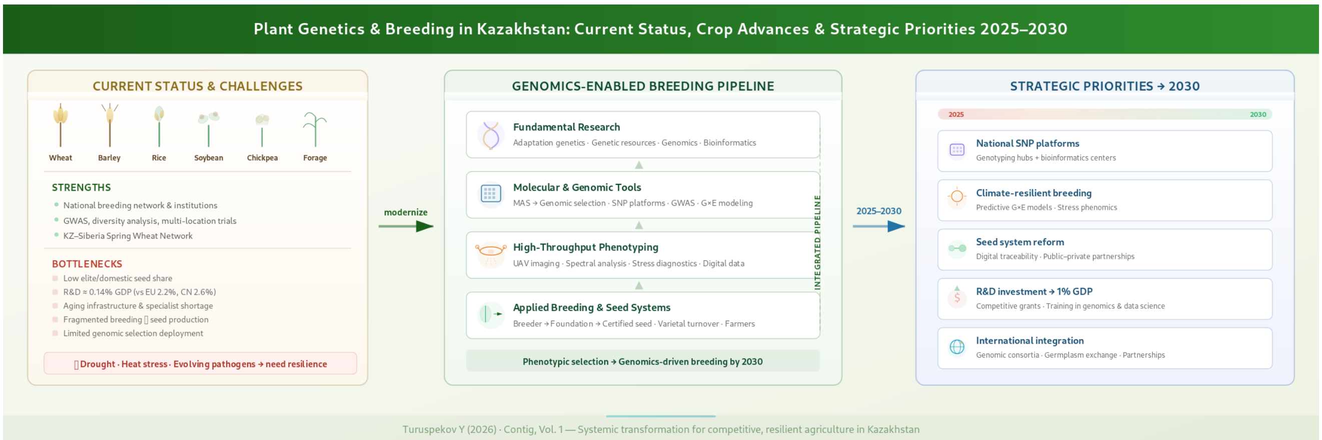
Graphical abstract



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Abstract

This review synthesizes the current status, challenges, and long-term development prospects of plant genetics and breeding research in the Republic of Kazakhstan, integrating institutional analysis for 2025-2030 with crop-specific genetic and breeding priorities projected to 2035. Kazakhstan has established a national network of research and breeding institutions that has enabled the development of numerous domestically bred crop varieties and supported the country's role as a major wheat exporter. However, systemic constraints persist, including a low share of elite and domestically produced seed material, fragmentation between breeding and seed production, aging research infrastructure, and a shortage of qualified young specialists. These factors limit the large-scale deployment of modern molecular and genomic technologies and slow the renewal of varietal diversity.

Against this institutional background, the review examines genetics- and genomics-enabled breeding progress in major cereal and legume crops, with emphasis on wheat, barley, rice, soybean, and chickpea. Increasing climate variability, recurrent drought, heat stress, and evolving pathogen populations intensify the demand for yield stability, durable disease resistance, and stress resilience. Recent Kazakhstan-focused studies employing genome-wide association mapping, genetic diversity analysis, and multi-location testing networks, including the Kazakhstan-Siberia Network on Spring Wheat Improvement, demonstrate that a solid scientific foundation for modern breeding is already in place.

Looking forward, priority directions include strengthening fundamental research in plant adaptation genetics, conservation and utilization of genetic resources, genomics, and bioinformatics; routine deployment of marker-assisted and genomic selection; development of interoperable genotype-phenotype-environment datasets; high-throughput phenotyping; and accelerated generation advance under controlled environments. The integration of these components into operational breeding and seed systems is essential for increasing genetic gain, reducing dependence on imported varieties, and enhancing the long-term competitiveness and sustainability of Kazakhstan's agriculture under climate uncertainty.

Chapter 1: Current Status and Prospects of Plant Genetics and Breeding Research in Kazakhstan (2025-2030)

This chapter analyzes the current state and development prospects of fundamental and applied research in plant genetics and breeding in the Republic of Kazakhstan for the period 2025-2030. Institutional, scientific-technological, and human-resource aspects of the sector are examined in the context of food security, climate challenges, and the need to reduce dependence on imported seed material. Kazakhstan has established a network of research and breeding institutions that has enabled the development of numerous domestically bred crop varieties. However, persistent systemic constraints remain, including a low share of elite and domestic seeds across several crop groups, fragmentation of the breeding and seed production system, aging infrastructure, and a shortage of qualified young specialists. These factors limit the large-scale adoption of modern molecular and genomic technologies and slow the renewal of varietal diversity. The review highlights the critical role of fundamental research in plant adaptation genetics, conservation and utilization of genetic resources, genomics, and bioinformatics as the scientific basis for transitioning to next-generation breeding. Marker-assisted and genomic selection, development of national gene banks, integration of genotype-phenotype-environment data, and digital breeding tools are identified as priority directions. The outlined development pathways are considered essential for enhancing the competitiveness and long-term sustainability of Kazakhstan's agricultural sector.

Current Status and Prospects of Plant Genetics and Breeding Research in Kazakhstan

Kazakhstan maintains an institutional network of research institutes, experimental stations, and agricultural universities engaged in plant breeding and genetic research. According to official data, 868 domestically developed varieties are registered in the State Register of Breeding Achievements, and breeding activities are conducted by 27 specialized institutions (Government of the Republic of Kazakhstan, 2024). Between 2018 and 2022, more than 100 new varieties and hybrids were developed and submitted for state testing under program-targeted funding schemes (Government of the Republic of Kazakhstan, 2024).

Research activities include classical breeding, evaluation of germplasm collections, and increasingly, molecular approaches such as DNA marker-assisted selection (MAS). Some laboratories have initiated genomic and bioinformatics analyses to improve drought tolerance, disease resistance, and yield stability under Kazakhstan's continental climate. Fundamental and applied research has traditionally focused on adaptation to arid and sharply continental environments, particularly in wheat and barley. Molecular studies of genetic diversity and population structure have revealed substantial allelic variation relevant to stress tolerance and yield stability (Turuspekov et al., 2016; Abugalieva et al., 2019; Turuspekov et al., 2017). Genome-wide association studies (GWAS) and QTL analyses conducted on wheat, barley, and soybean collections grown under Kazakhstan's conditions have identified loci associated with yield components, quality traits, and disease resistance (Turuspekov et al., 2017; Zatybekov et al., 2017; Amalova et al., 2021a,b; Genievskaya et al., 2023a,b).

Despite these advances, large-scale genomic selection and integrated phenomics platforms remain limited. National R&D expenditure remains low (~0.14% of GDP), constraining access to advanced genotyping, phenotyping, and bioinformatics infrastructure (World Bank, 2025). The integration of genotype-phenotype-environment (G×P×E) modeling, large SNP panels, and digital breeding platforms remains nascent, reflecting broader structural constraints in research funding and infrastructure. According to World Bank data, Kazakhstan's gross domestic expenditure on research and development (GERD) accounts for approximately 0.14% of GDP - substantially lower than that of major agricultural innovation economies.

Despite its scientific base, Kazakhstan's breeding system faces several structural challenges. First, high import dependence persists for vegetable, sugar beet, potato, and fruit crop seeds, where domestic coverage is estimated at less than 10% in certain segments (Government of the Republic of Kazakhstan, 2024). Such dependence reduces technological sovereignty and increases vulnerability to disruptions in global supply chains. Second, the innovation chain is fragmented, with insufficient integration among fundamental genetics research, breeding institutions, seed multiplication enterprises, and commercial producers. Weak public-private partnerships limit the commercialization and scaling of new varieties. Third, demographic challenges affect the sustainability of research: the average age of plant breeders exceeds 60 years in many institutions, while the influx of young specialists remains insufficient (Government of the Republic of Kazakhstan, 2024). Finally, limited research funding constrains modernization - Kazakhstan's R&D intensity (0.14% of GDP) is significantly lower than Russia (~0.9% of GDP), China (~2.6% of GDP), and the European

Union (2.24% of GDP in 2024) (World Bank, 2025).

In Russia, state programs aim to increase domestic seed self-sufficiency and strengthen breeding technologies. China exemplifies rapid technological advancement in agricultural genomics, with R&D expenditure exceeding 2.5% of GDP enabling national genomic platforms and large-scale breeding programs integrating CRISPR-based technologies and genomic selection. The European Union maintains one of the most advanced breeding ecosystems in the world - in 2024, EU R&D expenditure reached €403 billion, corresponding to 2.24% of GDP. Compared to these systems, Kazakhstan's breeding infrastructure remains in a transitional phase. While foundational expertise exists, scaling molecular breeding and achieving technological parity require sustained increases in R&D investment and systemic integration.

The Comprehensive Plan for the Development of Breeding and Seed Production (2024-2028), adopted by the Government of Kazakhstan, sets quantitative targets, including the development of 108 new varieties and the increased use of elite domestic seeds (Government of the Republic of Kazakhstan, 2024). From a scientific perspective, this period represents a critical window for modernization. For sustainable development through 2030, several strategic priorities emerge: (1) expansion of genomic selection and MAS across priority crops; (2) establishment of national genotyping platforms and integrated bioinformatics centers; (3) strengthening public-private partnerships in seed commercialization; (4) increasing GERD to at least 1% of GDP as a medium-term benchmark; and (5) enhancing international collaboration with leading breeding centers. Bridging the gap between classical breeding traditions and genomics-driven innovation will determine Kazakhstan's ability to enhance agricultural resilience and reduce import dependence.

Fundamental Research in Plant Genetics: Current Focus and Critical Bottlenecks

Fundamental research in Kazakhstan is increasingly focused on the genetic mechanisms underlying adaptation to drought, heat stress, salinity, and emerging pathogens, in line with regional climate projections (IPCC, 2021). Conservation and utilization of plant genetic resources represent another strategic priority, as emphasized in national analytical reports (National Academy of Sciences of the Republic of Kazakhstan, 2022). Nevertheless, several bottlenecks persist. The country remains unable to establish a National GenBank for the centralized collection of wild and cultivated genetic resources. Existing germplasm collections are distributed across many research organizations and lack comprehensive genomic passportization and standardized digital databases, limiting their effective integration into breeding pipelines.

As one of the world's largest countries with predominantly continental and arid climates, Kazakhstan requires crop varieties with enhanced drought tolerance, heat resistance, and adaptability to saline and marginal soils. Consequently, genetic studies of abiotic stress tolerance have become a strategic priority. Globally, understanding the molecular mechanisms underlying plant responses to drought, salinity, and temperature extremes relies on advances in functional genomics, transcriptomics, and systems biology (Varshney et al., 2021; Hickey et al., 2019). In Kazakhstan, research institutions have begun incorporating molecular marker systems and candidate gene approaches to study adaptive traits, particularly in wheat and barley. However, large-scale genomic selection platforms and high-density SNP genotyping arrays remain limited in scope.

The conservation and utilization of plant genetic resources is another critical area. The erosion of agro-biodiversity poses long-term risks to breeding sustainability. Internationally, gene banks and integrated germplasm characterization platforms serve as essential infrastructure for resilient breeding systems (FAO, 2010; Halewood et al., 2020). Kazakhstan maintains national collections of crop germplasm; however, comprehensive genomic passportization and the digital integration of these resources are still in their early stages. Genomic selection (GS), which uses genome-wide markers to predict breeding values, has significantly accelerated genetic gain in major crops worldwide (Hickey et al., 2017). While marker-assisted selection (MAS) is gradually being adopted in Kazakhstan, full-scale implementation of GS requires substantial computational infrastructure and standardized phenotypic data.

One of the most critical scientific questions for Kazakhstan concerns genotype-environment (G×E) interactions under increasingly unstable climatic conditions. Climate projections indicate increased drought frequency and greater temperature variability across Central Asia (IPCC, 2021). Globally, integrated G×E modeling and high-throughput phenotyping platforms have enhanced the precision of selecting climate-resilient genotypes (Araus et al., 2018). In Kazakhstan, although multi-location field trials are conducted, phenomic tools such as UAV-based remote sensing, spectral imaging, and automated stress diagnostics remain underutilized. This technological gap limits the predictive capacity of breeding programs under climate uncertainty.

Kazakhstan's R&D expenditure remains approximately 0.14% of GDP (World Bank, 2025), limiting sustained investment in sequencing facilities, high-throughput genotyping, and computational biology. The European Union invests over 2% of GDP in R&D, and China exceeds 2.5%, enabling large-scale genomic platforms and AI-assisted breeding systems. Without systematic investment in digital infrastructure and in training bioinformatics specialists, the transition from classical to genomics-driven breeding will remain incremental.

Human capital represents one of the most pressing bottlenecks. The aging of senior breeding specialists, combined with insufficient recruitment of young researchers, threatens the continuity of scientific schools and institutional memory. Expanding graduate programs in plant genomics, computational biology, and quantitative genetics is essential for sustaining innovation.

The analysis of current trends indicates several critical bottlenecks: (1) limited scale of genome-wide genotyping and genomic selection; (2) insufficient integration of phenomics and predictive modeling; (3) fragmented digital infrastructure and bioinformatics capacity; (4) inadequate R&D investment relative to international benchmarks; and (5) demographic imbalance in the research workforce. Addressing these bottlenecks requires coordinated policies that link fundamental research funding to applied breeding programs. Future priorities should include national SNP platforms for priority crops, integrated G×E modeling systems, digital germplasm databases, and international research partnerships.

Applied Research and Plant Breeding Systems

Applied research serves as the critical interface between fundamental genetic discoveries and their practical application in crop improvement. In modern breeding systems, applied research integrates classical selection methods with molecular tools, multi-environment testing, and seed multiplication to deliver competitive varieties adapted to specific agroecological conditions. In Kazakhstan, applied plant breeding remains predominantly based on conventional phenotypic selection and multi-year field trials, which have historically enabled the development of locally adapted cultivars, particularly for cereals such as wheat and barley. These approaches have ensured baseline yield stability under continental climatic conditions but are increasingly insufficient in the context of climate variability, shortened breeding cycles, and global competition (Tester & Langridge, 2010). International experience demonstrates that applied breeding systems capable of sustained genetic gain rely on integrating molecular breeding technologies, optimized breeding pipelines, and strong linkages with seed production and commercialization sectors (Hickey et al., 2017). While elements of marker-assisted selection (MAS) have been introduced in Kazakhstan, their application remains fragmented and limited to individual traits and crops.

Kazakhstan's applied breeding system is organized primarily within public research institutions and experimental stations, with limited participation from private breeding companies. This structure contrasts with systems in the European Union, China, and North America, where public-private partnerships dominate the development and commercialization of variety (OECD, 2015). Current breeding programs focus on yield stability under drought and heat stress, resistance to major fungal and bacterial diseases, and adaptation to low-input and marginal soil conditions. Despite these priorities, the rate of varietal turnover remains relatively low. In several crop groups, outdated varieties continue to occupy substantial portions of cultivated areas, reducing productivity gains. The limited scale of applied genomic selection, insufficient high-throughput phenotyping, and constrained access to elite parental lines further restrict breeding efficiency.

An effective seed system is a cornerstone of applied breeding success. Globally, seed systems are characterized by clear differentiation between breeder, foundation, and certified seed classes, supported by regulatory frameworks and quality assurance mechanisms (FAO & OECD, 2018). In Kazakhstan, the seed sector is structurally fragmented, with limited coordination among breeders, seed multipliers, and distributors. As a result, even scientifically promising varieties may fail to reach farmers at scale. The low share of elite and certified domestic seeds in certain crop segments reflects systemic inefficiencies in technology transfer. Without similar integration, the outputs of applied breeding in Kazakhstan risk remaining underutilized.

Digital transformation is increasingly redefining applied breeding systems. Advanced breeding pipelines incorporate digital field data capture, genomic prediction models, decision-support tools, and real-time monitoring of seed production (Crossa et al., 2017). In Kazakhstan, the digitalization of applied breeding is in its early stages, with limited adoption of integrated data management systems. The absence of unified breeding databases and standardized phenotyping protocols constrains the effective use of molecular data in selection decisions. Scaling digital breeding tools requires not only technological investment but also institutional reforms that promote data sharing and interdisciplinary collaboration.

The analysis of applied breeding systems in Kazakhstan reveals several persistent constraints: (1) dominance of classical breeding methods with limited genomic integration; (2) weak linkages between breeding programs and seed production chains; (3) low participation of the private sector in applied breeding; (4) insufficient digital infrastructure for data-driven selection; and (5) slow varietal turnover and limited farmer adoption of new cultivars. Strategic priorities for applied research include: expansion of MAS and genomic selection into routine breeding workflows; development of regional breeding programs tailored to agroecological zones; strengthening public-private partnerships in variety commercialization; investment in digital breeding platforms and decision-support systems; and alignment of breeding objectives with farmer needs and market demand.

Prospects and Strategic Directions for 2025-2030

The period 2025-2030 is a crucial phase for modernizing plant genetics and breeding in Kazakhstan. Global agricultural innovation is increasingly driven by genomics-enabled breeding pipelines that integrate high-density genotyping, phenomics, predictive modeling, and digital decision-support systems (Hickey et al., 2017; Crossa et al., 2017). Countries that have successfully accelerated genetic gain have transitioned from phenotype-dominant selection to genomics-assisted and genomic selection (GS) frameworks (Anilkumar et al., 2022). For Kazakhstan, a strategic priority is the gradual scaling of marker-assisted selection (MAS) toward routine implementation of genome-wide selection across priority crops. Establishing national SNP genotyping platforms and centralized bioinformatics hubs would significantly enhance breeding efficiency. Achieving this transition requires coordinated investments in laboratory infrastructure, high-throughput sequencing capacity, and computational resources. Importantly, modernization should prioritize crops critical to national food security and export potential, including wheat, barley, oilseeds, and forage crops.

Projected climate variability in Central Asia necessitates breeding strategies centered on resilience to drought, heat stress, salinity, and emerging pathogens (IPCC, 2021). Future breeding programs must incorporate climate modeling, genotype-environment (G×E) interaction analyses, and multi-location trials under simulated stress conditions. Integration of high-throughput phenotyping tools, such as UAV-based imaging, spectral reflectance analysis, and automated stress diagnostics, will allow more precise evaluation of adaptive traits (Araus et al., 2018). By 2030, Kazakhstan's breeding system should aim to shift from reactive selection (responding to observed stress) to predictive breeding frameworks that anticipate climate scenarios and incorporate long-term resilience metrics.

Between 2025 and 2030, Kazakhstan's strategic priorities for the seed system should include: (1) enhancing breeder-foundation-certified seed linkages; (2) expanding elite seed production capacity; (3) implementing digital traceability platforms for seed quality control; and (4) increasing private-sector participation in seed commercialization. Reducing dependence on imported seeds will require targeted investments in breeding and accelerated release pipelines.

One of the most critical determinants of long-term competitiveness is research intensity. Kazakhstan's R&D expenditure (~0.14% of GDP) remains substantially below that of Russia (~0.9%), China (~2.6%), and the EU (~2.24%) (World Bank, 2025; Eurostat, 2025). Strategic directions for 2025-2030 should therefore include: (1) gradual increase of GERD toward at least 1% of GDP as a medium-term target; (2) establishment of competitive grant programs focused on plant genomics and breeding innovation; (3) support for interdisciplinary research combining genetics, data science, and agronomy; and (4) expansion of doctoral and postdoctoral training programs in plant genomics and quantitative genetics.

Modern breeding innovation operates within transnational research networks. Participation in international genomic consortia, germplasm exchange programs, and collaborative breeding initiatives accelerates knowledge transfer and reduces technological isolation (Hickey et al., 2019). For Kazakhstan, strategic international partnerships with leading research centers in Europe and Asia could facilitate access to advanced breeding technologies, shared databases, and training opportunities. Between 2025 and 2030, Kazakhstan's breeding system should evolve from a nationally oriented structure to a regionally influential, internationally connected innovation ecosystem.

By 2030, an effective plant breeding system in Kazakhstan would ideally exhibit the following characteristics: (1) routine application of genomic selection in major crops; (2) integrated national germplasm databases with genomic passportization; (3) digitalized breeding pipelines linking field phenotyping with predictive analytics; (4) balanced public-private participation in seed production; (5) sustainable funding mechanisms supporting fundamental and applied research; and (6) renewed human capital with strong quantitative and bioinformatic competencies. Such a transformation would not only increase varietal productivity but also enhance resilience to climate stress and reduce reliance on external seed markets.

Conclusion

This review demonstrates that Kazakhstan possesses a substantial scientific and institutional foundation in plant genetics and breeding, yet its potential remains constrained by structural, financial, and demographic limitations. The gap between classical breeding approaches and modern genomics-enabled systems represents the central challenge for the coming decade. Sustainable progress through 2030 will require the systemic integration of fundamental and applied research, modernization of breeding pipelines, strengthening of seed systems, and a significant increase in research investment. International experience indicates that incremental reforms are insufficient; only coordinated transformation across the entire innovation chain can ensure long-term competitiveness.

The modernization of plant genetics and breeding in Kazakhstan during 2025-2030 requires systemic transformation rather than incremental adjustments. Transitioning to genomics-driven breeding, strengthening seed systems, increasing research investment, and integrating into international networks constitute interconnected pillars of sustainable development. If successfully implemented, the outlined strategic directions will enhance agricultural resilience, reduce dependence on imported seeds, and position Kazakhstan as a regionally influential player in plant breeding and agri-biotechnology.

Chapter 2: Genetics and Breeding of Cereal and Legume Crops in Kazakhstan: Development Prospects and a Forecast of Priority Directions (2026-2035)

Kazakhstan is a major wheat-exporting country and is rapidly expanding pulse crop production, creating strong incentives to modernize crop genetics and breeding to support yield stability, grain quality, and resilience to abiotic and biotic stresses. Wheat still dominates the arable area, while pulses (pea, lentil, chickpea) are gaining importance due to market demand and crop-rotation benefits. At the same time, increasing climate variability and recurrent drought risk constrain productivity and raise the value of drought tolerance, heat tolerance, and durable disease resistance. This review synthesizes the current state of genomics-enabled breeding in Kazakhstan with emphasis on wheat, barley, rice, soybean, and chickpea, drawing on recent association mapping studies, genetic diversity analyses, and collaborative multi-location testing networks, including the Kazakhstan-Siberia Network on Spring Wheat Improvement. A forward-looking forecast for 2026-2035 is presented, centered on multi-environment genomic prediction, marker-assisted and genomic selection pipelines, high-throughput phenotyping, and accelerated generation advance through controlled-environment protocols.

Production and Environmental Drivers Shaping Breeding Demand

The structure of Kazakhstan's agriculture strongly influences breeding demand, because breeding priorities must reflect both the dominant crop area and the economic incentives that shape adoption (Morgounov et al., 2024). Northern Kazakhstan remains the primary rainfed cereal region, where wheat occupies a large share of the sown area and is grown under conditions that are frequently moisture-limited and highly variable from year to year (Tajibayev et al., 2023).

Simultaneously, pulse crops are becoming increasingly important. Kazakhstan has strengthened its position as a producer and exporter of pulses, particularly lentils and peas, and the growth of these crops is reinforced by their rotation benefits in cereal-based systems (Zatybekov et al., 2025a). Pulses offer additional agronomic advantages through biological nitrogen fixation and diversification of pest and disease cycles, which can indirectly improve cereal performance in the rotation. From a breeding perspective, this expansion requires investment in locally adapted pulse varieties that match Kazakhstan's temperature regimes, daylength patterns, and terminal drought risks. A consistent feature across both cereals and pulses is year-to-year volatility. Official country monitoring systems frequently emphasize variability in cereal output linked to weather dynamics, and this volatility places strong selection pressure on breeding programs to prioritize stability and broad adaptation. The implication is clear: breeding success in Kazakhstan should be measured not only by potential yield in optimal seasons, but also by resilience and predictability of performance across a wide range of environmental conditions.

Kazakhstan's agriculture is broadly exposed to aridity and drought, and climate change intensifies the challenge of breeding. Multi-decade analyses of climate and yield relationships in Kazakhstan consistently point to warming, increased frequency of heat-stress events, and drought patterns that strongly influence wheat productivity (Genievskaya et al., 2022; Morgounov et al., 2024). Such trends shift the breeding target away from narrow adaptation and toward traits that confer resilience under stress combinations, including drought and heat. In practical breeding terms, this means that drought tolerance and heat tolerance must be addressed not as isolated traits, but as components of a broader adaptation strategy that includes optimized phenology, efficient use of available soil moisture, and maintenance of reproductive success under high temperature. Because drought and heat responses are strongly dependent on developmental stage, breeding efforts must also incorporate careful management of flowering time, grain-filling duration, and stress-avoidance phenotypes, such as early maturity, where appropriate.

Alongside abiotic stressors, wheat diseases remain a major constraint on productivity and varietal stability. Wheat rusts are particularly important, and both national and international disease surveillance emphasize the continuous evolution of rust populations and the risk of new virulence combinations (Malysheva et al., 2023; Genievskaya et al., 2022). Breeding strategies are increasingly focused on durable resistance combining adult-plant and quantitative resistance mechanisms (Morgounov et al., 2024). The long-term objective is to develop varieties that maintain stable resistance across years and locations, thereby reducing the likelihood of widespread susceptibility when new rust variants emerge.

Institutional and Network Foundations for Kazakhstan's Breeding System

Kazakhstan has established a public research infrastructure for genetics, breeding, and plant protection, providing a platform for modernizing crop improvement (Morgounov et al., 2024). The capacity to integrate molecular markers, evaluate resistance sources, and develop donor material for breeding programs is particularly valuable because disease resistance is among the most economically important targets for marker-guided improvement (Malysheva et al., 2023; Genievskaya et al., 2022). A representative example of genomics integration is the Institute of Plant Biology and Biotechnology, which reports active implementation of marker-assisted selection, rust resistance genetics, association mapping, and donor development, alongside germplasm curation and technical services (Genievskaya et al., 2022; Zatybekov et al., 2025b). Such institutional capability is crucial because sustained breeding modernization depends not only on individual research projects but also on stable service platforms that enable routine genotyping and data-supported selection within breeding pipelines.

International and regional collaboration is a critical multiplier of breeding capacity. The Kazakhstan-Siberia Network on Spring Wheat Improvement provides multi-location testing, germplasm exchange, and cooperative evaluation across Kazakhstan and neighboring regions (Morgounov et al., 2024). Such networks generate exactly the type of data required for modern breeding approaches: large, multi-environment datasets that capture variability in climate, soils, and disease pressure. From a strategic perspective, this network also represents a strong foundation for genomic prediction across environments. However, realizing that potential depends on standardized phenotyping, consistent trial management, coordinated genotyping, and shared data models. Without these components, the network's value remains primarily descriptive rather than predictive.

Case Wheat: Association Mapping, Rust Resistance, and Trait-Linked Markers

Wheat is the primary target for advanced breeding in Kazakhstan, and recent years show steady growth in the use of molecular and genomic tools. Studies increasingly employ genome-wide association studies and multi-environment analysis to identify marker-trait relationships for agronomic performance and disease resistance (Genievskaya et al., 2022; Malysheva et al., 2023; Morgounov et al., 2024). Work on durum wheat has similarly advanced, combining field performance evaluation with molecular characterization (Anuarbek et al., 2020; Tajibayev et al., 2023). Importantly, multiple studies have focused on rust resistance screening under Kazakhstan conditions and have demonstrated the practicality of linking resistance phenotypes to genetic markers for breeding.

Despite this progress, major drawbacks remain. The primary limitation is not the absence of scientific publications or marker discovery, but the incomplete integration of genomics into routine breeding decisions. The next step is to transform genotyping and marker application from an occasional, project-based activity into an operational component of every breeding cycle, including parental choice, early-generation selection, quality control, and variety identity verification.

Case Barley: Stress Resilience and Quality Genetics

Barley plays a significant role in Kazakhstan, supporting diversification and providing resilience in dryland systems. Genetic and physiological work relevant to Kazakhstan includes analyses of salinity responses and grain quality traits, as well as association mapping under stress conditions (Almerekova et al., 2021). Because barley often has smaller breeding populations than wheat and can be targeted to well-defined stress environments, it is well positioned to benefit from genomics-enabled breeding approaches. In particular, barley represents an attractive candidate for a second wave of genomic prediction initiatives, where training populations can be constructed with high-quality phenotypes under drought and salinity, enabling more efficient selection for stability and grain quality (Kushanova et al., 2023).

Case Rice: Salinity and Irrigated-System Traits

Rice breeding in Kazakhstan is strongly shaped by salinity in irrigated production areas. Studies that focus on selecting parental material and evaluating combining ability under salt stress align well with the needs of irrigated systems, where managed-stress screening can be implemented more consistently than in rainfed systems (Bataeva et al., 2017). Rice, therefore, offers an opportunity for relatively rapid progress through targeted deployment of salt tolerance loci and stable performance selection under field-relevant salinity regimes.

Case Soybean: Genomic Resources and Adaptation Breeding

Soybean is expanding in Kazakhstan, and a key enabling milestone is the availability of whole-genome resequencing analyses of Kazakhstan soybean accessions in a global context (Zatybekov et al., 2025). Such resources provide a strong foundation for haplotype-informed breeding and help define which genetic variants are present locally, which are missing, and which can be introduced through targeted crossing. Because soybean has a globally mature genomic toolkit and well-developed genetic resources, Kazakhstan can adopt advanced methods relatively quickly, provided that local adaptation targets (maturity, heat stress, drought risk, and irrigation response) are clearly defined.

Case Chickpea and Other Pulses: Diversity, Adaptation, and Market-Aligned Traits

Pulse crop research in Kazakhstan is expanding, including the characterization of local chickpea collections and practical selection work under conditions in southeast Kazakhstan (Zatybekov et al., 2025). The immediate breeding opportunity for pulses is to define locally adapted ideotypes that integrate maturity timing, heat and drought resilience, disease resistance, and seed quality traits aligned with market requirements (Zatybekov et al., 2025). Pulses also offer a strategic advantage for breeding modernization because their production expansion creates demand for varieties tailored to specific regions and export standards, encouraging faster adoption of new cultivars when they deliver clear economic benefits.

Priority Traits for Kazakhstan: A Breeding Target Map (2026-2035)

Across cereals and legumes, Kazakhstan's breeding priorities converge on a small set of high-value targets: stable yield under variable moisture and temperature, resistance to major diseases, and grain or seed quality traits demanded by processors and export markets. However, the trait emphasis differs by crop and production zone. Spring bread wheat in northern rainfed environments requires drought tolerance, heat tolerance, stable yield, grain quality, and durable resistance to rust diseases. Durum wheat breeding must combine yield with quality traits important for pasta markets, while also strengthening disease resistance. Barley improvement should focus on tolerance to drought and salinity while maintaining quality attributes relevant for feed and malting. Rice breeding priorities are dominated by salinity tolerance and stable productivity under irrigated management. Soybean improvement should emphasize adaptation to maturity, yield, protein and oil quality, and stress resilience. Pulses require integrated packages for drought and heat resilience, early maturity, disease resistance, and seed quality aligned with market classes.

Technology Forecast: What Will Matter Most

In the near term, the most realistic and cost-effective modernization pathway is broad deployment of marker-assisted selection. Marker-assisted selection is particularly effective for traits controlled by major genes or well-characterized genomic regions, including many disease resistance genes and certain quality traits. In Kazakhstan, where wheat disease resistance has strong institutional support, marker-assisted selection can deliver immediate gains by improving the efficiency of gene pyramiding, enabling early-generation selection, and reducing reliance on late-stage phenotyping alone (Morgounov et al., 2024). Priority actions include standardizing trait-linked marker panels for key resistance and quality targets, and establishing quality control protocols for marker-based seed purity testing and variety identity verification. These steps connect genomics directly to the seed system and adoption pipeline, where economic impact is realized.

Genomic selection is increasingly recognized as a major driver of accelerated genetic gain because it allows selection on genomic estimated breeding values rather than waiting for complete multi-year phenotyping (Crossa et al., 2017). For Kazakhstan, the most valuable application is multi-environment prediction: selecting lines that are likely to be stable across varying rainfall and temperature conditions. A practical implementation pathway begins with wheat and barley training populations anchored in multi-location testing networks, where historical data and new standardized phenotyping can be combined. Sparse testing strategies, in which not all lines are tested across all environments, can reduce field costs while expanding the number of genotypes evaluated through prediction.

Accelerated generation advance through controlled-environment protocols can reduce breeding cycle length by enabling multiple generations per year (Watson et al., 2018; Ghosh et al., 2018). This approach is especially valuable when the breeding cycle time is a binding constraint on genetic gain. In Kazakhstan, the most effective strategy is to combine accelerated generation advance with marker-assisted selection and genomic prediction, thereby increasing both selection intensity and cycle speed while maintaining field validation in target environments. As crop genomics moves from single-reference genomes to pangenomes that capture broader species diversity, breeding can increasingly focus on haplotypes and structural variation relevant to adaptation and disease resistance (Tiwari et al., 2024). This trend is particularly important for wheat and barley, where structural variation can strongly affect agronomic traits. Kazakhstan can leverage this shift by expanding local resequencing efforts and connecting them to phenotypic data, enabling more informed parental selection and introgression strategies based on haplotype composition rather than single-marker selection alone.

System Bottlenecks and Make-or-Break Enablers

Genomic methods cannot outperform poor phenotyping. Kazakhstan's modernization will therefore depend on improved phenotyping capacity across environments, including managed-stress screening sites for drought, heat, and salinity. Equally important is harmonizing protocols, including growth-stage definitions, trait-measurement standards, and disease-scoring systems. Data interoperability requires databases that ensure findability, accessibility, interoperability, and reusability through consistent metadata and curation practices, but these systems must remain practical and usable for breeders. Genetic progress has a limited impact if improved varieties are not multiplied, certified, and adopted at scale. Strengthening seed multiplication, certification, and traceability is essential, and marker-based purity testing can support reliable variety identity throughout the seed chain. Breeding targets must also align with end-use requirements, including grain protein and gluten-related traits for wheat and market-class traits for pulses, to ensure that new varieties deliver economic value that motivates adoption. High-performing breeding pipelines require integrated teams that include breeders, quantitative geneticists, molecular biologists, plant pathologists, agronomists, and data specialists. Kazakhstan already has specialized competence in wheat disease genetics and marker-assisted selection; scaling advanced breeding approaches requires sustained training and stable platforms that connect genotyping, phenotyping, and decision support.

A Practical Roadmap for Kazakhstan (2026-2035)

Phase I (2026-2028): Consolidate and Standardize

The first phase should focus on practical standardization. This includes national marker panels for cereals and legume disease resistance and key quality targets, applied routinely in breeding cycles. It also includes establishing reference phenotyping corridors representing the main target environments, such as northern rainfed cereal zones, southeastern cropping systems, and salinity-affected irrigated zones. Finally, shared training populations should be built for wheat, barley, and at least one pulse crop to enable early genomic prediction efforts.

Phase II (2028-2031): Scale Prediction and Accelerate Cycles

The second phase should scale genomic prediction in major cereal species, emphasizing multi-environment modeling and yield stability. At the same time, accelerated generation advance should be integrated into pre-breeding and early-generation selection to shorten cycle time, while maintaining rigorous field validation in representative environments.

Phase III (2031-2035): Precision Breeding and New Trait Frontiers

The third phase should expand haplotype-informed selection enabled by resequencing and pangenome resources, strengthening parental selection and introgression design. Speed breeding technology can become increasingly relevant for trait validation and potentially cultivar development, contingent on regulatory and market dynamics. Pulses should be expanded as climate-smart rotation crops supported by locally adapted varieties that deliver stable performance and consistent market quality.

Conclusions

Kazakhstan has strong scientific foundations in cereal and legume breeding, particularly in wheat adaptation and disease resistance. However, the decisive factor for 2026-2035 will be whether these foundations are integrated into operational breeding systems that combine high-quality phenotyping, routine genotyping, accelerated generation turnover, and predictive modeling across environments. A transition toward data-intensive breeding, supported by standardized trials, interoperable databases, strengthened seed systems, and multidisciplinary human capital, can significantly improve yield stability, stress resilience, and product quality in cereals and pulses. If responsible organizations successfully implement these enabling steps, they can increase genetic gain per unit time and strengthen competitiveness in global grain and pulse markets under increasing climate uncertainty. Recent Kazakhstan-focused GWAS and diversity studies in wheat, barley, chickpea, and soybean demonstrate that the scientific foundation is already in place. The decisive next step is operational: building interoperable phenotyping networks, scaling MAS and GS inside real breeding cycles, accelerating generation turnover via speed breeding, and preparing for pangenome/haplotype breeding. If these enablers are addressed, the 2026-2035 period can deliver substantial improvements in yield stability, stress resilience, and product quality for both staple cereals and rapidly growing pulse sectors.

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