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The Landscape of Genetic and Breeding Research in Kazakhstan: Insights from the 1st KOGiS Conference

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Abstract

The 1st Conference of the Kazakhstan Society of Geneticists and Breeders (KOGiS 2026), held at Semey Medical University from May 13 to 15, 2026, was a historical milestone in consolidating the nation's scientific potential across diverse biological disciplines. This review synthesizes the key scientific achievements, cross-disciplinary methodologies, and strategic resolutions presented across the four core sectors of the conference: human genetics, animal genetics and breeding, plant genetics and breeding, and microorganism genetics and breeding. In medical genomics, the focus centered on high-throughput sequencing to decode the genetic architecture of multifactorial and orphan diseases within the Kazakh population, driving progress in personalized medicine. In the agricultural sectors, presentations underscored the urgent transition from classic phenotypes to precision breeding. Livestock research highlighted genomic selection strategies to enhance productive traits while preserving the genetic diversity of native breeds. Plant genetics discussions addressed global climate shifts through marker-assisted selection, genome-wide association studies, and speed breeding technologies essential for ensuring regional food security. Complementing these areas, microbial genetics showcased innovative biocontrol agents, surveillance of phytopathogen strains, and industrial biotechnology solutions. By bridging fundamental omics technologies with translational clinical and field practices, this review outlines a unified roadmap for modernizing Kazakhstan's scientific infrastructure, fostering younger research cohorts, and strengthening international collaborations to address priority tasks in global biosecurity and sustainable development.

1. Introduction

The rapid evolution of post-genomic technologies, high-throughput sequencing, and computational biology has fundamentally transformed the landscape of modern life sciences, erasing the traditional boundaries between medical, agricultural, and industrial disciplines. In the 21st century, genetic security, biodiversity conservation, and precision biotechnology have emerged as core directions of national strategic development and public health management. For Kazakhstan a nation characterized by vast ecological diversity, a critical agricultural sector, and unique demographic and genetic architectures the institutionalization of genetic research has become a matter of growing strategic importance.

A historic landmark in this journey was the formal assembly of the 1st Conference of the Republican Public Association "Kazakhstan Society of Geneticists and Breeders" (ROO KOGiS), held from May 13 to 15, 2026, at Semey Medical University (Semey, Kazakhstan). Historically, genetic research in Kazakhstan developed within relatively isolated institutional groups, separating medical academies under the Ministry of Healthcare from agricultural research stations and academic institutes operating under the Ministry of Science and Higher Education. However, modern global crises - shifting climatic patterns in the Central Asian grain belt, the emergence of transboundary phytopathogens and zoonotic diseases, and the global push toward personalized healthcare - require a unified response. The KOGiS 2026 conference directly addressed this fragmented landscape by structuring its scientific program into four interconnected fields: Human Genetics and Medical Genomics; Animal Genetics and Breeding; Plant Genetics and Breeding; and Microorganism Genetics and Industrial Biotechnology.

This review provides a comprehensive synthesis of the key scientific discoveries, methodology updates, and strategic resolutions formulated during this landmark event. It emphasizes the urgent transition from classic, labor-intensive phenotypic observations to data-driven precision genomics, marker-assisted selection (MAS), and targeted gene-editing frameworks, and outlines systemic approaches to professional development of the younger generation of scientists, modernization of state-funded biobanking infrastructure, and expansion of multilateral international collaborations.

2. Human Genetics and Medical Genomics

The KOGiS conference, hosted at Semey Medical University, naturally positioned medical genomics and human genetics as central themes of the scientific agenda. Healthcare in Kazakhstan has initiated a paradigm shift from generalized therapeutic protocols toward predictive, preventive, and personalized medicine (PPM). The presentations clearly demonstrated that the successful implementation of PPM depends on two interdependent elements: the deep genetic characterization of the local population and the establishment of a robust digital infrastructure for multi-omics data.

A primary focal point was the ongoing effort to comprehensively sequence, assemble, and analyze the Kazakh reference genome. Given the unique historical ethnogenesis of the Kazakh population - characterized by extensive admixture and specific demographic histories - reliance on Western or East Asian reference panels often limits the accuracy of clinical variant interpretation. Mapping the unique genomic architecture of the Kazakh population, including population-specific single-nucleotide polymorphisms (SNPs) and structural variants, is critical for improving polygenic risk scores (PRS) and enhancing the detection of mutations associated with hereditary, oncological, and rare (orphan) diseases.

The session emphasized the urgent necessity for structured documentation of genomic results in centralized national databases, transitioning from fragmented lab-specific storage toward a unified national biorepository integrating clinical phenotypes with raw genomic files (FASTQ/BAM/VCF) while complying with strict ethical standards and patient confidentiality protocols. A substantial part of the discussion focused on high-performance bioinformatic analysis of Big Data, utilizing cloud computing, parallelized alignment algorithms, and machine-learning frameworks to identify genomic biomarkers for multifactorial disorders prevalent in the region, such as cardiovascular diseases, type 2 diabetes, and metabolic syndromes. The consensus was clear: building local bioinformatic capacity and training a new cohort of computational biologists are essential prerequisites for translating genomic Big Data into actionable clinical decisions in Kazakhstan.

3. Animal Genetics and Breeding

The livestock sector occupies a central position in Kazakhstan's agricultural economy, contributing significantly to rural livelihoods and food security. The KOGiS 2026 session on animal genetics reflected a decisive shift away from traditional, subjective phenotypic selection toward evidence-based genomic breeding. The core technological approach highlighted across presentations was Genomic Estimated Breeding Values (GEBVs): a framework that integrates dense SNP genotyping arrays with statistical mixed-model predictions to assign genomic merit scores to individual animals, enabling the early identification of elite producers before costly phenotypic testing is completed.

A particularly promising development discussed was the design and validation of cost-effective,

Kazakhstan-specific SNP panels tailored for the primary livestock species of national importance: cattle (Kazakh Whiteheaded and Auliekol breeds), sheep (Edilbaev, Kazakh fine-wooled), and horses (Kazakh breed). Rather than relying on imported commercial panels optimized for Western European breeds, researchers advocated for population-specific panels containing 15,000–50,000 informative SNPs - sufficient for high-accuracy GEBV computation at substantially reduced genotyping costs. These locally calibrated panels are designed to capture breed-specific linkage disequilibrium patterns and structural haplotypes absent from international platforms, thereby improving prediction accuracy for economically relevant production traits such as milk fat and protein composition, average daily gain, disease resistance, and reproductive efficiency.

The sessions also dedicated substantial attention to the conservation and molecular passportization of

Kazakhstan's indigenous livestock breeds. Native breeds such as the Kazakh horse, Edilbaev sheep, and Kazakh Whiteheaded cattle represent unique, centuries-evolved genetic repositories shaped by extreme continental climates and traditional nomadic management systems. Molecular passportization using microsatellite markers and SNP panels enables precise documentation of breed identities, ancestry coefficients, and inbreeding levels - critical information for maintaining optimal effective population sizes and establishing protected gene pools. Discussions emphasized the urgent need to establish a unified National Livestock Genetic Database integrating pedigree records, genomic profiles, phenotypic measurements, and veterinary health data, which would serve as the foundational infrastructure for national-scale genomic selection programs.

4. Plant Genetics and Breeding

As a leading wheat-exporting nation, Kazakhstan's agricultural stability is directly linked to the continuous improvement of its crop germplasm. The plant genetics and breeding sessions at KOGiS 2026 underscored a paradigm transformation: the integration of Genome-Wide Association Studies (GWAS) and Marker-Assisted Selection (MAS) into mainstream breeding programs is no longer an experimental luxury but an operational necessity. Researchers across multiple institutions reported successful mapping of QTLs (quantitative trait loci) governing drought tolerance, salt stress resistance, yield potential, and pathogen resistance in wheat, barley, millet, and sunflower cultivars.

Among the most critical biotic stress threats, presentations focused extensively on three major wheat pathogens currently challenging Central Asian grain production: *Puccinia graminis* (stem rust), *Puccinia striiformis* (stripe/yellow rust), and *Zymoseptoria tritici* (Septoria tritici blotch). The emergence of new virulent races of

Puccinia spp. - including races capable of overcoming previously durable resistance genes such as *Sr31* and *Sr38* - has intensified the need for continuous genomic surveillance and the stacking of multiple resistance loci. Delegates proposed accelerating the development of cultivars with pyramided resistance genes identified by molecular markers, combined with field screening under local agroclimatic conditions to ensure durable, broad-spectrum resistance.

One of the most technically innovative highlights of the plant genetics sessions was the comprehensive review of Speed Breeding (SB) technology and its implementation in Kazakhstani research stations. Unlike conventional breeding cycles spanning 7–10 years per variety, Speed Breeding exploits controlled photoperiod extension (20–22 hours of light per day), optimized temperature gradients, and early seed harvest protocols to complete 5–6 generations per year. For self-pollinating crops such as wheat, barley, and chickpea, this acceleration shortens a full breeding cycle from the standard 10 years to approximately 4–6 years - a transformative gain for national food security programming. Participants emphasized that combining Speed Breeding with GWAS-identified favorable alleles and high-throughput phenotyping platforms creates a highly efficient pipeline for developing climate-resilient, high-yielding varieties at unprecedented speed. The session also highlighted the establishment of the

National Genetic Bank of Kazakhstan, which consolidates and preserves the country's vast landraces and wild relative germplasm as the raw genetic diversity essential for future breeding programs.

5. Microorganism Genetics and Industrial Biotechnology

The microorganism genetics track at KOGiS 2026 presented some of the most immediately translational work of the conference, spanning three interconnected domains: antimicrobial resistance (AMR) surveillance, biological crop protection, and industrial strain engineering. A central methodological theme across all presentations was the deployment of Whole Genome Sequencing (WGS) as the gold standard for microbial characterization - enabling simultaneous identification of species, resistance gene profiles, virulence factors, and horizontal gene transfer events in a single analytical workflow.

In the context of AMR surveillance, presentations reported on WGS-based monitoring programs targeting priority zoonotic and agricultural pathogens, specifically *Brucella* spp. and *Salmonella* spp. - organisms of significant public health importance in Kazakhstan due to the country's extensive livestock sector and semi-arid ecological context. WGS analysis allows tracking of transmission chains, identification of resistance determinants (including *bla* beta-lactamase genes, plasmid-mediated colistin resistance genes *mcr*), and rapid outbreak source attribution. Participants called for systematic integration of WGS surveillance data into the national One Health framework, connecting veterinary, agricultural, and public health monitoring systems for a unified epidemiological response.

The biocontrol segment of the microbiology sessions attracted considerable interest, with multiple research teams presenting results on plant-growth promoting rhizobacteria (PGPR) and fungal antagonists for sustainable crop protection. Key organisms under active development include *Bacillus subtilis* and *B. amyloliquefaciens* strains producing antifungal lipopeptides (iturin, fengycin, surfactin), *Pseudomonas fluorescens* strains synthesizing 2,4-diacetylphloroglucinol (DAPG) and siderophores, and *Trichoderma harzianum* and *T. asperellum* strains as mycoparasites of soil-borne fungal pathogens. Genomic characterization of these strains allows precise annotation of biosynthetic gene clusters and facilitates targeted strain improvement via adaptive laboratory evolution or metabolic engineering. The industrial biotechnology subsection covered the optimization of microbial strains for fermentation-based food processing, bioremediation of heavy metal-contaminated soils (cadmium, lead, arsenic), and biodegradation of petroleum hydrocarbons in contaminated arid steppe soils - a pressing environmental challenge across Kazakhstan's oil-producing regions.

6. Discussion

The KOGiS 2026 conference collectively revealed that Kazakhstan's genetic and breeding research ecosystem has reached a pivotal juncture: the scientific infrastructure, human capital, and institutional will to integrate genomics into applied practice are measurably growing, yet significant structural gaps between fundamental discoveries and their commercial realization remain. A recurring theme across all four scientific tracks was the insufficient integration between academic research outputs and the commercial sector - a gap that KOGiS uniquely positioned itself to bridge by bringing together scientists, breeders, clinicians, and industry stakeholders under a single interdisciplinary umbrella.

Beyond the domain-specific insights, KOGiS 2026 highlighted several overarching systemic priorities: the urgent need to develop a national bioethics framework governing genomic data sovereignty and consent management; the necessity of establishing a network of certified genomic core facilities accessible to researchers at all institutional levels; and the critical importance of expanding international partnerships - particularly with CGIAR centers, FAO genomics programs, and European research consortia - to accelerate technology transfer and joint publication outputs. The conference also emphasized the foundational role of post-graduate education reform in building the next generation of bioinformaticians, genomicists, and computational breeders - specialists currently in critically short supply across Kazakhstan's research landscape.

Table 1. Maps the four scientific domains of KOGiS 2026 to their most strategically relevant commercial partners and the primary translational outputs expected from each domain.

Table 1. Mapping of KOGiS 2026 scientific domains to commercial partners and translational outputs.

Scientific Domain	Target Commercial Partners	Practical Translational Output
Human Genetics	Private healthcare, pharma, diagnostics	Diagnostic test kits, biobank pipelines, clinical genomic panels
Animal Genetics	Livestock holdings, dairy enterprises, breeding companies	GEBV programs, elite sire networks, breed passportization services
Plant Genetics	Seed firms, grain exporters, farming cooperatives	Climate-resilient cultivars, speed-bred lines, certified seed lots
Microbial Genetics	Biopesticide manufacturers, biorefineries, food technology companies	Bio-stimulants, microbial consortia products, industrial enzyme portfolios

7. Conclusion

The 1st KOGiS Conference in Semey, 2026, marked a transformative milestone for Kazakhstan's scientific community. By unifying human medical genomics, animal and plant breeding sciences, and microbial biotechnology under a single interdisciplinary platform, KOGiS has established itself as the primary national forum for coordinating genomic research priorities, sharing methodological innovations, and fostering science-to-business translation. The four scientific tracks collectively demonstrated that Kazakhstan possesses both the intellectual capacity and the institutional motivation to transition from phenotypic to precision genomic practices across all strategic biological sectors.

The strategic resolutions adopted at KOGiS 2026 outline a clear roadmap: the creation of a unified national multi-omics biorepository, the expansion of locally validated genotyping panels across all major livestock and crop species, the nationwide deployment of Speed Breeding infrastructure, and the integration of WGS-based AMR surveillance into the One Health framework. These initiatives, if supported by sustained governmental investment and international scientific partnerships, position Kazakhstan to emerge as a regional leader in applied genomics within the Central Asian scientific landscape.

The 2nd KOGiS Conference is scheduled for September 2027 at Zhangir Khan West Kazakhstan Agrarian-Technical University (Uralsk, Kazakhstan), where the scientific community will review progress made against these resolutions and advance the next generation of cross-disciplinary genomic initiatives. KOGiS thus stands not only as a conference but as an evolving institution - a catalyst for the long-term transformation of Kazakhstan's genetic research infrastructure into a globally competitive, nationally impactful scientific enterprise.

Data & Code Availability

No primary research datasets or custom code were generated in the preparation of this review article.

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Author Contributions

Y.T.: Conceptualization, writing - original draft, writing - review & editing.

Ethics Statement

This article is a review of presented conference proceedings. No human participants, patient data, or animal subjects were involved in the preparation of this manuscript.

Competing Interests

The author declares no competing interests.

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