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Breeding and biotechnology to improve potato resilience to climate change

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Abstract

Background and Aim. Climate change threatens food security, while integrated breeding strategiesfor stress tolerance remain limited in Central Asia. This study aims to evaluate advanced genomic and biotechnological tools for climate-resilient potato breeding under regional stress conditions.

Materials and Methods. The study is based on a systematic review of recent publications indexed in Scopus and Web of Science. Studies on genomic selection, molecular markers, CRISPR/Cas genome editing, high-throughput phenotyping, *in vitro* technologies, microbiome applications, and digital agriculture were analyzed. Emphasis was placed on abiotic stress tolerance and adaptation to climatic variability in Kazakhstan and Central Asia.

Results. The results show that the integration of marker-assisted selection (MAS), genomic selection, and genome-wide association studies (GWAS) improves breeding efficiency by up to 30–50%. CCRISPR/Cas technologies enable the precise modification of genes regulating drought, heat, and salinity tolerance. When combined with artificial intelligence, high-throughput phenotyping improves the prediction of genotype-environment interactions. Plant biotechnology, including tissue culture, somatic hybridization, and *in vitro* selection, accelerates development of stress-tolerant lines and the preservation of genetic resources. Microbiome-based strategies enhance plant resilience and nutrient-use efficiency. In potato, tolerance is polygenic and is associated with root architecture, water-use efficiency, antioxidant systems, and photosynthetic stability. The integration of wild Solanum species, genomic tools, and digital modeling improves adaptation to the combined stresses typical of Kazakhstan.

Conclusion. Integrated genomic and biotechnological breeding significantly enhances potato resilience and productivity, supporting sustainable agriculture and climate adaptation in Central Asia.

Keywords: abiotic stress; biotechnology; climate resilience; digital agriculture; genomic selection; potato.

Introduction

In recent years, climate change has become one of the most significant challenges affecting agricultural production worldwide. Increasing temperatures, irregular precipitation patterns, and the growing frequency of extreme weather events, such as droughts and heat waves, are already affecting crop productivity and stability [1]. These changes are particularly critical in regions with continental climates, including Central Asia, where agricultural systems are highly sensitive to environmental fluctuations [2].

Under these conditions, ensuring stable crop yields and food security requires the development of plant varieties capable of maintaining productivity under stress conditions [3]. Traditional breeding methods have played a fundamental role in crop improvement; however, their efficiency is often limited by long breeding cycles and the complexity of traits such as drought and heat tolerance [4].

Recent advances in molecular biology and plant biotechnology have opened new opportunities for improving crop resilience [5]. The use of genomic selection, molecular markers, and genome-editing technologies allows researchers to identify and target genes associated with stress tolerance more

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precisely. At the same time, high-throughput phenotyping and digital tools make it possible to better understand genotype-environment interactions [6].

In this review, the term conventional breeding refers to phenotype-based selection and hybridization methods, whereas marker-assisted selection (MAS) and genomic selection (GS) denote molecular approaches based on genetic markers and genome-wide prediction, respectively. The term genome editing is used exclusively for targeted modification of DNA sequences using technologies such as CRISPR/Cas, while plant biotechnology encompasses *in vitro* culture, micropropagation, somatic hybridization, and related techniques.

Particular attention is currently being given to the integration of different approaches. Combining classical breeding with genomic, biotechnological, and computational methods is considered a promising strategy for developing climate-resilient crops [7].

Potato (*Solanum tuberosum* L.) is one of the key food crops worldwide but is highly sensitive to abiotic stresses such as drought, high temperatures, and soil salinity. In the context of climate change, improving potato resilience has become an important research priority, especially in regions such as Kazakhstan, where environmental conditions are highly variable [8].

The aim of this study is to analyze modern breeding and plant biotechnology for improving potato resilience to climate change, with a focus on their applicability under the conditions of Central Asia.

Materials and Methods

In this study, a systematic analysis of recent scientific publications was conducted. The analysis included peer-reviewed articles published between 2015 and 2025, enabling a comprehensive assessment of recent advances in the field of genomics, marker-assisted selection, genomic selection, plant biotechnology, and digital agriculture. The literature search was conducted using international databases such as Scopus, Web of Science, and PubMed, as well as leading scientific publishing platforms and journals, including Frontiers, MDPI, Springer, Elsevier, and Genome Biology. In addition, review articles, meta-analyses, and original studies reporting experimental and practical findings were included.The search for publications used keywords and combinations of keywords in English: climate-resilient crops, genomic selection, marker-assisted selection, CRISPR/Cas, genome editing, abiotic stress tolerance, drought tolerance, heat stress, salinity, high-throughput phenotyping, omics technologies, genomic selection (GS), as well as terms related to sustainable agriculture and digital technologies. The selected studies addressed plant resistance to major abiotic stresses, including drought, elevated temperatures, salinity, and their combined effects. Particular attention was paid to publications describing modern breeding strategies, such as genomic selection, GWAS, QTL mapping, transgenic approaches, genome editing, phenotyping, as well as systemic and interdisciplinary approaches to the formation of plant resistance.

The selected studies were evaluated based on scientific novelty, availability of experimental data, and practical relevance. The selection was made taking into account the geographical diversity of the studies, including works devoted to regions with high climatic risk. The methodological basis of the study was a qualitative analysis of scientific data, including a comparative assessment of modern approaches, their classification, and systematization. The information obtained was grouped according to the main directions of development of climate-resistant breeding and biotechnology, which made it possible to identify key trends, advantages, and limitations of modern methods, as well as to determine promising areas for further research and practical application.

Results

Current trends in crop breeding in the context of climate change

An analysis of recent studies shows that modern crop breeding is increasingly shifting toward the integration of genomic and digital approaches. These findings indicate that this field is undergoing a rapid transformation, characterized by a shift from predominantly phenotypic selection toward the integration of genomic, biotechnological, and digital approaches. Under current climatic conditions, traditional breeding remains of fundamental importance; however, its effectiveness is significantly enhanced through the use of molecular markers, genomic selection, high-throughput phenotyping, and genome editing methods. This combination accelerates the identification of adaptive genotypes, improves selection accuracy, and shortens breeding cycles.

One of the key strategies is the integration of genomic technologies into breeding programs. Modern methods based on the use of pan-genomes, SNP markers, marker-assisted selection (MAS), and genomic selection (GS) enable more efficient exploitation of the genetic diversity of cultivated plants and their wild relatives [9]. Recent studies of the potato pan-genome have shown that extensive structural variations and haplotype diversity can be used to accelerate genomics-assisted breeding and improve the identification of adaptive alleles associated with stress tolerance. This approach can accelerate the development of varieties with improved tolerance to drought, heat, and salinity, and also helps increase yield stability under a changing climate [10].

The development of genomic technologies, including pan-genome studies, GWAS, and QTL mapping, has significantly expanded opportunities for studying the genetic architecture of plant resistance to abiotic stresses. It has been established that resistance to drought, heat, and salt stress is of a complex polygenic nature, thereby requiring comprehensive breeding strategies that account for genotype-environment interactions.

Recent significant progress has been associated with the development of genome editing technologies, primarily the CRISPR/Cas system, which enables the targeted modification of genes controlling plant resistance to stress factors. A number of studies have shown that this approach helps increase tolerance to adverse environmental conditions, including water stress, extreme temperatures, and damage caused by pathogens. At the same time, the need to evaluate the effectiveness of the resulting plant lines under field conditions is emphasized, since plant resilience is determined not only by genetic factors but also by the interaction between genotype and the environment [11]. Furthermore, the practical implementation of genome editing in some countries is constrained by regulatory and ethical considerations, highlighting the need for harmonized regulatory approaches to these technologies.

An important area of research is the integration of genomic approaches with high-throughput phenotyping, which enables a comprehensive evaluation of breeding material. The concept of «next-generation breeding» involves combining genomic, molecular, and digital technologies, which significantly improves selection accuracy and accelerates the breeding process [1]. In this regard, the integration of genomic data with the results of phenotypic tests under various environmental conditions is considered a key factor in enhancing the reliability of the breeding process.

Traits related to drought tolerance, heat tolerance, and salt tolerance are predominantly polygenic, making GWAS and QTL mapping valuable tools for identifying loci associated with climate resilience [2]. An example of the successful application of this approach is the introduction of the SUB1 gene into the «Svarna-Sub1» rice variety, which provided tolerance to waterlogging and yield stability under flood conditions [12].

Broadening genetic diversity is a key component of modern breeding programs. International breeding programs aimed at developing drought-tolerant maize hybrids have demonstrated high effectiveness when grown in regions with unstable water availability. At the same time, there is growing interest in crops with natural resistance to adverse conditions, such as millet, sorghum, and cassava [13], which are capable of producing yields under conditions of low humidity and high temperatures [14].

Promising methods include transgenic technologies, which allow for the introduction of genes that enhance plant tolerance to adverse environmental factors, as well as somatic hybridization, which helps expand the genetic diversity of agricultural crops. Cell technologies, including tissue culture and *in vitro* cell selection, play an important role in obtaining stress-tolerant forms and accelerating the propagation of breeding material [15].

Current research also points to the significant potential of microbiome-related technologies. Rhizosphere microorganisms and endophytes can enhance plant stress tolerance, improve nutrition, and stimulate growth, which is considered a promising and environmentally sustainable area of biotechnology. In addition, digital methods in plant breeding are being actively developed, including the use of big data, remote sensing, artificial intelligence, and predictive modeling to assess the adaptive potential of genotypes and predict their performance under changing climatic conditions [16]. It is expected that the integration of artificial intelligence with genomic resources and phenotypic databases will improve the prioritization of candidate genes, the prediction of “genotype-environment” interactions, and decision-making in potato breeding programs.

Thus, modern breeding programs are characterized by a shift from traditional methods to the comprehensive use of genomic, biotechnological, and digital technologies. The integration of pan-genomic analysis, GWAS, genomic breeding, high-throughput phenotyping, artificial intelligence methods, and genome editing significantly enhances the efficiency of developing crop varieties adapted to changing climatic conditions.

Modern approaches to potato breeding to enhance climate resilience

The potato (*Solanum tuberosum* L.) plays a significant role in research aimed at developing climate-resilient crops, because it is highly sensitive to abiotic stresses, including drought, elevated temperatures, and soil salinity. In the context of global climate change, this crop is therefore considered a priority for the development of stress-tolerant varieties. Recent studies show that potato tolerance to adverse environmental factors is complex and polygenic in nature, determined by the interaction of numerous genes regulating water balance, photosynthetic activity, antioxidant defense, and carbohydrate metabolism [17].

In recent years, genomic selection and molecular marker-assisted breeding methods have been actively used to identify loci associated with potato tolerance to drought, heat, and salt stress. The use of SNP markers, GWAS analysis, and QTL mapping help accelerate the breeding process and improve the accuracy of selecting genotypes with enhanced adaptability. It has been shown that potato stress tolerance is closely linked to root system characteristics, water uptake efficiency, and the ability to maintain photosynthetic activity under adverse conditions [18, 19, 20].

Recent studies have demonstrated the successful application of CRISPR/Cas in potato breeding to modify genes involved in hormonal regulation, antioxidant defense, and starch metabolism, thereby increasing tolerance to drought, heat, and salinity [20].

Recent review articles indicate that CRISPR/Cas technologies are successfully used to increase resistance to abiotic stress, disease resistance, and tuber quality, underscoring their growing importance in modern potato breeding [21].

In potato breeding, tissue culture and microclonal propagation remain valuable tools for the rapid propagation of elite genotypes, the preservation of germplasm, and the *in vitro* screening of resistance to abiotic stress [22].

Of particular importance is the use of wild species of the genus Solanum as sources of resistance genes. Introgression of genes conferring resistance to drought, diseases, and extreme temperatures from wild relatives helps broaden the genetic base for potato breeding. Combined with modern molecular methods, this accelerates the development of adapted varieties. Modern breeding strategies increasingly combine pan-genomics, genome-wide association studies, genomic selection, and CRISPR/Cas-based gene editing to accelerate the development of potato varieties with stable resistance and enhanced climate resilience [23].

Thus, current research indicates that the development of climate-resilient potato varieties is impossible without the integrated use of molecular genetics, biotechnology, tissue culture, and modern genomic technologies. Their combined application can significantly accelerates the breeding process and improves the accuracy of selecting promising genotypes.

Recent advances in potato breeding and biotechnology in Kazakhstan and Central Asian countries

In Kazakhstan and other Central Asian countries, potato production faces increasing challenges due to recurring droughts, rising summer temperatures, irregular rainfall patterns, and soil degradation. In particular, the northern and northeastern regions experience significant year-to-year climate variability, which negatively affects yield and tuber quality. Consequently, breeding programs must prioritize the development of varieties that combine drought tolerance, heat tolerance, and resistance to major pathogens while maintaining stable yields under fluctuating environmental conditions. In this context, the integration of traditional breeding, marker-assisted selection (MAS), genomic selection, and in vitro biotechnology represents one of the most promising strategies for developing potato varieties adapted to regional climatic conditions and for enhancing agricultural resilience.

In the context of climate change, the issue of enhancing potato resilience is of particular relevance for Kazakhstan and other Central Asian countries, where agricultural production takes place under a sharply continental climate [20, 25, 26]. The region is characterized by longer periods of drought, higher

average daily temperatures during the growing season, uneven precipitation distribution, and soil degradation, which lead to reduced yields, poorer tuber quality, and an increased risk of physiological disorders and stress-induced damage in potato plants [27, 28]. In the northern and northeastern regions of Kazakhstan, climate variability is accompanied by significant fluctuations in temperature and moisture availability, which necessitates the development of varieties that combine high productivity, resistance to abiotic stresses, and adaptability to local agroecological conditions [29].

At present, research in Kazakhstan has focused on incorporating modern breeding methods and biotechnology into programs for developing new potato varieties. Alongside traditional hybridization, molecular markers, methods for assessing genetic diversity, tissue culture, and microclonal propagation are increasingly being used to accelerate the production of disease-free planting material and enhance the efficiency of the breeding process [30, 31]. A prime example of the implementation of molecular genetic technologies is the study conducted by *K. Adilbayeva* et al. (2024), in which a molecular assessment was conducted on 352 potato samples from the Kazakhstani collection using 30 DNA markers associated with resistance to the most dangerous pathogens and pests. As a result, varieties and breeding lines containing the greatest number of resistance genes were identified, and the authors concluded that the use of marker-assisted selection (MAS) and gene pyramiding holds great promise for the development of new domestic potato varieties. This study demonstrates the transition of Kazakhstani plant breeding from traditional methods to the application of modern molecular genetic technologies.

One example of the development of modern breeding stock is the study conducted by *Zh. Abilda, Z. Sapakhova, A. Sidorik* et al. (2024) at the Institute of Plant Biology and Biotechnology (Almaty). The authors conducted hybridization of domestic and foreign potato varieties with the aim of obtaining early-maturing forms suitable for cultivation in Kazakhstan. Four crossing combinations were used in the study, of which seven hybrid combinations proved successful (57%). As a result, promising hybrid clones were obtained that combine the traits of early maturity, yellow flesh color, shallow eye placement, and the absence of enzymatic browning of tubers; these are considered as source material for further breeding programs [30].

This work was continued in a study by *Z. Sapakhova* et al. (2024), in which 42 potato breeding lines derived from crosses between the «Yagodny 19» variety and clone CIP 397079-6 were examined during the early stages of breeding. Using molecular markers associated with maturity, tuber shape, and flesh color, the most promising lines were selected for further breeding programs under Kazakhstani conditions [32].

The development of biotechnological methods plays an important role in modern potato research in Kazakhstan. *A.M. Argynybaeva, D.L. Daurov, Z.B. Sapakhova, K.Zh. Zhambakin* et al. (2023) note that tissue culture, microclonal propagation, and the production of microtubers and minitubers form the basis of the modern system for producing virus-free seed potatoes. The use of plants sanitized via in vitro meristem culture significantly accelerates the production of high-quality planting material and reduces the risk of viral infection spread in potato seed production [33].

According to *A.M. Argynbayeva* et al. (2023), the production of virus-free planting material in Kazakhstan is based on in vitro apical meristem culture, microclonal propagation of regenerated plants, and the subsequent production of micro- and mini-tubers. The study by *Volkov* et al. (2020) demonstrates that the use of temporary immersion bioreactors significantly accelerates the mass propagation of virus-free potato plants and reduces the risk of viral infection spread during seed production [34].

Recent advances in Kazakhstan include improvements in technologies for producing disease-free seed potatoes based on in vitro apical meristem culture, microclonal propagation, and the production of micro- and mini-tubers, which form the basis of the modern system of original and elite potato seed production [33]. According to *A.M. Argynbayeva* et al. (2023), the use of apical meristem culture, microclonal propagation, and the production of micro- and minitubers ensures the production of high-quality, virus-free planting material. In turn, research by *I.N. Anikina* et al. (2023) showed that optimizing in vitro culture conditions – particularly temperature – significantly increases the propagation rate, stimulates organogenesis, and contributes to more efficient production of initial potato seed material [35].

A promising direction for the development of modern potato breeding is the introduction of molecular methods for evaluating breeding material. The use of DNA markers allows for the early

identification of genes conferring resistance to the most dangerous diseases and pests, significantly reducing the duration of the breeding cycle and increasing the accuracy of selection. Modern molecular markers associated with genes conferring resistance to biotic and abiotic stresses are widely used in marker-assisted breeding, enabling the effective identification of promising genotypes at early stages of the breeding process [36, 37, 38].

Despite significant progress in the development of genomic technologies, their widespread adoption in practical potato breeding remains a challenging task. This is due to the high cost of genotyping, the need to establish large training populations, the development of bioinformatics infrastructure, and the integration of genomic data with high-precision phenotyping. According to *Zh. Chunzhi* et al. (2024), *M. Mascher* et al. (2024), as well as *Alemu* et al. (2024), further improvements in breeding efficiency will depend on the comprehensive use of genomic breeding, pan-genomic analysis, high-throughput phenotyping, artificial intelligence methods, and genome editing. This integrated approach is considered the most promising direction for developing climate-resilient potato varieties, and is of significant interest to breeding programs in Kazakhstan and other Central Asian countries [39, 40]. Thus, domestic research demonstrates a consistent trend toward integrating classical breeding with modern biotechnological and molecular-genetic methods. The development of microclonal propagation technologies, the production of disease-free planting material, marker-assisted breeding, and genotyping provides the scientific foundation for the accelerated development of potato varieties adapted to the soil and climatic conditions of Kazakhstan and other Central Asian countries.

Discussion

A review of the literature indicates that modern potato breeding is moving toward the integrated use of traditional breeding approaches, molecular genetic methods, and biotechnology. While classical breeding remains the foundation for developing new varieties, the use of molecular markers, genomic selection, *in vitro* technologies, and high-throughput phenotyping allows for a significant increase in selection accuracy and a reduction in the duration of the breeding process. Consequently, the effectiveness of developing climate-resilient varieties is determined not by the use of any single method, but by their comprehensive integration.

The analyzed studies demonstrate that different breeding approaches complement rather than replace each other. Marker-assisted selection (MAS) is highly effective for traits controlled by major genes, whereas genomic selection is more suitable for complex polygenic traits such as drought and heat tolerance. Genome editing technologies, including CRISPR/Cas, enable targeted modification of candidate genes but still require comprehensive field validation before their large-scale implementation in breeding programs. Therefore, the highest breeding efficiency can be achieved through the integration of these complementary approaches rather than by relying on any single technology.

To assess the capabilities of modern breeding approaches, a comparative analysis was conducted based on their main advantages, limitations, and potential applicability in potato breeding (Table 1).

Table 1. Comparative analysis of major breeding and biotechnological approaches for developing climate-resilient potato cultivars

Method	Advantages	Limitations	Example in potato	Potential applicability in Kazakhstan
Conventional breeding	Low cost, widely used	Long breeding cycles	Early-maturing cultivars	High
Marker-assisted selection (MAS)	Rapid identification of target alleles	Limited for polygenic traits	PVY resistance genes	High
Genomic selection (GS)	High predictive accuracy	Requires large datasets and bioinformatics	Drought tolerance prediction	High
CRISPR/Cas	Precise genome editing	Regulatory restrictions and public acceptance	StCDF1, StSP6A	Moderate

Continuation of Table 1

In vitro biotechnology	Rapid propagation and germplasm conservation	Requires laboratory infrastructure	Virus-free seed potatoes	High
AI-assisted phenotyping	Improves prediction of genotype × environment interactions	High equipment costs	Prediction of genotype × environment	Promising

As the comparative analysis shows, each of the methods considered has its own advantages and limitations. Traditional breeding remains the most accessible approach, but it takes a long time to develop new varieties. Marker-assisted breeding is most effective when working with individual resistance genes, whereas genomic breeding has advantages in evaluating complex polygenic traits, including resistance to drought and high temperatures. Therefore, the most promising approach is the integrated use of various breeding methods.

An analysis of domestic research shows that technologies for microclonal propagation, the production of disease-free planting material, and the molecular evaluation of breeding material are being successfully implemented in Kazakhstan. At the same time, the application of genomic selection, high-throughput phenotyping, and genome editing technologies is currently represented by only a limited number of studies. This underscores the need for further development of modern genomic and biotechnological infrastructure to enhance the effectiveness of domestic breeding programs.

Compared with leading international breeding programs, the implementation of advanced genomic technologies in Kazakhstan remains at an early stage. Nevertheless, recent studies demonstrate a clear transition from conventional breeding toward the application of DNA markers, microclonal propagation, and molecular evaluation of breeding material. Further development of genomic selection, artificial intelligence-assisted phenotyping, and bioinformatics infrastructure will be essential for accelerating the development of climate-resilient potato cultivars adapted to regional conditions.

At the same time, the effectiveness of modern breeding approaches still requires comprehensive evaluation under field conditions and across various agroecological zones. This is particularly important for crops such as potatoes, whose stress tolerance is determined by complex interactions between genotype and the environment. This is especially relevant for Kazakhstan, where potato plants are often simultaneously exposed to high temperatures, moisture deficiency, and sharp fluctuations in weather conditions during a single growing season.

Thus, the most promising approach to enhancing potato resilience to climate change is the integrated use of traditional breeding, molecular genetic methods, and biotechnology. For Kazakhstan, the further development of marker-assisted breeding, the improvement of technologies for producing disease-free planting material, and the expansion of research on evaluating new genotypes under the country's various soil and climate conditions are of particular importance. Integrating these approaches will accelerate the development of potato varieties adapted to current climatic conditions.

Conclusion

An analysis of current scientific research has shown that it is not possible to increase potato resilience to climate change through any single breeding approach. The most effective strategy is the comprehensive integration of traditional breeding, marker-assisted breeding, genomic breeding, genome editing technologies, and modern biotechnological methods. Their combined use can improve selection accuracy, shortens the breeding process, and accelerates the development of varieties resistant to major abiotic stresses.

An analysis of domestic research indicates that technologies for microclonal propagation, the production of disease-free planting material, and the molecular evaluation of breeding material are already being successfully implemented in Kazakhstan. At the same time, the further development of breeding programs should involve the broader use of genomic selection, high-throughput phenotyping, and digital technologies to accelerate the development of potato varieties adapted to the country's soil and climatic conditions.

Promising areas for further research include expanding the use of molecular genetic methods in domestic breeding, conducting comprehensive evaluations of new genotypes under various agroecological conditions in Kazakhstan, and integrating genomic, biotechnological, and digital technologies into practical potato breeding programs. Implementation of these approaches can enhance the adaptability of new varieties to changing climatic conditions and contribute to strengthening food security in Kazakhstan and other Central Asian countries. Overall, this review demonstrates that integrating conventional breeding with genomic, biotechnological, and digital approaches provides the most promising strategy for developing climate-resilient potato cultivars and adapted to the agroecological conditions of Kazakhstan and Central Asia.

Authors' Contributions

VZh: conceptualized the study, performed the literature analysis, and prepared the original draft of the manuscript. IA: contributed to the methodology, supervised the research process, and critically revised and edited the manuscript. All authors have read and approved the final version of the article.

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Климаттық өзгерістерге қарсы картоптың төзімділігін арттыру үшін селекция және биотехнология

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Түйін

Алғышарттар мен мақсат. Климаттың өзгеруі азық-түлік қауіпсіздігіне қауіп төндіреді; Орталық Азияда стреске төзімділікті арттыруға бағытталған кешенді селекциялық стратегияларды іске асыру мүмкіндіктері шектеулі. Осы зерттеудің мақсаты – өңірлік стресс жағдайында климатқа төзімді картоп селекциясы үшін озық геномдық және биотехнологиялық құралдарды бағалау.

Материалдар мен әдістер. Scopus және Web of Science дерекқорларындағы соңғы жарияланымдарға жүйелі шолу жүргізілді. Геномдық селекция, молекулалық маркерлер, CRISPR/Cas жүйесін пайдалана отырып геномды өңдеу, жоғары өнімді фенотиптеу, in vitro технологиялары, микробиомды қолдану және цифрлық ауыл шаруашылығы зерттеулері талданды. Атап айтқанда Қазақстанда және Орталық Азияда абиотикалық стреске төзімділік пен климаттың өзгергіштігіне бейімделуге ерекше назар аударылды.

Нәтижелер. Талдау көрсеткендей, MAS, геномдық селекция және GWAS-ты біріктіру селекцияның дәлдігін арттырып, өсіру циклдарын 30–50% қысқарту арқылы селекциялық жұмыстың тиімділігін жақсартады. CRISPR/Cas технологиялары құрғақшылыққа, ыстыққа және тұздылыққа төзімділікті реттейтін гендерді дәл түзетуге мүмкіндік береді. Жоғары өнімді фенотиптеу жасанды интеллектпен біріктірілгенде генотип-орта өзара әрекеттесуін болжауды жақсартады. Тіндік культура, соматикалық гибридизация және S селекция сияқты биологиялық технологиялар стресске төзімді линияларды дамытуды жеделдетіп, генетикалық ресурстарды сақтайды. Микробиомға негізделген стратегиялар өсімдіктердің төзімділігін және қоректік заттарды пайдалану тиімділігін арттырады. Картопта төзімділік полигендік сипатқа ие және тамыр жүйесінің құрылымы, суды пайдалану тиімділігі, антиоксиданттық жүйелер мен фотосинтез

тұрақтылығымен байланысты. Жабайы *Solanum* түрлерін, геномдық құралдарды және сандық модельдеуді біріктіру Қазақстанға тән аралас стресс жағдайларына бейімделуді жақсартады.

Қорытынды. Кешенді геномикалық және биотехнологиялық селекция картоптың төзімділігі мен өнімділігін айтарлықтай арттырады, бұл Орталық Азияда тұрақты ауыл шаруашылығын дамытуға және климаттық өзгерістерге бейімделуге ықпал етеді.

Кілт сөздер: абиотикалық стресс; биотехнология; климатқа төзімділік; сандық ауыл шаруашылығы; геномикалық селекция; картоп.

Селекция и биотехнологии для повышения устойчивости картофеля к изменению климата

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Аннотация

Предпосылки и цель. Изменение климата угрожает продовольственной безопасности; в Центральной Азии по-прежнему ограничены возможности применения комплексных селекционных стратегий, направленных на повышение стрессоустойчивости. Целью данного исследования является оценка передовых геномных и биотехнологических инструментов для селекции картофеля, устойчивого к климатическим изменениям, в условиях регионального стресса.

Материалы и методы. Был проведен систематический обзор недавних публикаций из баз данных Scopus и Web of Science. Были проанализированы исследования по геномной селекции, молекулярным маркерам, редактированию генома с помощью CRISPR/Cas, высокопроизводительному фенотипированию, технологиям in vitro, применению микробиома и цифровому сельскому хозяйству. Особое внимание уделялось устойчивости к абиотическому стрессу и адаптации к климатической изменчивости в Казахстане и Центральной Азии.

Результаты. Анализ показал, что интеграция MAS, геномной селекции и GWAS повышает эффективность селекции за счет повышения точности отбора и сокращения селекционных циклов на 30–50%. Технологии CRISPR/Cas позволяют точно модифицировать гены, регулирующие устойчивость к засухе, жаре и засоленности. Высокопроизводительное фенотипирование в сочетании с искусственным интеллектом улучшает прогнозирование взаимодействий генотип-окружающая среда. Биотехнологические подходы, включая культуру тканей, соматическую гибридизацию и селекцию *in vitro,* ускоряют разработку стрессоустойчивых линий и сохраняют генетические ресурсы. Стратегии, основанные на микробиоме, повышают устойчивость растений и эффективность использования питательных веществ. У картофеля устойчивость является полигенной и связана со строением корневой системы, эффективностью использования воды, антиоксидантными системами и стабильностью фотосинтеза. Интеграция диких видов *Solanum*, геномных инструментов и цифрового моделирования улучшает адаптацию к комбинированным стрессам, характерным для Казахстана.

Заключение. Комплексная геномная и биотехнологическая селекция значительно повышает устойчивость и продуктивность картофеля, способствуя устойчивому сельскому хозяйству и адаптации к изменению климата в Центральной Азии.

Ключевые слова: абиотический стресс; биотехнология; климатическая устойчивость; цифровое сельское хозяйство; геномная селекция; картофель.