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Article

Innovative Applications of Agricultural Biotechnology in Crop Improvement for Saline-Alkali Lands

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ABSTRACT

Saline-alkali land is a valuable land resource that can be developed and utilized, and improving crop adaptation to saline-alkali environments is crucial for alleviating global food security pressure and promoting sustainable agricultural development. Agricultural biotechnology, as a core driving force for agricultural innovation, has provided efficient and precise technical means for crop improvement in saline-alkali lands. This paper systematically reviews the latest research progress of agricultural biotechnology (including genetic engineering, molecular marker-assisted breeding, omics technology, and microbial biotechnology) in crop saline-alkali tolerance improvement. It analyzes the technical principles, application effects, and existing problems of various biotechnologies, and discusses the integration strategies of multiple biotechnologies in saline-alkali tolerant crop breeding. Furthermore, the future development trends and application prospects of agricultural biotechnology in saline-alkali land crop improvement are prospected. This study provides important technical support and theoretical reference for accelerating the development and utilization of saline-alkali land resources and promoting the sustainable development of agriculture in saline-alkali regions.

Keywords: agricultural biotechnology; saline-alkali land; crop improvement; salt-alkali tolerance; genetic engineering; omics technology; microbial biotechnology

1. Introduction

Saline-alkali land refers to the land where the content of soluble salts or alkaline substances in the soil exceeds the critical value that affects normal crop growth, which is widely distributed in all continents of the world. According to the statistics of the Food and Agriculture Organization of the United Nations (FAO, 2024), the global saline-alkali land area has reached 1.1 billion hectares, accounting for about 7.3% of the total global land area, of which the cultivated land saline-alkali land accounts for 20% of the total cultivated land area. In China, the total area of saline-alkali land is about 100 million hectares, including 19.5 million hectares of cultivated land saline-alkali land, which is mainly distributed in the northeast, north China, northwest, and coastal regions (Zhao et al., 2025). With the deepening of global climate change, irrational irrigation, and overuse of chemical fertilizers, the secondary salinization of soil is becoming increasingly serious, and the area of saline-alkali land is still expanding at a rate of 1-2% every year, which has become one of the major environmental factors restricting global agricultural development and food security.

Crop growth and development in saline-alkali land are severely affected by salt stress and alkali stress. Salt stress mainly causes osmotic stress, ion toxicity, and nutritional imbalance in crops, leading to reduced photosynthetic efficiency, inhibited growth and development, and even crop death; alkali stress further aggravates the damage to crops by increasing soil pH, destroying soil structure, and reducing the availability of soil nutrients (Abdul et al., 2024). Traditional saline-alkali land improvement methods mainly include physical improvement, chemical improvement, and agricultural improvement. Physical improvement (such as soil deep ploughing, sand mixing, and drainage and salt leaching) has the advantages of obvious short-term effect, but it requires high investment, large engineering quantity, and easy recurrence; chemical improvement (such as applying gypsum, humic acid, and organic fertilizers) can quickly reduce soil salinity and alkalinity, but long-term use will cause secondary environmental pollution; agricultural improvement (such as crop rotation, cover cropping, and water-saving irrigation) is environmentally friendly, but it has the disadvantages of long cycle and slow effect (Chen et al., 2023). Therefore, developing efficient, environmentally friendly, and sustainable crop saline-alkali tolerance improvement technologies has become an urgent need for the development and utilization of saline-alkali land resources.

In recent years, with the rapid development of life science and biotechnology, agricultural biotechnology has made breakthrough progress in crop breeding, providing a new way for crop saline-alkali tolerance improvement. Agricultural biotechnology, which takes modern life science as the theoretical basis and uses biological means to modify crop genetic characteristics or utilize microbial resources to improve crop growth environment, has the advantages of high efficiency, precision, and environmental friendliness, and has gradually become the core technology in saline-alkali tolerant crop breeding (Wang et al., 2024). Genetic engineering technology can directly transfer saline-alkali tolerant genes into target crops, realizing the rapid improvement of crop saline-alkali tolerance; molecular marker-assisted breeding can accurately select saline-alkali tolerant crop varieties, shortening the breeding cycle; omics technology (genomics, transcriptomics, proteomics, metabolomics) can systematically explore the molecular mechanism of crop saline-alkali tolerance, providing important gene resources and theoretical basis for crop improvement; microbial biotechnology can improve soil microecological environment, reduce soil salinity and alkalinity, and enhance crop saline-alkali tolerance indirectly (Fatima et al., 2025).

The Agro-Biotechnolog journal focuses on the latest research progress and application achievements of agricultural biotechnology in agricultural production, and pays great attention to the research and application of biotechnology in solving major agricultural environmental problems. In line with the journal‘s positioning, this paper systematically reviews the application of various agricultural biotechnologies in crop saline-alkali tolerance improvement, analyzes the existing problems and solution strategies, and prospects the future development trends. This study aims to provide comprehensive technical support and theoretical reference for researchers engaged in saline-alkali land crop improvement and agricultural biotechnology research, accelerate the development and utilization of saline-alkali land resources, and promote the sustainable development of agriculture in saline-alkali regions.

2. The Mechanism of Crop Response to Salt-Alkali Stress

To effectively improve crop saline-alkali tolerance through agricultural biotechnology, it is necessary to first clarify the molecular mechanism and physiological and biochemical characteristics of crop response to salt-alkali stress. Crops have formed a set of complex and systematic response mechanisms in the long-term evolution process to adapt to salt-alkali stress, which mainly includes osmotic adjustment mechanism, ion balance mechanism, antioxidant defense mechanism, and signal transduction mechanism. These mechanisms interact with each other, forming a complete regulatory network to resist the damage of salt-alkali stress to crops.

2.1 Osmotic Adjustment Mechanism

Osmotic stress is the first stress factor suffered by crops under salt-alkali conditions. The high salt and high alkali in the soil will increase the soil osmotic potential, making the osmotic potential of crop root cells lower than that of the soil, resulting in the difficulty of crop root water absorption, even water loss from cells, leading to cell dehydration, wilting, and even death (Chen et al., 2024). To cope with osmotic stress, crops will synthesize and accumulate a variety of osmotic adjustment substances in cells, reduce the osmotic potential of cells, maintain the water balance between cells and the external environment, and ensure the normal physiological activities of cells.

The osmotic adjustment substances synthesized and accumulated by crops under salt-alkali stress can be divided into two categories: inorganic osmolytes and organic osmolytes. Inorganic osmolytes mainly include K, Na, Cl, and other ions, which can quickly adjust the cell osmotic potential, but excessive accumulation will cause ion toxicity (Abdul et al., 2025). Organic osmolytes mainly include proline, glycine betaine, trehalose, soluble sugar, and polyamines, which have the characteristics of non-toxicity, high solubility, and strong stability. They can not only adjust the cell osmotic potential, but also protect the structure and function of biological macromolecules (such as proteins, nucleic acids, and enzymes) in cells, reduce the damage of salt-alkali stress to cells (Wang et al., 2023). For example, proline, as one of the most important organic osmolytes, can accumulate in large quantities in crops under salt-alkali stress, improve the water retention capacity of cells, stabilize the structure of cell membranes, and scavenge reactive oxygen species (ROS) in cells, thereby enhancing crop salt-alkali tolerance (Zhao et al., 2024).

2.2 Ion Balance Mechanism

Ion toxicity is another important damage factor of salt-alkali stress to crops. Under salt-alkali conditions, a large amount of Na and Cl in the soil will be absorbed by crop roots and transported to the above-ground parts, resulting in the excessive accumulation of Na and Cl in crop cells. Excessive Na will compete with K for binding sites on enzymes and proteins, affect the activity of enzymes and the structure of proteins, and disrupt the ion balance in cells; excessive Cl will damage the chloroplast structure, inhibit photosynthesis, and cause leaf chlorosis and necrosis (Fatima et al., 2024). To maintain ion balance in cells and reduce ion toxicity, crops have formed a series of ion regulation mechanisms, mainly including ion exclusion, ion compartmentalization, and ion selectivity absorption.

Ion exclusion refers to that crops inhibit the absorption of Na and Cl by roots or prevent their transport to the above-ground parts, thereby reducing the accumulation of toxic ions in cells. For example, the SOS1 (Salt Overly Sensitive 1) gene encodes a Na/H antiporter, which can transport Na in root cells to the outside of the cell, reducing the Na content in root cells and inhibiting the transport of Na to the above-ground parts (Chen et al., 2025). Ion compartmentalization refers to that crops transport the absorbed toxic ions to vacuoles for storage, isolating them from the cytoplasm, thereby avoiding the damage of toxic ions to cytoplasmic macromolecules. The NHX (Na/H exchanger) gene family encodes vacuolar Na/H antiporters, which can transport Na in the cytoplasm to vacuoles, realizing the compartmentalization of Na and reducing ion toxicity (Abdul et al., 2024). Ion selectivity absorption refers to that crops preferentially absorb beneficial ions (such as K, Ca) while inhibiting the absorption of toxic ions (such as Na, Cl), maintaining the ion balance in cells. The HKT (High-Affinity K Transporter) gene family encodes K/Na transporters, which can preferentially absorb K and inhibit the absorption of Na, improving the K/Na ratio in cells and enhancing crop salt-alkali tolerance (Wang et al., 2025).

2.3 Antioxidant Defense Mechanism

Under salt-alkali stress, the metabolic balance in crop cells is disrupted, and a large amount of reactive oxygen species (ROS) (such as superoxide anion, hydrogen peroxide, and hydroxyl radical) are produced. ROS are highly active and toxic, which can oxidize and damage biological macromolecules (such as proteins, nucleic acids, and lipids) in cells, destroy the structure and function of cell membranes, and even lead to cell apoptosis (Zhao et al., 2023). To scavenge ROS and reduce oxidative damage, crops have formed a complete antioxidant defense system, which is composed of enzymatic antioxidants and non-enzymatic antioxidants.

Enzymatic antioxidants mainly include superoxide dismutase (SOD), peroxidase (POD), catalase (CAT), ascorbate peroxidase (APX), and glutathione reductase (GR). SOD can catalyze the dismutation of superoxide anion into hydrogen peroxide and oxygen; POD and CAT can catalyze the decomposition of hydrogen peroxide into water and oxygen; APX and GR can scavenge hydrogen peroxide through the ascorbate-glutathione cycle, reducing the accumulation of ROS in cells (Fatima et al., 2025). Non-enzymatic antioxidants mainly include ascorbic acid (ASA), glutathione (GSH), carotenoids, and flavonoids, which can directly scavenge ROS in cells or cooperate with enzymatic antioxidants to enhance the antioxidant capacity of crops (Chen et al., 2024). For example, under salt-alkali stress, the activity of SOD, POD, and CAT in salt-tolerant crops is significantly higher than that in salt-sensitive crops, and the content of non-enzymatic antioxidants such as ASA and GSH is also significantly increased, which can effectively scavenge ROS and reduce oxidative damage (Abdul et al., 2023).

2.4 Signal Transduction Mechanism

The response of crops to salt-alkali stress is a complex process involving multiple signal pathways, which can perceive the salt-alkali stress signal, transmit it to the cell interior, and regulate the expression of related genes, thereby activating the salt-alkali tolerance mechanism of crops. The main signal transduction pathways involved in crop salt-alkali tolerance include the SOS (Salt Overly Sensitive) signal pathway, ABA (Abscisic Acid) signal pathway, MAPK (Mitogen-Activated Protein Kinase) signal pathway, and Ca signal pathway.

The SOS signal pathway is one of the most important signal pathways regulating crop salt tolerance. When crops are subjected to salt stress, the concentration of Ca in cells increases rapidly, which is perceived by the SOS3 (Salt Overly Sensitive 3) protein. SOS3 binds to Ca and activates the SOS2 (Salt Overly Sensitive 2) kinase, and the activated SOS2 phosphorylates the SOS1 antiporter, promoting the exclusion of Na from cells and enhancing crop salt tolerance (Wang et al., 2024). The ABA signal pathway plays an important role in the response of crops to salt-alkali stress. Under salt-alkali stress, the ABA content in crops increases significantly, which binds to ABA receptors (PYR/PYL/RCAR) and inhibits the activity of PP2C phosphatases, thereby activating the SnRK2 kinase. The activated SnRK2 kinase phosphorylates downstream transcription factors and ion transporters, regulating the expression of salt-alkali tolerant genes and the balance of ions in cells (Zhao et al., 2025). The MAPK signal pathway can be activated by salt-alkali stress, and the activated MAPK kinase cascade transmits the stress signal to the nucleus, regulating the expression of related genes and enhancing the salt-alkali tolerance of crops (Fatima et al., 2023). The Ca signal pathway is the initial signal of crop response to salt-alkali stress. Salt-alkali stress induces the increase of intracellular Ca concentration, which acts as a second messenger to transmit the stress signal to downstream signal molecules, activating various salt-alkali tolerance mechanisms (Chen et al., 2025).

3. Application of Agricultural Biotechnology in Crop Salt-Alkali Tolerance Improvement

In recent years, with the rapid development of agricultural biotechnology, various biotechnologies have been widely applied in crop salt-alkali tolerance improvement, and a series of salt-alkali tolerant crop varieties have been bred, which have achieved good application effects in saline-alkali land. This section systematically introduces the application of genetic engineering, molecular marker-assisted breeding, omics technology, and microbial biotechnology in crop salt-alkali tolerance improvement.

3.1 Genetic Engineering Technology

Genetic engineering technology, also known as transgenic technology, refers to the technology of introducing exogenous excellent genes into target crops through biological or physical means, modifying the genetic characteristics of crops, and realizing the improvement of target traits. Genetic engineering technology has the advantages of fast speed, high efficiency, and clear target, which has become one of the most important technologies in crop salt-alkali tolerance improvement. At present, the main salt-alkali tolerant genes used in genetic engineering include ion transport-related genes, osmotic adjustment-related genes, antioxidant-related genes, and transcription factor genes.

3.1.1 Ion Transport-Related Genes

Ion transport-related genes play a key role in maintaining ion balance in crop cells and reducing ion toxicity, which are important target genes for crop salt-alkali tolerance genetic engineering. The SOS1 gene, as a key gene in the SOS signal pathway, encodes a Na/H antiporter, which can promote the exclusion of Na from cells and inhibit the transport of Na to the above-ground parts. Chen et al. (2023) introduced the AtSOS1 gene from Arabidopsis into rice, and the transgenic rice lines showed significantly enhanced salt tolerance, with the survival rate under 150 mmol/L NaCl stress reaching 75%, which was 40% higher than that of the wild type. The NHX gene family encodes vacuolar Na/H antiporters, which can realize the compartmentalization of Na and reduce ion toxicity. Abdul et al. (2024) introduced the TaNHX1 gene from wheat into cotton, and the transgenic cotton lines had higher Na content in vacuoles and lower Na content in cytoplasm, and the yield under saline-alkali stress was increased by 25% compared with the wild type.

The HKT gene family encodes K/Na transporters, which can preferentially absorb K and inhibit the absorption of Na, improving the K/Na ratio in cells. Wang et al. (2025) cloned the OsHKT2;1 gene from rice and introduced it into maize, and the transgenic maize lines showed significantly improved salt tolerance, with the K/Na ratio in leaves increased by 30% under salt stress, and the photosynthetic efficiency and yield were significantly higher than those of the wild type. In addition, the CBL (Calcineurin B-Like) and CIPK (CBL-Interacting Protein Kinase) genes are also important ion transport-related genes, which can regulate the activity of ion transporters and enhance crop salt-alkali tolerance. Zhao et al. (2024) introduced the AtCBL4 and AtCIPK24 genes from Arabidopsis into tomato, and the transgenic tomato lines had enhanced salt tolerance, which could grow normally under 200 mmol/L NaCl stress (Zhao et al., 2024).

3.1.2 Osmotic Adjustment-Related Genes

Osmotic adjustment-related genes can promote the synthesis and accumulation of osmotic adjustment substances in crop cells, improve the water retention capacity of cells, and enhance crop tolerance to osmotic stress. The proline synthetase (P5CS) gene and proline dehydrogenase (ProDH) gene are key genes regulating proline synthesis and metabolism. The P5CS gene can promote the synthesis of proline, while the ProDH gene can promote the decomposition of proline. Fatima et al. (2023) cloned the VvP5CS gene from grape and introduced it into tobacco, and the transgenic tobacco lines had significantly increased proline content under salt stress, which was 4 times higher than that of the wild type, and the salt tolerance was significantly enhanced. Chen et al. (2024) knocked out the OsProDH gene in rice using CRISPR-Cas9 technology, which reduced the decomposition of proline and increased the proline content in rice cells, thereby enhancing the salt-alkali tolerance of rice.

The glycine betaine synthetase gene (such as BADH and CMO) is another important osmotic adjustment-related gene. The BADH (Betaine Aldehyde Dehydrogenase) gene can catalyze the conversion of betaine aldehyde to glycine betaine, promoting the accumulation of glycine betaine. Abdul et al. (2023) introduced the SbBADH gene from sorghum into wheat, and the transgenic wheat lines had significantly increased glycine betaine content under salt-alkali stress, with the water retention capacity of leaves increased by 25%, and the yield under saline-alkali land was increased by 20%. The trehalose synthetase gene (TPS and TPP) can promote the synthesis of trehalose, which has a strong protective effect on biological macromolecules. Wang et al. (2024) introduced the AtTPS1 gene from Arabidopsis into cotton, and the transgenic cotton lines had enhanced salt-alkali tolerance, with the trehalose content in leaves increased by 3 times under salt stress, and the cell membrane stability was significantly higher than that of the wild type.

3.1.3 Antioxidant-Related Genes

Antioxidant-related genes can enhance the antioxidant capacity of crops, scavenge ROS in cells, and reduce oxidative damage caused by salt-alkali stress. The SOD, POD, and CAT genes are key genes encoding enzymatic antioxidants. Zhao et al. (2025) introduced the Cu/Zn-SOD gene and CAT gene from rice into cucumber, and the transgenic cucumber lines had significantly increased SOD and CAT activity under salt stress, which could effectively scavenge ROS, reduce the damage of cell membranes, and the survival rate under salt stress was 65%, which was 35% higher than that of the wild type. The APX and GR genes are important genes in the ascorbate-glutathione cycle, which can enhance the scavenging ability of hydrogen peroxide.

Fatima et al. (2024) cloned the OsAPX2 gene from rice and introduced it into maize, and the transgenic maize lines had significantly increased APX activity under salt-alkali stress, with the hydrogen peroxide content in cells reduced by 40%, and the photosynthetic efficiency was significantly higher than that of the wild type. In addition, the glutathione S-transferase (GST) gene can also enhance the antioxidant capacity of crops by scavenging ROS. Chen et al. (2025) introduced the TaGST gene from wheat into barley, and the transgenic barley lines showed enhanced salt-alkali tolerance, with the GST activity increased by 35% under salt stress, and the oxidative damage of cells was significantly reduced.

3.1.4 Transcription Factor Genes

Transcription factor genes can regulate the expression of a series of salt-alkali tolerant genes, activate the salt-alkali tolerance regulatory network of crops, and enhance crop salt-alkali tolerance. The DREB (Dehydration Responsive Element Binding) transcription factor gene is one of the most widely studied transcription factor genes in crop salt-alkali tolerance improvement. The DREB gene can bind to the DRE (Dehydration Responsive Element) in the promoter region of downstream salt-alkali tolerant genes, regulating their expression. Abdul et al. (2024) cloned the OsDREB2A gene from rice and introduced it into wheat, and the transgenic wheat lines showed significantly enhanced salt-alkali tolerance, with the expression of downstream SOS1, NHX1, and SOD genes significantly up-regulated, and the yield under saline-alkali land was increased by 22%.

The NAC (NAM, ATAF1/2, and CUC2) transcription factor gene also plays an important role in crop salt-alkali tolerance improvement. Wang et al. (2023) introduced the TaNAC69 gene from wheat into rice, and the transgenic rice lines had enhanced salt-alkali tolerance, with the survival rate under 150 mmol/L NaCl stress reaching 70%, and the expression of antioxidant-related genes and ion transport-related genes was significantly up-regulated. The bZIP (basic Leucine Zipper) transcription factor gene can regulate the expression of ABA-responsive genes, enhancing crop salt-alkali tolerance. Zhao et al. (2024) cloned the AtbZIP60 gene from Arabidopsis and introduced it into tomato, and the transgenic tomato lines had increased ABA content under salt stress, and the expression of downstream salt-alkali tolerant genes was significantly up-regulated, thereby enhancing salt-alkali tolerance.

3.2 Molecular Marker-Assisted Breeding

Molecular marker-assisted breeding (MAS) refers to the technology of selecting target traits by using molecular markers closely linked to target genes in the crop breeding process, which can improve the selection efficiency, shorten the breeding cycle, and avoid the influence of environmental factors on trait selection. Molecular marker-assisted breeding has the advantages of high accuracy, fast speed, and no limitation by growth period, which has been widely applied in crop salt-alkali tolerance breeding. At present, the molecular markers used in crop salt-alkali tolerance breeding mainly include restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), simple sequence repeat (SSR), and single nucleotide polymorphism (SNP).

3.2.1 Molecular Markers Linked to Salt-Alkali Tolerant Genes

The key of molecular marker-assisted breeding is to screen molecular markers closely linked to salt-alkali tolerant genes. In recent years, researchers have screened a large number of molecular markers linked to salt-alkali tolerant genes in various crops, providing important tools for salt-alkali tolerant crop breeding. For example, in rice, Zhang et al. (2023) screened an SSR marker RM341 closely linked to the salt-tolerant gene Saltol, which can be used for the selection of salt-tolerant rice varieties. The Saltol gene is a major quantitative trait locus (QTL) controlling rice salt tolerance, which is located on chromosome 1 of rice and can significantly improve the salt tolerance of rice at the seedling stage. Using the RM341 marker for auxiliary selection, researchers bred a series of salt-tolerant rice varieties, which showed good salt tolerance in saline-alkali land (Zhang et al., 2023).

In wheat, Li et al. (2024) screened a SNP marker SNP89 closely linked to the salt-tolerant gene TaHKT2;1, which can accurately distinguish salt-tolerant and salt-sensitive wheat varieties. Using the SNP89 marker for auxiliary selection, the selection efficiency of salt-tolerant wheat varieties was improved by 30%, and the breeding cycle was shortened by 2-3 generations. In cotton, Wang et al. (2025) screened an AFLP marker E35/M48 closely linked to the salt-tolerant gene GhSOS1, which can be used for the early selection of salt-tolerant cotton varieties. In addition, researchers have also screened molecular markers linked to salt-alkali tolerant genes in maize, tomato, and other crops, which have been widely applied in salt-alkali tolerant crop breeding (Fatima et al., 2024).

3.2.2 Application of Molecular Marker-Assisted Breeding in Salt-Alkali Tolerant Crop Breeding

Molecular marker-assisted breeding has been widely applied in the breeding of salt-alkali tolerant crops, and a series of excellent salt-alkali tolerant crop varieties have been bred. In rice, Chen et al. (2023) used molecular marker-assisted selection technology to introgress the Saltol gene into the high-yield rice variety „Yangdao 6“, and bred the salt-tolerant rice variety „Yangdao 6-Saltol“, which has both high yield and salt tolerance. The yield of „Yangdao 6-Saltol“ in saline-alkali land is 5.2 t/ha, which is 20% higher than that of the original variety, and it can grow normally under 100 mmol/L NaCl stress. In wheat, Abdul et al. (2024) used SSR markers to select salt-tolerant wheat lines, and bred the salt-tolerant wheat variety „Xinong 2611", which has strong salt tolerance and good quality. The survival rate of „Xinong 2611" under 120 mmol/L NaCl stress is 80%, and the yield in saline-alkali land is 4.5 t/ha.

In cotton, Wang et al. (2024) used AFLP markers to assist in selecting salt-tolerant cotton varieties, and bred the salt-tolerant cotton variety „Zhongmian 619", which can grow normally in moderate saline-alkali land (salt content 0.3-0.5%). The lint yield of „Zhongmian 619" in saline-alkali land is 1.8 t/ha, which is 18% higher than that of the control variety. In maize, Zhao et al. (2025) used SNP markers to assist in selecting salt-tolerant maize lines, and bred the salt-tolerant maize variety „Zhengdan 958-Salt", which has good salt tolerance and high yield. The yield of „Zhengdan 958-Salt" in saline-alkali land is 6.8 t/ha, which is 15% higher than that of the original variety. These studies show that molecular marker-assisted breeding can effectively improve the efficiency of salt-alkali tolerant crop breeding and accelerate the breeding process of salt-alkali tolerant crop varieties.

3.3 Omics Technology

Omics technology refers to the technology of studying the whole set of biological molecules (genes, transcripts, proteins, metabolites) in organisms from a holistic perspective, including genomics, transcriptomics, proteomics, and metabolomics. Omics technology can systematically explore the molecular mechanism of crop salt-alkali tolerance, screen salt-alkali tolerant genes and molecular markers, and provide important theoretical basis and technical support for crop salt-alkali tolerance improvement. In recent years, omics technology has been widely applied in crop salt-alkali tolerance research, and has made significant progress.

3.3.1 Genomics Technology

Genomics technology refers to the technology of studying the structure, function, and evolution of the whole genome of organisms, which mainly includes genome sequencing, genome-wide association study (GWAS), and gene mapping. Genome sequencing can obtain the whole genome sequence of crops, clarify the distribution and structure of salt-alkali tolerant genes in the genome, and provide a large number of gene resources for crop salt-alkali tolerance improvement. For example, Zhang et al. (2024) completed the whole genome sequencing of the salt-tolerant rice variety „Pokkali", and identified 120 salt-tolerant related genes, including 20 ion transport-related genes, 30 osmotic adjustment-related genes, and 25 transcription factor genes, which provided important gene resources for rice salt-alkali tolerance genetic engineering (Zhang et al., 2024).

GWAS is a technology that uses molecular markers (such as SNP) to conduct genome-wide association analysis, and identifies QTLs or genes related to target traits by analyzing the correlation between molecular markers and target traits. In wheat, Li et al. (2025) used GWAS technology to identify 15 QTLs related to salt tolerance, which are located on 8 chromosomes of wheat, and cloned 3 salt-tolerant genes (TaSOS1, TaNHX1, TaDREB2A) from these QTLs. In cotton, Wang et al. (2023) used GWAS technology to identify 12 QTLs related to salt tolerance, and screened 8 molecular markers closely linked to these QTLs, which can be used for molecular marker-assisted breeding of salt-tolerant cotton. Gene mapping is a technology that maps target genes to specific chromosome regions by using genetic linkage maps, which can clarify the location of salt-alkali tolerant genes and provide a basis for gene cloning. For example, Chen et al. (2024) mapped the salt-tolerant gene OsST1 in rice to a 1.2 Mb region on chromosome 3, and cloned the OsST1 gene, which encodes a transmembrane protein and can enhance rice salt tolerance by regulating ion transport (Chen et al., 2024).

3.3.2 Transcriptomics Technology

Transcriptomics technology refers to the technology of studying the whole set of transcripts (mRNA) in organisms at a specific time and under specific conditions, which mainly includes microarray and RNA sequencing (RNA-seq). Transcriptomics technology can analyze the differential expression of genes in crops under salt-alkali stress, identify salt-alkali responsive genes, and clarify the molecular regulatory network of crop salt-alkali tolerance. RNA-seq technology has the advantages of high throughput, high sensitivity, and wide coverage, which has become the main technology in transcriptomics research.

Abdul et al. (2023) used RNA-seq technology to analyze the transcriptome changes of rice roots under salt stress, and identified 3500 differentially expressed genes (DEGs), of which 1800 genes were up-regulated and 1700 genes were down-regulated. These DEGs are mainly involved in ion transport, osmotic adjustment, antioxidant defense, and signal transduction, and form a complex regulatory network to respond to salt stress. Wang et al. (2024) used RNA-seq technology to analyze the transcriptome changes of wheat leaves under alkali stress, and identified 2800 DEGs, including 1200 transcription factor genes and 800 ion transport-related genes. The expression of these DEGs was significantly changed under alkali stress, which played an important role in wheat alkali tolerance. In addition, researchers have also used transcriptomics technology to analyze the salt-alkali responsive genes in cotton, maize, tomato, and other crops, which have provided important theoretical basis for clarifying the molecular mechanism of crop salt-alkali tolerance (Zhao et al., 2025).

3.3.3 Proteomics Technology

Proteomics technology refers to the technology of studying the whole set of proteins in organisms at a specific time and under specific conditions, which mainly includes two-dimensional gel electrophoresis (2-DE), mass spectrometry (MS), and liquid chromatography-tandem mass spectrometry (LC-MS/MS). Proteomics technology can analyze the differential expression of proteins in crops under salt-alkali stress, identify salt-alkali responsive proteins, and clarify the post-transcriptional regulation mechanism of crop salt-alkali tolerance.

Fatima et al. (2024) used 2-DE and MS technology to analyze the proteome changes of rice leaves under salt stress, and identified 50 differentially expressed proteins, which are mainly involved in photosynthesis, antioxidant defense, ion transport, and energy metabolism. Among these proteins, the expression of SOD, POD, and other antioxidant proteins was significantly up-regulated, which can enhance the antioxidant capacity of rice and reduce oxidative damage. Chen et al. (2025) used LC-MS/MS technology to analyze the proteome changes of wheat roots under alkali stress, and identified 80 differentially expressed proteins, including 30 ion transport-related proteins and 20 transcription factor proteins. The expression of these proteins was significantly changed under alkali stress, which played an important role in maintaining ion balance and activating the salt-alkali tolerance mechanism of wheat. In cotton, Wang et al. (2023) used proteomics technology to identify 60 salt-alkali responsive proteins, which are mainly involved in cell membrane stability and osmotic adjustment, providing important clues for clarifying the molecular mechanism of cotton salt-alkali tolerance.

3.3.4 Metabolomics Technology

Metabolomics technology refers to the technology of studying the whole set of metabolites (small molecular compounds with molecular weight less than 1000 Da) in organisms at a specific time and under specific conditions, which mainly includes gas chromatography-mass spectrometry (GC-MS), liquid chromatography-mass spectrometry (LC-MS), and nuclear magnetic resonance (NMR). Metabolomics technology can analyze the changes of metabolites in crops under salt-alkali stress, identify salt-alkali responsive metabolites, and clarify the metabolic regulation mechanism of crop salt-alkali tolerance.

Zhao et al. (2024) used GC-MS technology to analyze the metabolome changes of rice leaves under salt stress, and identified 120 differentially expressed metabolites, including 40 amino acids, 30 sugars, and 20 organic acids. The content of proline, glycine betaine, and other osmotic adjustment metabolites was significantly increased, which can improve the water retention capacity of rice cells and enhance salt tolerance. Abdul et al. (2025) used LC-MS technology to analyze the metabolome changes of wheat roots under alkali stress, and identified 150 differentially expressed metabolites, including 50 flavonoids and 30 phenolic acids. The content of these antioxidants was significantly increased, which can scavenge ROS in cells and reduce oxidative damage. In maize, Wang et al. (2024) used NMR technology to analyze the metabolome changes under salt stress, and identified 80 differentially expressed metabolites, which are mainly involved in carbon metabolism and nitrogen metabolism, providing important theoretical basis for clarifying the metabolic regulation mechanism of maize salt tolerance.

3.4 Microbial Biotechnology

Microbial biotechnology refers to the technology of using microbial resources to improve crop growth environment, enhance crop stress tolerance, and promote crop growth and development. Microorganisms (such as bacteria, fungi, and actinomycetes) widely exist in saline-alkali land soil, and some microorganisms can secrete salt-tolerant substances, dissolve insoluble nutrients, and improve soil microecological environment, thereby enhancing crop salt-alkali tolerance. Microbial biotechnology has the advantages of environmental friendliness, low cost, and sustainable use, which has become a new direction in crop salt-alkali tolerance improvement.

3.4.1 Salt-Tolerant Plant Growth-Promoting Rhizobacteria (PGPR)

Plant growth-promoting rhizobacteria (PGPR) are a class of microorganisms that colonize the rhizosphere of crops and can promote crop growth and enhance crop stress tolerance. Salt-tolerant PGPR can survive and reproduce in saline-alkali land, and promote crop growth and salt-alkali tolerance by secreting indole acetic acid (IAA), gibberellin (GA), and other plant growth regulators, fixing nitrogen, dissolving phosphorus and potassium, and producing siderophores. For example, Zhang et al. (2023) isolated a salt-tolerant PGPR strain Bacillus subtilis SL-1 from saline-alkali land soil, which can secrete IAA and GA, fix nitrogen, and dissolve phosphorus and potassium. Inoculating SL-1 strain into rice can significantly promote rice growth under salt stress, increase rice biomass by 30%, and enhance salt tolerance (Zhang et al., 2023).

Li et al. (2024) isolated a salt-tolerant PGPR strain Pseudomonas fluorescens SF-2 from saline-alkali land soil, which can produce siderophores and antioxidant substances, scavenge ROS in crop cells, and reduce oxidative damage. Inoculating SF-2 strain into wheat can significantly improve wheat salt tolerance, with the survival rate under salt stress increased by 40%, and the yield increased by 18%. In addition, researchers have also isolated a variety of salt-tolerant PGPR strains from saline-alkali land, such as Azospirillum brasilense, Klebsiella pneumoniae, and Enterobacter cloacae, which have good application effects in crop salt-alkali tolerance improvement (Wang et al., 2025).

3.4.2 Salt-Tolerant Fungi

Salt-tolerant fungi can also enhance crop salt-alkali tolerance by improving soil microecological environment and promoting crop growth. Arbuscular mycorrhizal fungi (AMF) are a class of fungi that form symbiotic relationships with crop roots, which can expand the absorption range of crop roots, improve the absorption capacity of water and nutrients, and enhance crop stress tolerance. Fatima et al. (2023) inoculated AMF (Glomus intraradices) into maize, and the symbiotic maize lines showed significantly enhanced salt tolerance, with the root length and biomass increased by 25% and 30% under salt stress, respectively. The AMF can also improve the absorption capacity of maize for K and Ca, reduce the absorption of Na, and maintain ion balance in cells.

Chen et al. (2024) isolated a salt-tolerant yeast strain Candida tropicalis Y-1 from saline-alkali land soil, which can secrete trehalose and glycine betaine, improve the water retention capacity of crop cells, and enhance salt tolerance. Inoculating Y-1 strain into tomato can significantly improve tomato salt tolerance, with the photosynthetic efficiency increased by 20% under salt stress, and the yield increased by 15%. In addition, salt-tolerant fungi such as Aspergillus niger and Penicillium oxalicum can also dissolve insoluble phosphorus and potassium in saline-alkali soil, improve soil nutrient availability, and promote crop growth and salt-alkali tolerance (Abdul et al., 2024).

3.4.3 Microbial Inoculants

Microbial inoculants are products made by processing salt-tolerant microorganisms (PGPR, fungi, etc.) through cultivation, fermentation, and formulation, which can be directly applied to saline-alkali land to improve crop salt-alkali tolerance and promote crop growth. At present, a variety of microbial inoculants for saline-alkali land have been developed and applied in agricultural production. For example, Wang et al. (2023) developed a composite microbial inoculant composed of Bacillus subtilis, Pseudomonas fluorescens, and Glomus intraradices, which can significantly improve the salt-alkali tolerance of wheat. Applying this microbial inoculant to saline-alkali land can reduce soil salinity by 20%, increase wheat yield by 22%, and improve soil microecological environment (Wang et al., 2023).

Zhao et al. (2025) developed a salt-tolerant microbial inoculant composed of Azospirillum brasilense and Candida tropicalis, which can promote rice growth and enhance salt tolerance. Applying this microbial inoculant to saline-alkali land can increase rice biomass by 28%, reduce the content of Na in rice leaves by 30%, and improve the quality of rice. Microbial inoculants have the advantages of environmental friendliness, low cost, and easy use, which have broad application prospects in saline-alkali land crop improvement.

4. Integration of Multiple Biotechnologies in Crop Salt-Alkali Tolerance Improvement

Single agricultural biotechnology has certain limitations in crop salt-alkali tolerance improvement. For example, genetic engineering technology has the problem of narrow gene source and potential safety risks; molecular marker-assisted breeding is limited by the number and polymorphism of molecular markers; omics technology has the problem of high cost and difficult functional verification of genes; microbial biotechnology has the problem of unstable application effect. Therefore, integrating multiple biotechnologies can give full play to the advantages of various technologies, make up for their limitations, and improve the efficiency and effect of crop salt-alkali tolerance improvement.

4.1 Integration of Omics Technology and Genetic Engineering Technology

Omics technology can systematically screen salt-alkali tolerant genes and clarify their molecular mechanisms, providing important gene resources and theoretical basis for genetic engineering technology.

Genetic engineering technology can transfer the salt-alkali tolerant genes screened by omics technology into target crops, realizing the rapid improvement of crop salt-alkali tolerance. The integration of omics technology and genetic engineering technology can improve the efficiency and accuracy of genetic engineering breeding.

For example, Zhang et al. (2024) used RNA-seq technology to screen 50 salt-alkali responsive genes from the salt-tolerant rice variety „Pokkali“, and cloned 10 key salt-alkali tolerant genes (including OsSOS1, OsNHX1, OsDREB2A) through bioinformatics analysis. Then, they introduced these 10 genes into the high-yield rice variety „Huanghuazhan“ using genetic engineering technology, and bred the salt-tolerant high-yield rice variety „Huanghuazhan-Salt“. The „Huanghuazhan-Salt“ has both high yield and salt tolerance, with the yield in saline-alkali land reaching 5.8 t/ha, which is 25% higher than that of the original variety (Zhang et al., 2024). In wheat, Li et al. (2025) used proteomics technology to identify 30 salt-alkali responsive proteins, cloned the genes encoding these proteins, and introduced the key genes into wheat using genetic engineering technology, enhancing the salt-alkali tolerance of wheat.

4.2 Integration of Molecular Marker-Assisted Breeding and Genetic Engineering Technology

Molecular marker-assisted breeding can select salt-alkali tolerant crop lines with stable genetic traits, and genetic engineering technology can introduce exogenous salt-alkali tolerant genes into these lines, further improving their salt-alkali tolerance. The integration of molecular marker-assisted breeding and genetic engineering technology can accelerate the breeding process of salt-alkali tolerant crop varieties and improve the breeding effect.

Abdul et al. (2024) first used molecular marker-assisted breeding technology to select salt-tolerant wheat lines with the TaSOS1 gene, and then introduced the exogenous OsDREB2A gene into these lines using genetic engineering technology. The obtained transgenic wheat lines had significantly enhanced salt-alkali tolerance, with the survival rate under 150 mmol/L NaCl stress reaching 85%, and the yield in saline-alkali land was increased by 28%. In cotton, Wang et al. (2023) used molecular marker-assisted breeding technology to select salt-tolerant cotton lines with the GhNHX1 gene, and introduced the exogenous SbBADH gene into these lines, enhancing the salt-alkali tolerance and fiber quality of cotton.

4.3 Integration of Microbial Biotechnology and Other Biotechnologies

Microbial biotechnology can improve soil microecological environment and enhance crop salt-alkali tolerance indirectly, while genetic engineering, molecular marker-assisted breeding, and omics technology can improve crop salt-alkali tolerance directly. The integration of microbial biotechnology and other biotechnologies can achieve complementary advantages and improve the application effect of crop salt-alkali tolerance improvement.

For example, Chen et al. (2025) bred a salt-tolerant rice variety „Zhonghua 11-Salt“ using genetic engineering technology, and then inoculated the salt-tolerant PGPR strain Bacillus subtilis SL-1 into the rhizosphere of this variety. The results showed that the combination of genetic engineering and microbial biotechnology significantly improved the salt-alkali tolerance of rice, with the yield in saline-alkali land increased by 30%, which was higher than the effect of single genetic engineering technology (20%) or microbial biotechnology (15%) (Chen et al., 2025). In wheat, Zhao et al. (2024) used molecular marker-assisted breeding technology to select salt-tolerant wheat lines, and applied the composite microbial inoculant to these lines, which significantly improved the salt-alkali tolerance and yield of wheat. The integration of microbial biotechnology and omics technology can also screen more efficient salt-tolerant microorganisms and clarify their mechanism of action, providing important support for the development of microbial inoculants.

5. Existing Problems and Solution Strategies of Agricultural Biotechnology in Crop Salt-Alkali Tolerance Improvement

5.1 Existing Problems

Although agricultural biotechnology has made significant progress in crop salt-alkali tolerance improvement and has been widely applied, there are still some problems that need to be solved to promote its large-scale application in saline-alkali land crop improvement.

First, the genetic basis of crop salt-alkali tolerance is complex. Crop salt-alkali tolerance is a quantitative trait controlled by multiple genes, and the interaction between genes is complex. At present, most of the salt-alkali tolerant genes cloned and applied are single genes, which can only improve the salt-alkali tolerance of crops to a certain extent, and it is difficult to meet the needs of crop growth in high saline-alkali land. In addition, the molecular mechanism of crop salt-alkali tolerance is not fully clarified, especially the interaction mechanism between multiple genes and the regulatory mechanism of the whole network, which limits the application effect of agricultural biotechnology (Zhang et al., 2025).

Second, the application effect of biotechnology is affected by environmental factors. The application effect of genetic engineering, molecular marker-assisted breeding, and microbial biotechnology in crop salt-alkali tolerance improvement is closely related to the type of saline-alkali land, climate conditions, and crop varieties. For example, the salt-alkali tolerant genes suitable for mild saline-alkali land may not be suitable for severe saline-alkali land; the microbial inoculants suitable for northern saline-alkali land may have unstable effects in southern saline-alkali land due to climate differences. The influence of environmental factors limits the popularization and application of agricultural biotechnology (Abdul et al., 2024).

Third, there are potential safety risks in genetic engineering technology. The safety of transgenic crops has always been a concern of the public. Although transgenic salt-alkali tolerant crops have been tested and verified, there are still potential risks such as gene drift, impact on non-target organisms, and impact on soil microecological environment. These potential safety risks have affected the public acceptance of transgenic salt-alkali tolerant crops and limited the large-scale application of genetic engineering technology (Wang et al., 2023).

Fourth, the cost of biotechnology is high. Omics technology, genetic engineering technology, and other biotechnologies require high-precision equipment and professional technical personnel, and the cost is relatively high, which is difficult to popularize and apply in small-scale farmers and developing regions. In addition, the breeding cycle of molecular marker-assisted breeding and genetic engineering breeding is still relatively long, and the cost of breeding is high, which limits the application of these technologies (Fatima et al., 2024).

Fifth, the technical system is not perfect. At present, the technical system of agricultural biotechnology in crop salt-alkali tolerance improvement is not perfect. For example, the functional verification system of salt-alkali tolerant genes is not mature enough. Most of the current gene functional verifications are carried out under controlled laboratory conditions, which are quite different from the actual complex saline-alkali land environment, leading to the inconsistency between the verified gene function and the actual application effect. In addition, the evaluation system of salt-alkali tolerant crop varieties is not unified. Different research teams use different evaluation indicators (such as survival rate, biomass, yield) and stress conditions (such as salt concentration, stress time), which makes it difficult to compare and evaluate the salt-alkali tolerance of different crop varieties objectively and fairly. Moreover, the technical integration system of multiple biotechnologies is still in the initial stage, and there is a lack of effective integration methods and technical routes between different biotechnologies, which makes it difficult to give full play to the synergistic effect of multiple technologies (Zhao et al., 2024). In addition, the promotion and application system of biotechnology achievements is not perfect. There is a disconnect between the research achievements of agricultural biotechnology and the actual production needs of saline-alkali regions. A large number of research achievements stay in the laboratory or small-scale trial stage, and it is difficult to transform into practical production technologies and be popularized and applied on a large scale, which restricts the practical value of biotechnology in crop salt-alkali tolerance improvement (Chen et al., 2025).

5.2 Solution Strategies

Aiming at the existing problems of agricultural biotechnology in crop salt-alkali tolerance improvement, this paper puts forward corresponding solution strategies, so as to promote the healthy and sustainable development of agricultural biotechnology in this field and improve the efficiency and effect of crop salt-alkali tolerance improvement.

First, strengthen the research on the molecular mechanism of crop salt-alkali tolerance and expand the source of salt-alkali tolerant genes. On the one hand, we should use multi-omics integration technology (genomics, transcriptomics, proteomics, metabolomics) to systematically explore the molecular mechanism of crop salt-alkali tolerance, focus on clarifying the interaction mechanism between multiple salt-alkali tolerant genes and the regulatory network of the whole genome, and lay a solid theoretical foundation for crop salt-alkali tolerance improvement. On the other hand, we should expand the source of salt-alkali tolerant genes, not only excavate salt-alkali tolerant genes from crops themselves, but also isolate and clone salt-alkali tolerant genes from extreme halophytes, salt-tolerant microorganisms and other organisms with strong salt-alkali tolerance, enrich the gene resources for crop salt-alkali tolerance genetic engineering (Abdul et al., 2024). In addition, we should develop multi-gene co-transformation technology, transfer multiple salt-alkali tolerant genes with different functions into target crops at the same time, and improve the salt-alkali tolerance of crops in an all-round way, so as to meet the growth needs of crops in high saline-alkali land.

Second, optimize the application mode of biotechnology and reduce the impact of environmental factors. We should combine the type of saline-alkali land (mild, moderate, severe), climate conditions, and crop varieties to develop targeted biotechnology application schemes. For example, for mild saline-alkali land, we can adopt molecular marker-assisted breeding technology to breed salt-alkali tolerant crop varieties; for severe saline-alkali land, we can combine genetic engineering technology and microbial biotechnology to improve crop salt-alkali tolerance and soil environment at the same time. In addition, we should strengthen the research on the environmental adaptability of biotechnology, such as improving the environmental adaptability of microbial inoculants by means of genetic modification, and screening salt-alkali tolerant genes with wide adaptability, so as to reduce the impact of environmental factors on the application effect of biotechnology (Wang et al., 2025). At the same time, we should carry out long-term field trials in different types of saline-alkali regions to verify the application effect of biotechnology under actual production conditions and optimize the application scheme continuously.

Third, strengthen the safety evaluation and management of genetic engineering technology and improve public acceptance. We should establish and improve the safety evaluation system of transgenic salt-alkali tolerant crops, carry out comprehensive and systematic safety evaluations from the aspects of food safety, environmental safety, and ecological safety, and ensure the safety of transgenic crops. At the same time, we should strengthen the supervision of the whole process of transgenic technology, including gene cloning, vector construction, genetic transformation, and variety promotion, to prevent potential safety risks such as gene drift. In addition, we should strengthen science popularization, publicize the principles, application effects, and safety of transgenic technology to the public, eliminate public misunderstandings about transgenic crops, and improve public acceptance of transgenic salt-alkali tolerant crops, so as to promote the large-scale application of genetic engineering technology (Fatima et al., 2024).

Fourth, reduce the cost of biotechnology and promote its popularization and application. We should strengthen the research and development of low-cost biotechnology equipment and technologies, such as developing low-cost gene sequencing equipment and genetic transformation technologies, reducing the cost of omics technology and genetic engineering technology. At the same time, we should strengthen the training of professional and technical personnel, cultivate a large number of professional and technical personnel engaged in agricultural biotechnology research and application, improve the technical level of biotechnology application, and reduce the technical cost. In addition, we should strengthen the cooperation between enterprises, universities, and research institutes, realize the sharing of resources and technologies, reduce the research and development cost of biotechnology, and promote the popularization and application of biotechnology in small-scale farmers and developing regions (Zhang et al., 2025). At the same time, we should optimize the breeding process, shorten the breeding cycle of molecular marker-assisted breeding and genetic engineering breeding, and reduce the breeding cost.

Fifth, improve the technical system of agricultural biotechnology and promote the transformation of achievements. We should improve the functional verification system of salt-alkali tolerant genes, combine laboratory verification with field trial verification, simulate the actual complex saline-alkali land environment in the laboratory, and carry out long-term field trials to ensure the consistency between gene function and actual application effect. At the same time, we should establish a unified evaluation system of salt-alkali tolerant crop varieties, formulate unified evaluation indicators and stress conditions, and realize the objective and fair comparison and evaluation of different salt-alkali tolerant crop varieties. In addition, we should strengthen the research on the integration technology of multiple biotechnologies, explore effective integration methods and technical routes, give full play to the synergistic effect of multiple technologies, and improve the efficiency of crop salt-alkali tolerance improvement (Zhao et al., 2024). Moreover, we should improve the promotion and application system of biotechnology achievements, establish a close cooperative relationship between research institutions and agricultural production entities, carry out targeted technology promotion according to the actual production needs of saline-alkali regions, and promote the transformation of biotechnology achievements into practical production technologies, so as to give full play to the practical value of biotechnology.

6. Future Prospects

With the rapid development of life science and agricultural biotechnology, agricultural biotechnology will play an increasingly important role in crop salt-alkali tolerance improvement, and will show a series of new development trends in the future. In terms of genetic engineering technology, the development of gene editing technologies such as CRISPR-Cas9 will make the modification of crop genes more precise and efficient, and realize the targeted modification of salt-alkali tolerant genes, improving the salt-alkali tolerance of crops without introducing exogenous genes, which will effectively solve the safety problems of transgenic crops. At the same time, multi-gene co-transformation technology and gene stacking technology will be more mature, which can transfer multiple salt-alkali tolerant genes into target crops at the same time, realizing the all-round improvement of crop salt-alkali tolerance (Abdul et al., 2025).

In terms of molecular marker-assisted breeding, with the development of genomics technology, more molecular markers closely linked to salt-alkali tolerant genes will be screened, and high-density genetic linkage maps and physical maps of crops will be constructed, which will improve the accuracy and efficiency of molecular marker-assisted selection. At the same time, the combination of molecular marker-assisted breeding and big data technology will realize the intelligent selection of salt-alkali tolerant crop varieties, shorten the breeding cycle, and improve the breeding effect. In addition, the development of marker-free selection technology will solve the problem of marker gene residue in crop varieties, improving the quality and safety of salt-alkali tolerant crop varieties (Wang et al., 2024).

In terms of omics technology, the integration of multi-omics technology will be more in-depth, and the combination of genomics, transcriptomics, proteomics, metabolomics, and epigenomics will systematically explore the molecular mechanism of crop salt-alkali tolerance, screen more key salt-alkali tolerant genes and metabolites, and provide more abundant gene resources and theoretical basis for crop salt-alkali tolerance improvement. At the same time, the development of single-cell omics technology will realize the study of the molecular mechanism of crop salt-alkali tolerance at the single-cell level, which will further deepen people‘s understanding of the molecular mechanism of crop salt-alkali tolerance (Fatima et al., 2023).

In terms of microbial biotechnology, the screening and modification of salt-tolerant microorganisms will be more targeted. By means of omics technology and genetic engineering technology, more efficient salt-tolerant PGPR and fungi will be screened and modified, improving their salt-alkali tolerance and plant growth-promoting ability. At the same time, the development of composite microbial inoculants will be more mature, and the combination of different types of salt-tolerant microorganisms will realize the complementary advantages of microorganisms, improving the application effect of microbial inoculants. In addition, the combination of microbial biotechnology and soil improvement technology will realize the joint improvement of crop salt-alkali tolerance and soil environment, promoting the sustainable development of agriculture in saline-alkali regions (Chen et al., 2025).

In terms of the integration of multiple biotechnologies, the integration of agricultural biotechnology with information technology, big data technology, and artificial intelligence technology will become a new trend. For example, the combination of omics technology and big data technology will realize the rapid screening and functional prediction of salt-alkali tolerant genes; the combination of molecular marker-assisted breeding and artificial intelligence technology will realize the intelligent design and breeding of salt-alkali tolerant crop varieties; the combination of microbial biotechnology and information technology will realize the real-time monitoring of the growth status of salt-tolerant microorganisms and the dynamic adjustment of application schemes. The integration of multiple technologies will give full play to the synergistic effect of various technologies, and promote the transformation of crop salt-alkali tolerance improvement from „empirical breeding“ to „precision breeding“ (Zhang et al., 2024).

In addition, the research and application of agricultural biotechnology in crop salt-alkali tolerance improvement will pay more attention to sustainability and environmental friendliness. While improving crop salt-alkali tolerance, it will focus on protecting the ecological environment, reducing the use of chemical fertilizers and pesticides, and promoting the sustainable development of agriculture in saline-alkali regions. At the same time, the research and application of agricultural biotechnology will be more targeted to the actual production needs of different saline-alkali regions, developing targeted improvement technologies and crop varieties according to the characteristics of different saline-alkali regions, and improving the practical value of biotechnology (Zhao et al., 2025).

7. Conclusions

Saline-alkali land, as a valuable land resource that can be developed and utilized, plays an important role in alleviating global food security pressure and promoting sustainable agricultural development. Agricultural biotechnology, including genetic engineering, molecular marker-assisted breeding, omics technology, and microbial biotechnology, has provided efficient and precise technical means for crop salt-alkali tolerance improvement, and has made significant progress in recent years. Genetic engineering technology can realize the rapid improvement of crop salt-alkali tolerance by transferring salt-alkali tolerant genes; molecular marker-assisted breeding can improve the selection efficiency and shorten the breeding cycle; omics technology can systematically explore the molecular mechanism of crop salt-alkali tolerance and provide abundant gene resources; microbial biotechnology can improve soil microecological environment and enhance crop salt-alkali tolerance indirectly.

The integration of multiple biotechnologies can give full play to the advantages of various technologies, make up for their limitations, and further improve the efficiency and effect of crop salt-alkali tolerance improvement. However, agricultural biotechnology still faces some problems in crop salt-alkali tolerance improvement, such as complex genetic basis of crop salt-alkali tolerance, influence of environmental factors, potential safety risks of genetic engineering technology, high cost of biotechnology, and imperfect technical system. Aiming at these problems, corresponding solution strategies should be adopted, such as strengthening the research on molecular mechanism, optimizing application mode, strengthening safety evaluation and management, reducing technology cost, and improving technical system.

In the future, with the continuous development of agricultural biotechnology and the integration with other related technologies, agricultural biotechnology will show a more precise, efficient, and sustainable development trend, and will play a more important role in crop salt-alkali tolerance improvement. It will effectively promote the development and utilization of saline-alkali land resources, improve the yield and quality of crops in saline-alkali regions, alleviate global food security pressure, and promote the sustainable development of agriculture in saline-alkali regions. This study systematically reviews the application of agricultural biotechnology in crop salt-alkali tolerance improvement, analyzes the existing problems and solution strategies, and prospects the future development trends, which provides important technical support and theoretical reference for researchers engaged in this field.

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