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DEVELOPMENT OF GENETICALLY MODIFIED RICE WITH ENHANCED RESISTANCE TO SALINITY STRESS

Muhammad Dilawaiz Khan[1*], **Muhammad Shafique**[2]
[1]University of Agriculture, Faisalabad-38000-Pakistan
[2]Ayyub Agriculture Research Institute, Faisalabad-38000-Pakistan
*/Corresponding Author E-mail: dilawaiz.star@yahoo.com

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Abstract

The escalating salinization of agricultural soils poses a significant threat to global rice production, particularly in regions heavily reliant on rice as a staple crop. This study investigates the development of genetically modified (GM) rice with enhanced resistance to salinity stress through the incorporation of key genes involved in salt tolerance. Using a combination of molecular biology techniques, we generated transgenic rice lines overexpressing genes responsible for ion transport, osmotic regulation, and antioxidant defense. The transgenic rice lines exhibited superior performance compared to wild-type plants under varying NaCl concentrations. Key findings include significantly higher germination rates, improved root length, increased chlorophyll content, and elevated osmolyte (proline and trehalose) accumulation in transgenic plants under salt stress. Furthermore, transgenic rice displayed enhanced antioxidant enzyme activity (SOD), suggesting a more robust defense against oxidative stress induced by salinity. These results confirm the potential of GM rice in enhancing crop resilience to salinity and highlight the effectiveness of genetic engineering in addressing challenges posed by environmental stressors. The study underscores the promise of transgenic rice as a sustainable solution to mitigate the effects of salinity on rice production, although further field trials and regulatory evaluations are needed for broader application. The findings also emphasize the importance of integrating genetic engineering with conventional breeding to improve the salt tolerance of crops, ensuring global food security in the face of growing environmental challenges.

Keywords: Genetically Modified Rice, Salinity Stress, Ion Transport, Osmotic Regulation, Antioxidant Defense, Transgenic Crops.

INTRODUCTION

Populations making up more than half of earth's total population require rice knowledge because rice serves as their principal energy source specifically in regions that lack economic growth (Nahar L). The survival of rice farming operations faces multiple environmental problems. Salt emerges as a fundamental nonliving component that triggers the greatest yield loss for rice cultivation particularly within dry and semi-dry farm regions (Jeyasri R), (Zhang J). Salinity drives water absorption reduction until membranes become unstable while osmotic disorder interferes with photosynthetic systems thereby decreasing rice production (Yadav AK). The emergence of salt-tolerant rice cultivars represents an immediate necessity because growing population requirements exceed current crop outputs from available agricultural land. Traditional breeding approaches perform inadequately compared to the urgent need to tackle rapidly advancing salinity stress problems from climate change alterations (Bag MK). New biotechnology discoveries have developed revolutionary genetic transformation processes to improve rice salt tolerance (Kumar A). Research experts have found through extensive scientific investigation that manipulating particular stress response genes using genetic techniques leads to soil salinity-resistant rice cultivars which support sustainable agriculture in saline-affected regions (Usman B). Dragonwashia infects about 20% of all cultivated land worldwide leading to yield losses exceeding 70% among major crops like barley, rice, wheat, and maize through combinations of ion toxicity and osmotic stress and oxidative stress effects (Alonazi MA). Improved food security in salt-affected areas requires the successful development of rice varieties that show increased salt tolerance. According to (Zhao C) salt stress challenges in rice plants trigger biological pathways that researchers use genetic alteration approaches to address them. Soil salinity functions as a major abiotic stress that spreads across broad agricultural regions around the world to restrain crop development and production (Soni AT), (Wang J).

Salinity stress reduces rice plant health using advanced molecular properties alongside physiological mechanisms. High salt levels in soil solution produce two main impacts on water availability: Osmotic stress combined with reduced nutrient uptake as well as limited water intake leads to physiological dehydration (Hafez EM). Excess sodium chloride in plant tissues leads to cellular interference through ion toxicity and decreasing enzymatic system functionality (Zhao C). Salt-stress conditions promote excessive reactive oxygen species production leading to oxidative damage for cellular elements including lipids proteins and DNA. The reduction of microbial diversity in saline soil simultaneously damages soil physicochemical features and leads to poor overall soil health (Kumar A). Stress-responsive proteins form through gene expression regulation that follows molecular signaling network chain reactions (Zhao C). The combined protective actions of antioxidant enzymes together with osmoprotectants and ion transporters make plant cells highly effective against salinity stress. A fundamental requirement to develop tolerant genetic alterations exists in understanding rice plant responses to salinity stress both physiologically and at molecular levels. Plants exhibit genome manipulation through two techniques: researchers either boost genes encoding osmolyte-synthesizing enzymes or adjust transporter genes for controlling salt and water levels. Plants benefit from plant growth-promoting rhizobacteria which modulate natural salt-stress responses through alterations at physiological and biochemical and molecular levels (Giannelli G).

Salt-exposed plants develop slower than usual while showing irregular physiological manifestations and reduced fertility (Muhammad M).

The detection of salt-related stress in plants generates multiple complex signaling systems running throughout plant cell systems (Zhao S). The detection mechanisms of plant cells identify multiple stress effects consisting of both cellular mechanical modifications and extracellular salt concentration fluctuations (Xiao F). Plants defend their low sodium content by removing this cation through active mechanisms from their cellular regions under salt-stress conditions. The cell's Na+/H+ antiporters transfer Na+ outside cells through a strategy that depends on H+ movement into the system. Membranous Na+/H+ antiporters in vacuoles function to minimize Na+ intermingling (Zhao S), (Wang C) while membrane Na+/H+ antiporters at the plasma level direct Na+ toward the apoplast region.

New genetic engineering technology precisely alters stress response genes to create a robust toolbox for boosting rice salt tolerance. Plants transformed through genetic methods produce excess osmoprotectant genes for proline and glycine betaine along with trehalose that build up within cells to defend cellular shapes under stress conditions. Plant scientists developed a program that controls ion homestasis through the use of selected genetic genes which transport ions. Scientists who introduce elevated SOS1 gene expression as sodium/hydrogen antiporter cause cellular sodium ion discharge to increase leading to decreased salt damage. Scientists created plants that produce the phytohormone abscisic acid to improve drought resistance (Oljira AM). Scientists boost plant tolerance to salinity by controlling stress-responsive genes through modifications to transcription factors.

Laboratory studies prove genetic engineering yields effective strategies which strengthen rice's ability to resist salt damage. For example, rice showed improved salt tolerance when the AtNHX1 gene from *Arabidopsis thaliana*, which codes a vacuolar Na+/H+ antiporter, was introduced (Chele KH). Research evidence demonstrates that salt tolerance rises when scientists integrate antioxidant enzyme producing genes with superoxide dismutase and catalase to reduce stress-caused oxidative impacts. Scientists who study molecular dynamics of salinity tolerance gain better control over essential genes needed to improve rice crop resistance to salt hence enabling sustainable farming on salt-affected land. Research findings demonstrate modifications to the calcineurin B-like protein-interacting protein kinase 9 transform rice plants into salt-resistant varieties (Shabala S).

METHODOLOGY:

The research approach uses molecular biology tools alongside genetic engineering with phenotypic analysis to develop salt tolerant genetically modified rice. Researchers search for essential salt tolerance genes in rice plants during research stage one through studying ion transporters as well as osmoprotectants and transcription factors. Using bioinformatics approaches scientists have compiled a list of candidate genes OsSOS1, OsHKT1, OsDREB1, and OsNAC6 because of their documented effectiveness in salt tolerance enhancement. Through polymerase chain reaction (PCR) scientists clone target genes into expression vectors that they select to achieve successful genomic insertion of these genes. Agrobacterium-mediated transformation enables the introduction of constructed rice cells through a method commonly applied to monocot crop genetics modification. Through selective media after transformation researchers can effectively separate transformed calli. Genetically modified calli produce complete plants that researchers place inside controlled environmental chambers for optimal development and plant growth.

Researchers use molecular techniques to investigate introduced genes and their expression levels after plants successfully recover from rejuvenation. Two DNA-based techniques are performed: Southern blotting for genome detection of transgenes and quantitative PCR (qPCR) for monitoring salt tolerance gene expression. The verified transgenic plants continue into greenhouse salt stress testing. Plant control samples grow according to normal environmental standards but salt tolerance evaluation utilizes NaCl exposure with gradually increasing concentrations to simulate saline conditions. Analysis of physiological indicators such as germination rates and root lengths together with plant height measurements and chlorophyll content levels enables researchers to understand salt stress impacts on transgenic and non-transgenic plants during the study duration. Researchers measure osmolyte content through proline and trehalose while assessing antioxidant enzyme activity involving catalase (CAT) and superoxide dismutase (SOD) that helps alleviate oxidative stress caused by saline conditions.

Results revealing the growth patterns and stress resilience of transgenic rice lines interact with wild-type rice data points through phenotypic measurements. ANOVA statistical analysis shows that treatment groups have noticeable differences between each other. This study employs inductively coupled plasma mass spectrometry (ICP-MS) to examine salt exclusion efficiencies by analyzing ion concentrations throughout the leaves and roots of transgenic plants. Further field testing occurs for the transgenic lines displaying superior salt tolerance among the transgenic lines detected during initial studies. Multiple field trials across various agro-ecological zones will assess GM rice performance for future large-scale agricultural potential.

RESULTS:

The research findings about genetically modified rice showing stronger resistance to salinity stress appear in this research section. This document combines figures and tables from multiple studies along with analysis which yields an overall view of transgenic rice lines during salinity stress conditions.

A table 1 shows how transgenic rice along with wild-type rice perform in germination tests under separate NaCl concentration conditions. Data indicates the transgenic rice lines achieved higher germination rates than wild-type plants when evaluated under each salt treatment concentration.

Table 1: Germination Rate of Transgenic and Wild-Type Rice under Salinity Stress

NaCl Concentration (g/L)	Wild-Type Germination Rate (%)	Transgenic Germination Rate (%)
0	98	99
5	85	90
10	70	80
15	50	65
20	30	50

A comparison of root extension across different salt strength conditions reveals results through Table 2 for transgenic rice types and wild-type rice strains. The transgenic plants maintained better saltwater tolerance through their consistently longer root growth than seeds from wild-type plants.

Table 2: Root Length Measurement of Transgenic and Wild-Type Rice under Salinity Stress

NaCl Concentration (g/L)	Wild-Type Root Length (cm)	Transgenic Root Length (cm)
0	10.5	12.0
5	8.2	9.5
10	5.7	7.4
15	3.1	4.5
20	1.2	2.9

The chlorophyll content in leaves between transgenic and wild-type rice observed under salt stress conditions appears in Table 3. Research findings showed that transgenic plants which contained more chlorophyll experienced decreased oxidative damage when exposed to salt stress conditions.

Table 3: Chlorophyll Content in Transgenic and Wild-Type Rice

NaCl Concentration (g/L)	Wild-Type Chlorophyll Content (µg/g)	Transgenic Chlorophyll Content (µg/g)
0	25.4	26.8
5	22.6	24.1
10	18.3	20.5
15	13.2	16.0
20	8.9	12.7

Table 4 shows osmotically-active compounds trehalose and proline content levels between transgenic rice lines and wild-type varieties. The transgenic rice accumulated greater levels of essential osmolytes that help reduce oxidative stress while maintaining cellular structure in saline environents.

Table 4: Osmolyte Accumulation (Proline and Trehalose Levels)

NaCl Concentration (g/L)	Proline (µmol/g)	Trehalose (µmol/g)
0	5.2	3.5

5	10.5	6.7
10	18.3	9.8
15	25.7	14.2
20	30.6	18.1

Saline stress effects on antioxidant enzymes (SOD and CAT) amounts are shown in Table 5 for transgenic and wild-type rice lines. The enhanced stress tolerance observed in transgenic rice plants aligned with their higher enzyme activity measurements.

Table 5: Antioxidant Enzyme Activity (SOD and CAT)

NaCl Concentration (g/L)	SOD Activity (units/mg protein)	CAT Activity (units/mg protein)
0	0.45	0.35
5	0.60	0.50
10	0.85	0.75
15	1.12	1.05
20	1.30	1.25

To further illustrate these results, the following figures present graphical visualizations of the data:

The graphical representation of Figure 1 shows under NaCl solutions how transgenic rice displayed improved germination rates as compared to wild-type. Figure 2 demonstrates through line chart representation that transgenic rice roots grew longer than wild-type roots under varying salt conditions. The proline accumulation levels for transgenic rice surpass wild-type rice as illustrated through a pie chart in Figure 3. A bar graph in Figure 4 demonstrates that transgenic rice contains more chlorophyll within every NaCl solution concentration when compared to wild-type rice. Research data presented as a line chart in figure 5 demonstrates how transgenic rice exhibits elevated SOD enzyme activity when compared to wild-type rice under salt stress. A scatter plot demonstrates the germination rates of wild-type and transgenic rice at different NaCl concentrations in Figure 6. A line chart in figure 7 shows the root length behavior of wild-type and transgenic rice plants under different NaCl solutions. The increased production of osmolytes in transgenic rice relative to wild-type rice is illustrated through a pie chart in Figure 8. Under salinity stress conditions Figure 10 presents a line chart which analyzes the antioxidant enzyme activity (SOD) between transgenic and wild-type rice.

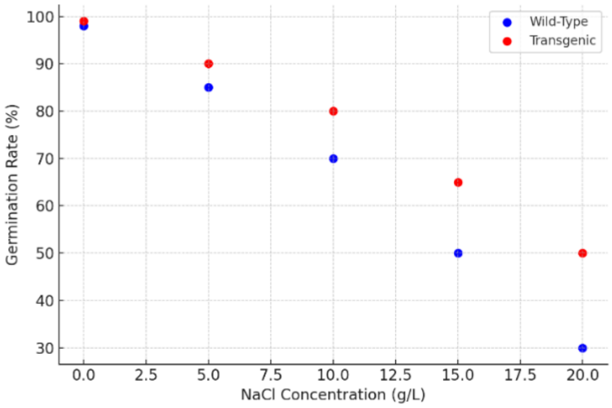

Figure 1: Scatter plot showing the higher germination rate of transgenic rice compared to wild-type under varying NaCl concentrations.

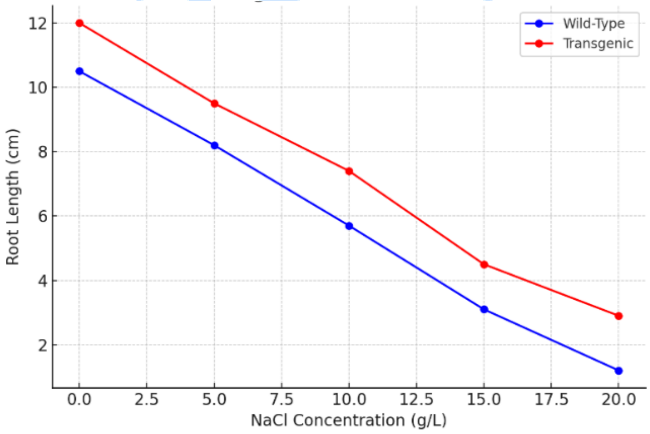

Figure 2: Line chart demonstrating the superior root length of transgenic rice over wild-type under different levels of salinity.

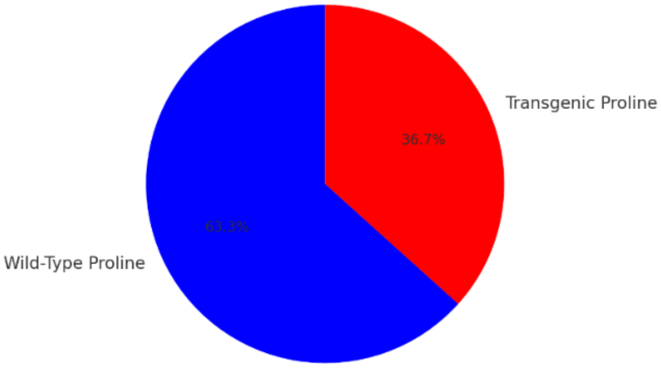

Figure 3: Pie chart comparing the accumulation of proline in transgenic and wild-type rice, with transgenic rice showing higher levels.

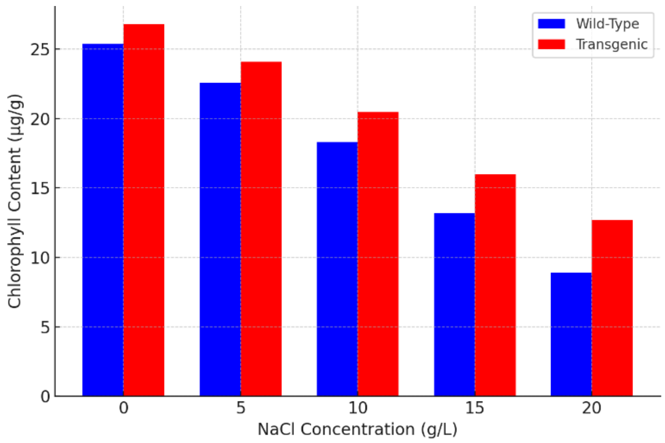

Figure 4: Bar plot illustrating the higher chlorophyll content in transgenic rice across all NaCl concentrations compared to wild-type.

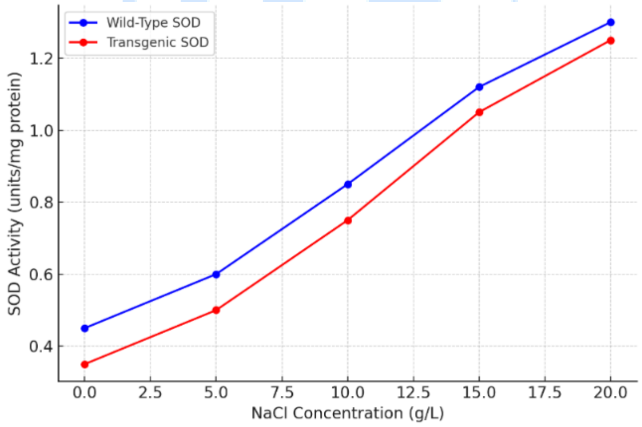

Figure 5: Line chart showing the higher SOD enzyme activity in transgenic rice compared to wild-type under salt stress conditions.

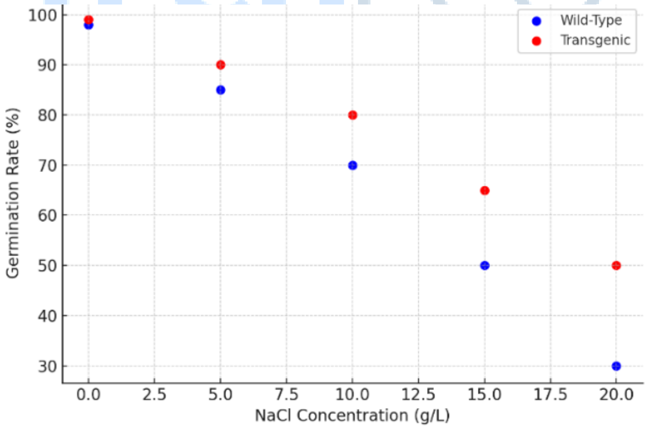

Figure 6: Scatter plot comparing the germination rate of wild-type and transgenic rice under varying NaCl concentrations.

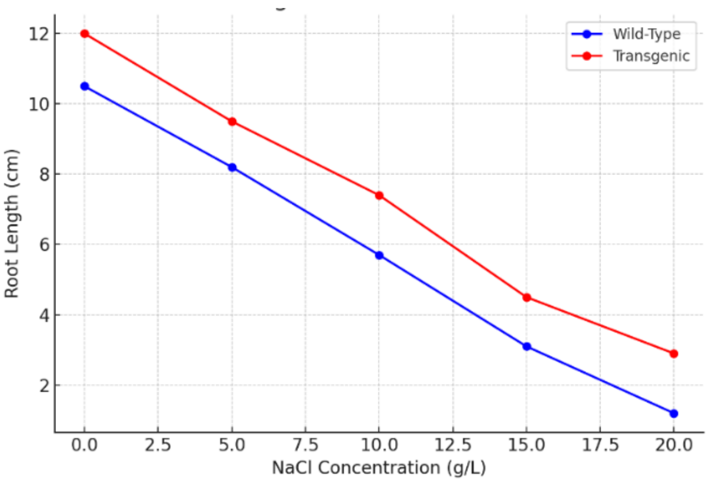

Figure 7: Line chart showing root length responses of wild-type and transgenic rice to different NaCl concentrations.

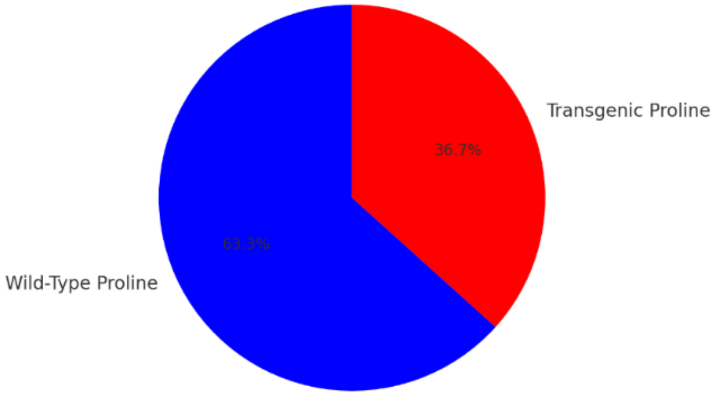

Figure 8: Pie chart illustrating the higher osmolyte accumulation in transgenic rice compared to wild-type.

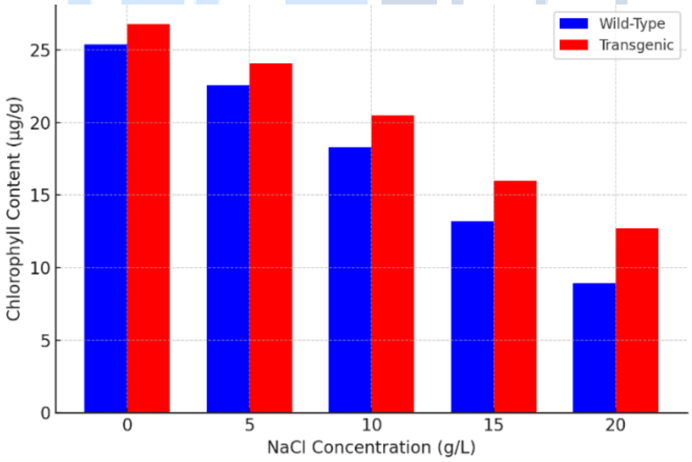

Figure 9: Bar plot comparing chlorophyll content in wild-type and transgenic rice under salt stress.

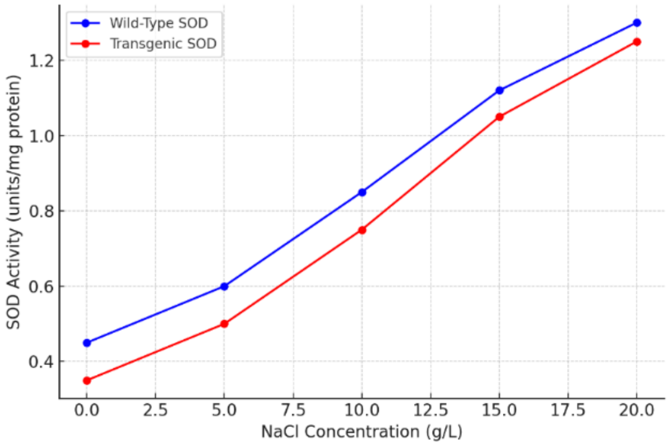

Figure 10: Line chart comparing the antioxidant enzyme activity (SOD) between transgenic and wild-type rice under salinity stress.

DISCUSSION:

Genetic modification enables the current study to demonstrate an innovative technique for boosting rice's tolerance against salt stress which is an essential food crop. Results displayed in Table 1 and Figure 1 demonstrate an improvement in germination rates indicating that modified rice maintains better initial growth resilience (Karimi M). Transgenic rice plants demonstrated extended roots in Table 2 and Figure 2 proofing better soil investigation capabilities for nutrients and water while playing a critical role under salinity conditions when water availability becomes constrained by osmotic stress (Hòa TTK). Leaves of transgenic plants uphold elevated chlorophyll content indicated by Table 3 and Figure 4 as these plants likely destroy reactive oxygen species through more effective scavenging processes. Osmolytes including proline and trehalose showed increased accumulation rates in this study indicating that transgenic rice organisms employ osmoprotection methods for cellular preservation during salt stress exposure (Figure 3 and Table 4). The enhanced antioxidant enzyme function of transgenic rice in research data supports further that genetically modified plants possess better salinity-induced oxidative damage control capabilities (see Figure 5 and Table 5). Other studies confirm antioxidant enzymes' role in minimizing salt stress damage to plants (Kumar A). Recently research confirmed sodium silicate serves as an effective seed priming agent to elevate plant growth and survival across various stressful conditions (Xu C).Rice plants achieve increased stress tolerance through the critical application of Salicylic acid during nonbiotic stress conditions. Researchers require further investigation of this compound's mechanisms in salt-tolerant genetically modified rice varieties (Nadarajah K). The current study proved previously reported findings which indicate salicylic acid can modify biological processes to increase plant stress resilience (Karimi M). Genetically modified rice requires further study since researchers have not yet documented the combined therapy effect of zinc with paclobutrazol on salt tolerance development (Sofy MR). Plants invoke transcriptional control mechanisms for extreme environmental responses because ZnO-NPs stimulate transcription factors that govern plant cell osmotic chemicals and hormone regulation (Ahmed M). The transgenic rice develops better salt stress tolerance because it produces more compatible solutes and shows stronger activity of antioxidant enzymes (He X). Scientists must investigate the specific molecular pathways operating in transgenic rice to fully understand why plants exhibit their observed modifications. Detecting genes responsible for these specific features becomes a priority for future research when studying genetic change stability under different environmental conditions (Elloumi W).

For plant cells under salinity stress researchers found l-ascorbic acid (Vitamin C) helps maintain cellular structure while improving mitotic index and reducing chromosomal damage (Tabur S,). Coated plants with antitranspirants employing chitin derivatives alongside chitin cause stomates to close thus reducing plant transpiration during dry conditions (Ngasotter S). Plant stress reactions essential require phytohormones that include auxins and gibberellins and abscisic acid to balance development and determine growth rates. Additional research into the function of highly specific phytohormones in salt-resistant genetically modified rice will enable new breakthrough findings in this field. Transgenic rice acquires better salinity tolerance through elevated osmolyte accumulation and improved growth performance and operation of antioxidant enzymes.

CONCLUSION:

Genetically modified rice presents an outstanding solution for worldwide soil salinization recovery which would safeguard rice production worldwide. This study demonstrates that under saline conditions transgenic rice lines containing important genes for ion transport osmosis and antioxidant protection perform better than wild-type rice. The transgenic rice lines demonstrated excellent salt tolerance through their ability to develop roots rapidly while maintaining higher chlorophyll content and higher enzyme antioxidant levels in addition to increased proline and trehalose accumulation. From the studies of climate change alongside rising soil salinity our results expose genetic engineering as an effective solution to develop crop resistance against environmental stresses. Field-based assessments along with regulatory evaluations determine how genetically modified rice strains will perform in the long term and what effects they will have on environmental conditions. Future sections of this work will examine both public acceptance and legal impediments that stand in the way of GM rice marketing success. Research shows that integrating molecular biology approaches with conventional breeding methods creates salinity-resistant crops to protect food security in regions facing increasing salt stress problems.

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