

LITERATURE ASSESSMENT OF RESILIENT SOYBEAN GENOTYPES BASED ON PHYSIOLOGICAL INDICATORS AND MOLECULAR MARKERS IN THE CONDITIONS OF KARAKALPAKSTAN

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Abstract

In this article, soybean (*Glycine max* (L.) Merr.) The scientific and methodological foundations for assessing the resistance of Merr. genotypes to abiotic stress based on physiological indicators and molecular markers are highlighted. The research concept provides for the harmonization of physiological indicators such as plant growth rate, relative leaf water content, chlorophyll status, root system development, biomass accumulation, and the ratio of sodium and potassium ions with genotypic data. Therefore, combining phenotypic assessment with molecular markers can increase the efficiency of selecting genotypes suitable for the conditions of Karakalpakstan. Based on this approach, the article proposes the organization of field and control experiments, the determination of physiological indicators, DNA isolation and marker analysis, as well as comprehensive evaluation criteria.

Keywords: soy, *Glycine max*, Karakalpakstan, salinization, drought, abiotic stress, physiological indicators, molecular marker, SNP, SSR, GmSALT3, genotype.

Introduction

Abiotic factors such as climate change, limited water resources, and soil salinization are increasingly impacting agricultural crop yields. Especially in dry and arid regions, the accumulation of salts in the soil can hinder the plant's absorption of water and mineral substances, leading to the disruption of growth, photosynthesis, and reproductive processes. In the conditions of Karakalpakstan, taking these factors into account, identifying genotypes resistant to salinization and suitable for local agro-ecological conditions is an important scientific and practical task.

Soybean is one of the important crops for food, fodder, and industry, rich in protein and oil. However, soybeans are among the most sensitive crops to salt stress. In saline environments, osmotic stress, ionic toxicity, and oxidative stress can affect the normal physiological state of the plant. Modern research indicates that there are significant genetic differences in salt tolerance among soybean genotypes.

Soybean salt tolerance is a complex, multi-gene trait that is difficult to reliably evaluate based on a single morphological indicator. Combining physiological phenotyping with DNA markers can provide valuable information for early genotype selection and marker-assisted selection. Modern reviews point to Na^+/K^+ homeostasis in the shade, ion distribution in tissues, osmotic adaptation, and stress-responsive genes as important parts of salt tolerance mechanisms.

Purpose of the research

The aim of the study is to comprehensively evaluate the resistance of soybean genotypes based on physiological indicators and molecular markers in the conditions of saline soils and water scarcity in Karakalpakstan, isolate promising genotypes, and create a scientific basis for further breeding research.

Research objectives

Determination of the growth and development characteristics of soybean genotypes tested under the conditions of Karakalpakstan.

Assessment of physiological indicators such as relative leaf water content, chlorophyll status, leaf area, root length, and biomass under salt stress conditions.

Determination of Na^+ and K^+ levels in plant tissues, as well as the Na^+/K^+ ratio, and analysis of their relationship with resistance.

Assessment of DNA polymorphism in selected genotypes based on SSR and/or SNP.

Assessment of the feasibility of using candidate genes and markers mentioned in the scientific literature related to salt tolerance.

Development of criteria for selecting promising genotypes by integrating physiological and molecular data.

Materials and research methods

Various genotypes and varieties of soybeans were selected as the object of study. When selecting genotypes, their genetic diversity, specific reaction to salinization, and the possibility of cultivation in the agro-ecological conditions of Karakalpakstan are taken into account.

The experiment can be organized under two main conditions: control conditions and salt stress conditions. In the field experiment, the electrical conductivity, pH, mechanical composition, humus content, and primary ion composition of the soil are determined. In laboratory or greenhouse experiments, salt stress levels are monitored. This approach allows for the comparison of natural variability in field conditions with controlled stress in laboratory conditions.

During physiological assessment, the relative water content of the leaf, chlorophyll index, leaf area, root length, dry mass of the root and shoot, growth rate, and fruit elements are recorded. Biochemical indicators such as proline and malondialdehyde can also be additionally assessed if the necessary laboratory capabilities are available.

Ion homeostasis is of particular importance in understanding salt tolerance. Therefore, it is recommended to determine the Na^+ and K^+ concentrations in plant tissues and calculate the Na^+/K^+ ratio. The literature indicates that one of the important mechanisms in the soybean salt response is the restriction of excessive intake of Na^+ into tissues and the maintenance of K^+ homeostasis.

Genome DNA is isolated from young leaf samples for molecular analysis. DNA quality and concentration are assessed by spectrophotometry or fluorimetry. Then methods such as PCR/KASP can be used for selected SSR or SNP markers. When selecting markers, their association with salt resistance in scientific literature, polymorphism, and reliable amplification in laboratory conditions are taken into account.

There is information that the GmCHX1/GmSALT3 gene and some of its allelic variants are associated with salt tolerance in soybeans. Additionally, certain SNP markers on chromosome 3 and QTL regions on other chromosomes are associated with salt tolerance phenotypes.

Assessment of physiological indicators

The relative water content of a leaf is one of the important indicators used to assess the water state of a plant. The maintenance of relative water levels under stress conditions may reflect the ability of cells to maintain a stable water regime.

Chlorophyll status is important for assessing the stress response of the photosynthetic apparatus. When salt stress increases, changes in photosynthesis and chloroplast function can be observed; therefore, the chlorophyll index can be used as an additional indicator in physiological screening. The length of the root system and dry mass are also important indicators. A well-developed root system in saline soils may be linked to a strategy for absorbing water and minerals. However, instead of interpreting each indicator separately, it is advisable to analyze them together with yield and ion homeostasis.

Scientific basis for the use of molecular markers

Since salt tolerance is a multi-gene and complex trait, it is advisable to use several markers in genetic analysis. In soy research, genomic regions associated with salt tolerance were identified through QTL mapping, GWAS, and SSR/SNP markers. For example, it has been shown that markers associated with Glyma03g32900/GmCHX1 on chromosome 3 are associated with the salt tolerance phenotype. The primary advantage of molecular markers is the ability to detect genetic differences before the phenotype is fully formed. However, it is not automatically possible to conclude that the association of a marker in one population works to the same extent in another geographic or genetic material. Therefore, it is necessary to validate the selected markers in the conditions of Karakalpakstan in combination with phenotypic indicators in the local or test genotype set.

Statistical data analysis

It is advisable to obtain physiological and agronomic data in at least three biological replications and to evaluate the interaction between genotype and the stress factor using statistical methods. Dispersion analysis (ANOVA), correlation analysis, and, if necessary, regression methods can be used. If there are different scales between the indicators, they can be standardized and the complex endurance index can be calculated.

For molecular data, allele frequencies by genotypes, genetic distances, and associations with physiological phenotypes are evaluated. When interpreting marker-phenotype relationships, sample size and statistical reliability must be taken into account separately.

Expected scientific results and discussion

The study is expected to reveal differences in the physiological response to salt stress between soybean genotypes. In a number of genotypes, relative water content, chlorophyll status, and root development are relatively stable, while in other genotypes, a significant decrease in growth and biomass accumulation can be observed.

Combining physiological indicators with Na^+/K^+ ratio and molecular marker data allows for the simultaneous assessment of various components of salt tolerance. Such an integrated approach corresponds to the principles of phenotypic and genomic screening used in modern soybean breeding. It is noted in the literature that several QTL and candidate genes for soybean salt tolerance have been identified. At the same time, it is noted that resistance can change depending on the genotype, stage of development, and level of stress. Therefore, it is more correct to evaluate data from local agro-ecological conditions as an independent basis than to directly compare the results obtained in the conditions of Karakalpakstan with the results of other regions.

Conclusion

A promising scientific approach is the combination of physiological phenotyping and molecular markers in determining resistant soybean genotypes in the saline soil conditions of Karakalpakstan. A comprehensive assessment of relative leaf water content, chlorophyll status, root system, biomass, Na^+/K^+ ratio, and yield elements allows for a broader description of the stress response of genotypes.

At the molecular level, SSR and SNP markers can be used, including markers corresponding to regions associated with soybean salt tolerance in the literature. However, the study of markers together with phenotypic data in the studied

genotypes in Karakalpakstan is an important stage before their use for breeding purposes.

As a result of the proposed approach, a scientific basis can be created for the selection of soybean genotypes suitable for the conditions of Karakalpakstan, the effective use of saline lands and the formation of genetic resources for further breeding research.

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