

THE EFFECT OF SALTS ON NODULE BACTERIA OF ALFALFA SYMBIONTS AND THEIR GENETIC CHARACTERISTICS

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Abstract: Based on an analysis of the results of previous studies, a review of theoretical and practical data is devoted to the study of salt tolerance and genetic determination of this trait in nodule bacteria *Sinorhizobium meliloti* - alfalfa symbionts. Extensive modern data are presented on genes that affect the adaptivity of proteobacteria and on groups of genes which activity varies depending on the osmolarity of the medium. The structural and functional polymorphism of *bet* genes involved in the synthesis and transport of betaines in *S. meliloti* is discussed. The phenotypic and genotypic polymorphism of 282 natural rhizobia strains isolated at alfalfa diversity centers under the influence of aridity and salinity is considered.

Keywords: *Sinorhizobium meliloti*, *betC*, *betB* and *betT* genes, *Medicago* spp., Salt tolerance, symbiotic effectiveness, nodule and soil isolates.

Introduction. Improving soil fertility is one of the most important tasks of modern agronomic science. Microorganisms play a significant role in the mineral nutrition of plants, including biological nitrogen fixation. Despite the significant successes of scientists achieved in research on this problem, the practical use of effective plant-microbial systems remains at a low level [1].

Salinity, drought, and extreme temperatures are the most common climatic and edaphotopic stress environmental factors that limit the growth and productivity of practically valuable plant species. Ionic and osmotic stress affect the structure of membrane complexes in soil bacteria. Intensive introduction of nitrogen-fixing symbioses based on rhizobia and legume plants, as well as legume-grass mixtures is an effective and environmentally friendly way to improve the quality and quantity of fodder and restore vegetation on degraded soils [5].

The plant-microbial symbiotic interaction is a unique highly specific biological system for the fixation of atmospheric nitrogen and its transformation into compounds accessible to living organisms. A fundamentally new approach could be the creation of a system for genetic monitoring of the stability of economically valuable strains of symbionts in microbiomes of agroecosystems. Comparison of the genomic characteristics of symbiotic active strains can make it possible to identify functionally significant marker sequences and become the basis for creating such a system [2].

Purpose of research: to study the genetic diversity and phylogeny of nodule bacteria, and to determine the morphology and genetics of new strains of nodule

bacteria, alfalfa symbionts and the classification of these strains, to identify conditions under which symbiosis will be more effective.

Materials and methods of research. The material for the article is information from scientific papers analyzed by us on the basis of previous publications and data from Russian researchers.

Results:

1. Diversity and salt resistance of rhizobia:

A positive correlation between the signs of salt tolerance and symbiotic efficiency was shown for strains isolated from nodules of wild plants [3]. In addition, there is evidence that strains with a higher level of salt resistance, in contrast to salt-sensitive isolates, form a symbiosis predominantly with increased efficiency (comparative assessment of the mass of inoculated and uninoculated plants) [4].

The vast majority (71.4%) of natural strains of *S. meliloti* are able to grow under laboratory conditions at 0.6 M NaCl. This is true for rhizobia isolated from nodules and soils. Alfalfa rhizobia is characterized by natural resistance to relatively high concentrations of sodium ions (Na⁺). Thus, the strain *S. meliloti*102F34 is resistant to 0.3 M NaCl, which is significantly higher than the resistance of host plants, *M. varia*. A similar level of resistance is shown for *Agrobacterium tumefaciens* GMI 9023, while typical strains of other rhizobia species, for example, *R. tropici* (strain IIB), *S. fredii*, *Mezorhizobium huakuii* are resistant to 0.2 M, and representatives of the species *R. leguminosarum* (all biovars), *R. etli*, *A. rhizogenes*, and *Bradyrhizobium japonicum* are sensitive to 0.1 M.

2. Genomic organizations *S. Meliloti*

The genome of alfalfa nodule bacteria consists of a chromosome (SMc; 3650 kbp) and two highly molecular, so-called symbiotic megaplasmids SMa and SMb, which are 2.7 and 2.2 times smaller than SMc. About 86% of the natural strains of *S. meliloti* contain from 1 to 4 cryptic plasmids with a molecular weight of from 40 to 440 kb, which, as a rule, are not transmissible.

Cryptic plasmids, regardless of their molecular weight, can have homologous sequences, and the composition of plasmids can change under the influence of host plants. It was shown that strains containing 2-3 plasmids were significantly more likely to have a reduced level of salt tolerance. Analysis of the symbiotic and cultural-biochemical properties of natural strains made it possible to predict that genes affecting the adaptive properties and symbiotic effectiveness of rhizobia are localized on *S. meliloti* cryptic plasmids 140–200 kbp in size. The functional significance of cryptic plasmids was brilliantly proven in the study of pSmeSM11a and pSmeSM11b strain *S. meliloti* SM11. Analysis of the nucleotide sequences of plasmids revealed the presence of typical and atypical genes for rhizobia, and it was also suggested that plasmids were formed as a result of combining portions of replicons from different bacterial hosts. Both plasmids revealed a repABC replication system typical of α -proteobacteria (I-st segregation system), while pSmeSM11a also has a second replication system A (II) described for *S. meliloti* GR4 plasmid [5].

All the considered features of the structure of cryptic plasmids, including the fact that replicons are saturated with IS elements and transposons, indicate their active participation in horizontal gene transfer, which increases the possibility of

introducing foreign genes, in particular, affecting the resistance to rhizobia, with a subsequent change in their adaptive potential [5].

Analysis of the nucleotide and amino acid sequences of the E-type allele of the Le-C gene allowed to conclude that the fixing of this allele in the population occurred as a result of positive selection. It is concluded that *B. teSHOON* actively undergoes the process of diversification of functionally diverse Le genes, which have a significant effect on the salt tolerance and symbiotic effectiveness of rhizobi [5].

Conclusion. Symbiotic studies of nitrogen fixation should be carried out with the advent of new varieties and preparations of nodule bacteria, taking into account the new conditions of the changing climate. Thus, preliminary treatment of seeds with various strains of bacterial preparations based on nodule bacteria increases the yield and increases the production of crude protein per unit area.

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BIRD COMMUNITIES IN MOSCOW CITY PARKS

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Abstract. Some results of the research of bird fauna in seven Moscow city parks conducted in 2018-2019 are presented in this article. It is shown that the one of the key factors affecting bird communities in city parks may rather be the quality of habitats than their area.