Proteomic and metabolomic analysis of the ntrc mutant azospirillum brasiliense.

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Abstract

Bacterial chemotaxis enables mobile microorganisms to explore their surroundings in search of growth and survival niches. Chemotaxis relies on chemoreceptor signalling arrays that interact with cytoplasmic proteins to regulate the direction of movement at the molecular level. Two separate chemotaxis pathways, Che1 and Che4, mediate chemotaxis in Azospirillum brasilense. In the free-living and plant-associated lifestyles of A. brasilense, Che1 and Che4 are both essential. Here, we investigate the function of chemotaxis in A. brasilense physiology using whole-cell proteomics and metabolomics. We discovered that chemotaxis-unrelated processes, including as significant alterations in transcription, signalling trafficking, and cell metabolism, are impacted in mutants lacking either CheA1 or CheA4 or both. We uncover particular impacts of CheA1 and CheA4 on nitrogen metabolism, such as nitrate absorption and nitrogen fixation, which may be dependent, at the very least, on the transcriptional control of RpoN, which encodes RpoN, a worldwide regulator of metabolism, including nitrogen. We also find unique, as of yet uncharacterized, transcriptional and posttranscriptional regulatory layers for regulators of nitrogen metabolism. Our data show that CheA1 and CheA4 play important roles in chemotaxis and nitrogen metabolism, possibly by controlling global regulatory networks. Salt-tolerant materials responded to salt stress at the protein and metabolic levels more favourably than salt-sensitive materials did. These findings collectively imply that salt-tolerant germplasm may improve resilience through the repair of intracellular structures, stimulation of lipid metabolism, and elevation of osmotic metabolites. These findings offer fresh perspectives on how seeds respond to salt stress as well as new avenues for research into the molecular processes and metabolic homeostasis of seeds during the early abiotic stresses of germination.

Keywords: Azospirillum, Chemotaxis, Nitrate assimilation, Nitrogen fixation, Metabolomics, Nitrogen metabolism, Proteomics.

Introduction

One of the main environmental issues affecting plant development and crop yield globally is salt stress. A major abiotic factor impeding agricultural productivity, particularly in arid and semi-arid regions, is soil salinity, which is promoted by industrial pollution, inefficient irrigation techniques, and growing populations [1]. It is anticipated that roughly of arable soils will experience salt by and without the implementation of effective management measures. One of the most significant salts in soil is sodium chloride, which is widely distributed and highly soluble. The impact of salinity factors on plant growth and productivity result in substantial agricultural production losses. As the most important stage of the life cycle, seed germination is particularly vulnerable to abiotic stimuli like salt stress [2].

The term "seed germination" describes the process in which, following seed imbibition, metabolism is increased, critical germination genes start to be expressed, and the radicle gradually lengthens before finally breaking through the endosperm and seed coat. The main ways that salt stress inhibits seed germination include osmotic stress, the build-up of too many reactive oxygen species, the breakdown of cell structure, and changes to the balance of phytohormones, all of which decrease germination rate and lengthen germination time [3]. Salt stress had a considerable impact on several metabolic functions, such as starch hydrolysis, sucrose transport, and amino acid metabolism. Sulfhydryl redox is controlled by thioredoxins, versatile proteins having catalytic activity. In transgenic tobacco, the thioredoxin protein-encoding gene MsTRX has been shown to increase salt tolerance by preserving osmotic equilibrium. When controlling the germination of Arabidopsis seeds under salt stress, the abscisic acid insensitive 4 (ABI4) gene directly binds to RbohD and Vitamin C Defective 2, regulating the formation and clearance of reactive oxygen species (ROS) and the metabolism of ROS [4].

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Deep gene expression changes are necessary for salt stress tolerance, along with modifications to the plant transcriptome, metabolome, and proteome. Integration of several "omics" technologies has been proven to be a successful tactic for understanding environmental stress response systems. Quantitative proteomics now uses data-independent acquisition (DIA), which uses delicate techniques to carry out and find abiotic stress-responsive proteins in plants. DIA can offer a reliable, reproducible, and accurate solution to cover deeper data from several complicated samples in less time than earlier proteomics methods. The efficacy of melatonin to mitigate the impacts of drought on soybean growth has been investigated using ultra-performance liquid chromatography-tandem mass spectrometry [5].

Conclusion

The biosynthesis pathways of phenylpropanoids, flavonoids, lignin, and lysophospholipids have been discovered to play essential roles in determining the salt tolerance of millet using the combined transcriptome and metabolome investigation of two millet genotypes with varied tolerances under salt stress. More effective ion channels and antioxidant systems, which offer millet a comprehensive regulatory network to handle salt and some inspiration from other cereal crops' salt tolerance, are primarily responsible for the salt tolerance of tolerant cultivars. It is possible to conduct more thorough and systematic research of the mechanisms by which seed germination may tolerate salt thanks to the combination of omics techniques.

References

1. Rajjou L, Duval M, Gallardo K, et al. Seed germination and vigor. Annu Rev Plant Biol. 2012;63:507-533.
2. Shu K, Qi Y, Chen F, et al. Salt stress represses soybean seed germination by negatively regulating GA biosynthesis while positively mediating ABA biosynthesis. Front Plant Sci. 2017;8:1372.
3. Duan X, Wang Z, Zhang Y, et al. Overexpression of a thioredoxinprotein-encoding gene, MsTRX, from medicago sativa enhances salt tolerance to transgenic tobacco. Agronomy. 2022;12:1467.
4. Yang F, Chen H, Liu C. Transcriptome profile analysis of two vicia faba cultivars with contrasting salinity tolerance during seed germination. Sci Rep. 2020;10:7250.
5. Liu L, Wu X, Sun W, et al. Galactinol synthase confers salt-stress tolerance by regulating the synthesis of galactinol and raffinose family oligosaccharides in poplar. Ind Crops Prod. 2021;165:113432.

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