Journal of Plant Growth Regulation
https://doi.org/10.1007/s00344-024-11377-w

Xerophyte-Derived Synthetic Bacterial Communities Enhance Maize Drought Tolerance by Increasing Plant Water Use Efficiency

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Received: 25 November 2023 / Accepted: 17 May 2024

Abstract

We had assembled a synthetic bacterial community (SynComH) from the rhizosphere microbiota of *Haloxylon ammodendron*, which enhance drought tolerance in *Arabidopsis thaliana* under laboratory conditions. Here we assessed the efficacy of SynComH, alone or in combination with SynComS, a consortium of previously identified growth-promoting bacteria from *Crocus sativus*, in increasing maize plants' fitness under optimal and water-deficit conditions. We were also interested in unveiling the mechanisms by which the bacteria confer drought tolerance. We first performed detailed greenhouse experiments on maize plants that were artificially inoculated with SynComS, SynComH, and SynComH+S, and measured 22 different plant morphological, physiological, biochemical, and histological traits under optimal and water-deficit conditions. Data were analyzed by different univariate and multivariate statistical methods. Lastly, we tested the effects of the SynComs on maize in field in a split-plot experiment with two irrigation regimes as main plots and SynComs as subplots. Results from both greenhouse and field experiments showed that all three SynComs had growth-promoting properties and improved growth-related traits, but only SynComH and SynComH+S were effective in ameliorating the drought stress. SynComH substantially enhanced drought tolerance by increasing stomatal conductance, photosynthesis rate, and proline content, while decreasing transpiration rate, leading to up to 700% increase of water use efficiency. Morphological and histological investigations suggested that these positive effects are probably attributed to modulation of plant stomatal density and xylem structure by SynComH. Besides the significance for practical agronomic use, our results suggest unprecedented capabilities of non-pathogenic bacteria in modulation of plant stomatal density.

Keywords Desert microbiome · Structural equation modeling · Stomatal conductance · Stomatal density · Xylem · Rhizobacteria

Introduction

Developing climate-resilient crops is a necessity for approaching global food security under climate variability and extremes. Drought, which is already considered the major climate factor in reducing agricultural productivity (Food and Agriculture Organization 2021), is predicted to be more severe and widespread in the future (Dai 2013). The complex inheritance of plant drought tolerance (Yang and Qin 2023; Hu and Xiong 2014) and the fact that usually combined environmental stresses occur in field conditions (Shaar-Moshe et al. 2017; Zandalinas et al. 2021; Mittler 2006) challenge the efficacy of crop breeding and genetic engineering strategies for improving crop drought tolerance.

In the last decade, the potential of plant microbiota, the microorganisms that are naturally associated with different parts of plants (Trivedi et al. 2020; Bulgarelli et al. 2012), has been explored for improving plant drought tolerance with encouraging outcomes (Liu et al. 2020). The results of a meta-analysis of 57 studies suggested that the plant-associated bacteria help plants, particularly the C_4 plant species, to recover more efficiently from water-deficit stress by enhancing photosynthesis and reducing oxidative stress, leading to increasing plant biomass (Zhao et al. 2023). In

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Handling Editor: Puneet Singh Chauhan

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