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Molecular Evidence of Crosstalk Between Bacterial Endophytes and Plant Transcriptome in *Brassica juncea*

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Abstract

The beneficial effects of endophytes on plant growth, development and yield are well known. Modulating plant growth-promoting substances and ameliorating biotic and abiotic stresses are some of the key mechanisms that are deployed by endophytes to facilitate host growth and defence. However, the understanding of the plant's genome response to their presence is still limited. Therefore, this study provides an insight into the microbiome of *B. juncea* seeds as well as leaves, and its impact on plant growth and development. It also correlates their presence with the changes in plant. Removal of seed-borne culturable endophytes resulted in trade-off of accelerated growth with decreased biomass. 16S metagenomics revealed that bacterial endophyte diversity and density varied with stage of the plant. We found that 22 endophytic genera including *Enterococcus, Halobacteroides, Planktothrix* and *Streptomyces* were observed irrespective of Bavistin treatment and age of the plant. Removal of culturable endophytes also led to downregulation of crucial genes involved in growth, photosynthesis (Photosystem I assembly protein, Photosystem II reaction center protein and Rubisco), transport (nitrate transporter; *NRT*) and regulation of plant hormones (auxin homeostasis and signalling; *CYP83A1*) in *B. juncea*. To the best of our knowledge, this is the first report of the response of plant' transcriptome to changes in endophyte composition indicating a strong possibility of host gene regulation by the endophytic partner. The exact mechanism of the same needs to be further explored.

Keywords Indian mustard · Seed-borne endophytes · 16S metagenome · Photosynthesis · Ion transport · Phytohormones

Introduction

The association of endophytes with plants dates back to 350 million years ago, and has played an important role in plant evolution (Heckman et al. 2001). Bacteria, cyanobacteria, microalgae and fungi are some of the prominent groups of microbes associated with higher plants (Hardoim et al. 2015; Alvarez et al. 2021). Their density as well as diversity vary with the type of host, parts of the plant, growth stage, environmental conditions and the presence of other cohabitating microbes (Dastogeer et al. 2020). These endophytes are transmitted through seeds, vegetative parts and even rhizosphere (Compant et al. 2010; Shahzad et al. 2018). They are commensals, mutualists or symbionts, and confer several direct as well as indirect benefits to plants through the production of phytohormones, enzymes, antimicrobial compounds and secondary metabolites that can also influence the structure and nutritional status of soil (Brader et al. 2017; Eid et al. 2021; Fadiji and Babalola 2020; Mathur and Ulanova 2022). This mainly facilitates plant growth through interrelated mechanisms such as phytostimulation (through phytohormones), biofertilization (increasing accessibility to soil nutrients) and biocontrol (production of antibiotics and siderophores) (Bloemberg and Lugtenberg 2001). Thus, their presence in plants has a positive impact on the development and yield as well as the resistance to biotic and abiotic stresses (Cipollini et al. 2012; Santoyo et al. 2016). In exchange, the host provides carbohydrates, amino acids, inorganic nutrients and habitat to the microbial partner for

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