

Genome-wide Association Studies Reveal Candidate Genes Important for the Interaction of *Bacillus pumilus* with *Arabidopsis thaliana*

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Abstract

The plant growth promoting bacterium (PGPB) *Bacillus pumilus* is a nitrogen fixing and a gibberellin producer that increases the nitrogen content and shoot length and surface in plants. In addition, this PGPB has the capability of improving plant growth under drought and saline conditions. The strain *Bacillus pumilus* TUAT-1 can increase rice's roots and biomass and the content of nitrogen and chlorophyll. In this study, through genome-wide association study (GWAS), we evaluated the interaction between TUAT-1 and *Arabidopsis thaliana*. In order to do that, 288 *A. thaliana* accessions were screened for root architecture traits: main root length (MRL), number of lateral roots (NLR), branched zone (BZ), total root length (TRL) and lateral root length (LRL). GWAS accelerated mixed model analysis was performed for the 5 traits within 288 ecotypes. Several ecotypes responded significantly to TUAT-1 inoculation: MRL (52.7%), NLR (14.2%), BZ (8.3%), TRL (21.2%) and LRL (19.1%). Many inoculated ecotypes were significantly affected in more than one trait. However, only one ecotype showed a significant difference between control and inoculated plants for all the traits. While some of the ecotypes either did not respond or responded positively for growth, a few ecotypes showed inhibition of root growth upon inoculation. Significant single nucleotide polymorphisms (SNPs) were detected in all the traits evaluated. 34% of the significant SNPs were associated with more than one trait and, 1 SNP was associated with 4 different traits. Causative SNPs were selected according to missense or nonsense alterations and produced a list of candidate genes related to hormone production, defense response, root development, autophagy, and fatty acid metabolism. Candidate genes were very likely associated with the interaction between TUAT-1 and *Arabidopsis* and the plant growth promotion. In this study, we validated previously reported *Bacillus* spp. and its plant interaction and growth promotion genes and highlight the potential genes involved in these mechanisms. The results of this work showed that some of the root architecture characteristics are genetic separable traits associated with the plant growth. We suggest that plant-bacteria interaction and the plant growth promotion are quantitative and multigene traits. This knowledge expands our understanding of the functional mechanisms driving the plant growth promotion by PGPB.

Funding: Supported by INCT-FBN, CNPq, Fundação Araucária and CAPES