

**TITLE:** MODULATION OF GENE EXPRESSION BY THE INOCULATION OF *Herbaspirillum seropedicae* IN MAIZE ROOTS.

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**ABSTRACT:**

*Herbaspirillum seropedicae* is an endophytic diazotrophic bacterium that is widely recognized for its potential in promoting plant growth and use in agricultural bioinoculants. Nevertheless, many molecular details underlying plant-*H. seropedicae* interactions remain unclear. In this direction, genome-wide transcriptional profiling using second-generation sequencing technologies (RNA-Seq) constitutes an important tool for the identification of metabolic pathways related to plant growth promotion efficiency. Thus, the objective of this work is to elucidate how the colonization by *H. seropedicae* modulates gene expression in maize roots. Maize (Dekalb 7815 var.) seeds were disinfected and germinated on Germitex paper for 72 hours in a BOD chamber. Seedlings with 2.5cm radicles were transplanted into 2L pots with Furlani solution ( $\frac{1}{4}$  of the ionic strength) and kept in a growth chamber. After 24 hours of adaptation, an aliquot of 20mL of the inoculum containing  $\sim 2 \times 10^7$  cells mL<sup>-1</sup> of *H. seropedicae* strain HRC54 were applied. Five days after inoculation, eight seedlings were processed for biometric analysis and roots of 18 seedlings collected in three groups (biological triplicates) were used for RNA extraction, cDNA library construction and sequencing on an Illumina Hi-Seq 2500 instrument. Differential expression analysis revealed 4964 and 5955 genes up- and down-regulated by *H. seropedicae* inoculation, respectively. We found a number of interesting candidates, such as: GM70087, phosphate transporter; G180490, phototropism-related; G125557, dormancy/auxin signaling; G332660, calcium dependent protein; G175562, photosystem II and; G062527, gibberellin-regulated protein. These genes were up-regulated by 29, 17.7, 8.6, 43, 9.95 and 5.1-fold, respectively. Regarding alterations in important plant traits, we found a statistically significant increase of root (242 and 73%) and shoot biomass (166.7 and 188%), in this order for fresh and dry mass. We estimated a concentration of  $5 \times 10^7$  bacterial cells per g of roots with populations 3 log<sub>10</sub> units higher than control plants. In this work, we presented preliminary evidence supporting the modulation by *H. seropedicae* of important biochemical pathways in maize roots.

**Keywords:** RNAseq, beneficial bacteria, bioinoculants.

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