

CHARACTERIZATION OF LONG NON-CODING RNAs (LncRNAs) IN MAIZE SUBJECTED TO COLONIZATION BY THE ENDOPHYTIC DIAZOTROPHIC BACTERIA *HERBASPIRILLUM SEROPEDICAE* AND ADDITION OF HUMIC ACID

III Simpósio Internacional de Atualização em Genética e Melhoramento de Plantas, 0ª edição, de 24/05/2021 a 26/05/2021
ISBN dos Anais: 000

SILVA; Leandro de Oliveira ¹, VIEIRA; Lucas Maciel ², WALTER; Maria Emilia M. T. ³, VENÂNCIO; Thiago M. ⁴, OLIVARES; Fábio Lopes ⁵, GRATIVOL; Clícia ⁶

RESUMO

Maize (*Zea mays*) is one of the most important cereal crops, used in human food, production of animal feed and bioenergy. To optimize your cultivation, it is possible to use diazotrophic and growth-promoting bacteria. However, the complex beneficial plant-bacterial relationship has not yet been elucidated, which includes the role of long non-coding RNAs (lncRNAs). The present work aims to characterize lncRNAs expressed in maize submitted to colonization by the diazotrophic bacteria *Herbaspirillum seropedicae* with the addition of humic acid. Reads of RNA-seq libraries were aligned to the *Z. mays* genome by the use of HISAT2, and StringTie was used to assemble the transcripts. The differential expression of lncRNAs was calculated using DESeq2. A model based on machine learning was created to increase the accuracy of predicting new lncRNAs in maize. The search of lncRNAs in maize returned 124,739 different known lncRNAs. Through BLASTN with the transcriptome, 32,645 known lncRNAs were identified. Of these, 3,263 lncRNAs were differentially expressed (1,502 up-regulated and 1,761 down-regulated). The assembled transcripts were submitted to different tools, as a way to identify the new lncRNAs: size filter; calculation of the protein coding potential (CPC); calculation of the size of the ORF; alignment against a Rfam database and, finally, analysis with the model. A total of 6,736 new highly confidence lncRNAs were identified, 1,050 of which are differentially expressed (480 up-regulated and 570 down-regulated). The next steps include: prediction of the target genes of lncRNAs and characterization using Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG); verification of alternative splicing mechanisms; mapping of lncRNAs in public miRNA libraries and validating their targets through degradoma libraries; construction of a network of maize lncRNA-miRNA interaction. This work can contribute to a greater understanding of the roles played by maize lncRNAs.

PALAVRAS-CHAVE: *Zea mays*, non-coding sequences, diazotrophic bacteria

¹ Universidade Estadual do Norte Fluminense Darcy Ribeiro, oliveiradasilvaleo@gmail.com

² Universidade de Brasília, lucas.maciel.vieira@gmail.com

³ Universidade de Brasília, memtwalter@gmail.com

⁴ Universidade Estadual do Norte Fluminense Darcy Ribeiro, thiago.venancio@gmail.com

⁵ Universidade Estadual do Norte Fluminense Darcy Ribeiro, fabioliv@uenf.br

⁶ Universidade Estadual do Norte Fluminense Darcy Ribeiro, cgrativol@uenf.br