

ANALYSIS OF LONG NON-CODING INTERGENIC RNAs (LINC RNAs) OF *SPORISORIUM SCITAMINEUM* IN INTERACTION WITH SUGARCANE

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Abstract:

Sugarcane plays a crucial global role, serving not only in sugar production but also as a source of renewable energy (ethanol, biodiesel) and biomaterials. However, sugarcane smut, caused by the fungus *Sporisorium scitamineum*, poses a serious threat to the crop, significantly impacting productivity due to its difficult containment and rapid spread. Long intergenic non-coding RNAs (lincRNAs) are critical elements in gene expression regulation. While transcriptome studies have traditionally focused on protein-coding genes, little is known about the universe of non-coding RNAs in phytopathogens. The main objective of this project is to identify and profile the expression of lincRNAs in *S. scitamineum*, under *in vitro* growth conditions and when inoculated *in planta*, to understand the molecular dynamics of these transcripts in relation to the fungus's pathogenesis. By reassembling the transcriptome, we identified 1563 long non-coding RNAs (lncRNAs), of which 69 are intergenic (lincRNAs). Among the lincRNAs identified and located in the genome of *S. scitamineum*, 6 transcripts were associated with the mitochondria. All lincRNAs are expressed *in vitro* experiments with the fungus, and 6 are expressed *in planta*, using minimum expression and repeatability criteria. This study expands the understanding of lncRNAs in *S. scitamineum*, revealing the complexity of gene regulation during the pathogenesis of sugarcane smut. The identification and transcriptional profiling of lincRNAs will provide new perspectives for disease control and crop sustainability.

Palavras-chave: LincRNAs; Sugarcane; *Sporisorium scitamineum*; Smut;

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