EPIGENETIC APPROACH TO THE STUDY OF SECONDARY METABOLISM OF MACROPHOMINA PHASEOLINA

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INTRODUCTION: Macrophomina phaseolina is a necrotrophic plant pathogenic fungus that infects over 500 plant hosts. This pathogen causes significant economic losses in crops. It is the causative agent of diseases such as mildew, charcoal rot, stem rot, the root rot and stem canker, the latter is among the five diseases of major soybean causing great economic losses in producing countries.

The recent sequencing of the genome of M. phaseolina revealed that this pathogen has an arsenal of 75 genes possibly associated with secondary metabolism, mainly genes encoding polyketide synthases (PKS), non-ribosomal peptide synthases (NRPS) and hybrid PKS-NRPS. Few secondary metabolites have been reported in this fungus, so there is a huge chemical unexplored richness in the metabolome M. phaseolina. Many of these metabolites could be phytotoxins, signaling molecules and/or communication molecules between and within species, or even act as agents for controlling the growth of other organisms.

OBJECTIVE: This work aims to explore the potential of M. phaseolina for the production of bioactive secondary metabolites using epigenetic modifiers.

MATERIALS AND METHODS: The fungus was grown in liquid culture media Czapek-Dox (CZP), in the presence of epigenetic modifiers valproic acid (VA) and sodium butyrate (SB), the comparative analysis of organic extracts was performed by chromatographic methods: TLC, HPLC-PDA, UPLC-MS/MS.

RESULTS AND DISCUSSION: Analysis of the extracts by HPLC and UPLC-MS/MS identified the differential production of secondary metabolites and allowed to determine the possible presence of phaseolinone in the organic extracts, and other metabolites that could be involved in virulence of the pathogen and which differentially produced in vitro.

CONCLUSIONS: Chemical epigenetic modifiers are a powerful tool for obtaining diversity of molecules that are produced only under certain conditions and that could have a key role in plant pathogen interaction process.

Key words: Macrophomina phaseolina, epigenetic modification, secondary metabolites