



Proteomics analysis and mining of effector weaponries of *Cochliobolus lunatus* reveals CL[xxx]LHM-motif during colonization of potato leaf

Name: Bengyella Louis^{1*}, Naser Aliye Feto¹

¹Omics Research Group, Department of Biotechnology, Faculty of Applied and Computer Sciences, Vaal University of Technology, Gauteng, South Africa

*Corresponding author: Tel: 0027 712781091, E-mail: bengyellalouis@gmail.com

Cochliobolus lunatus is fungi pathogen that causes devastating losses to plant and animals, yet the effectoromics is unknown. In an attempt to mine the secretome weaponries of C. lunatus, the pathogen was interacted with potato leaf, and secretome weaponries mined using proteomics tools and a cohort of in silico pipelines. It is shown that secretome weaponries of C. lunatus interacting with potato leaf at different temperature regimes bear a CL[xxx]LHM-motif. Furthermore, pathogenicity studies revealed C. lunatus adopt different but highly successful strategies on potato cultivars to incite brown-to-black leaf spot disease but the most affected component of potato physiological process remain uncovered. Long-lasting defense during infection requires an upsurge in proteome changes particularly pathogenesis related proteins (PrPs) chiefly under the control of nonexpresser of pathogenesis related proteins. In order to gain molecular insights, we examine the changes in proteome and potato nonexpresser of pathogenesis related proteins (StNPR1) during the infection process. It is shown that C. lunatus significantly (P < 0.05) inhibited the host functional proteome by 96 h after infection (hai), principally, affecting the expression of ribulose bisphosphate carboxylase enzyme, plastidic aldolase enzyme, alcohol dehydrogenase 2 and photosystem II protein prior to the formation of brown-to-black leaf spot disease. Strongest host-response was observed at 24 hai hallmarked by 307 differentially expressed peptide spots concurring with the active phase of production of penetrating hyphae. Additionally, C. lunatus differentially down-regulate StNPR1 transcript by 8.19 fold by 24 hai. This study is the first to elucidate that C. lunatus transiently down-regulate the expression of StNPR1 at the onset of infection, and as a whole, infection negatively affects the expression of proteome components involve in photosynthesis, carbon fixation and light assimilation. This study contributes towards better understanding of the mechanism underlining the invasion strategies of C. lunatus.

Keywords: Western blotting, Proteome, motif search, effector, MALDI-TOF MS/MS, plant-pathogen interaction

Dr. Louis Bengyella has completed his PhD at the age of 37 years from the University of Burdwan, India and postdoctoral studies from the University of the Witwatersrand School of Cell and Molecular Biology, and Department of Biotechnology, The Vaal University of Technology, South Africa. He has published 30 papers in reputed journals and has been serving as an editorial board member for Springer, Elsevier, Sciencealert and Academic publishers.

Presenting author details

Full name: Dr. Louis Bengyella Contact number: 0027 712781091 Twitter account: @louisbengyella Linked In account: https://www.linkedin.com/in/dr-louis-bengyella-6075ab46?trk=nav_responsive_tab_profile_pic