

CO-ORGANIZED EVENT

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Microbial metabolomics: new biomarkers describing biological mechanisms related to *M. tuberculosis* growth, virulence, drug resistance, and host-microbe adaptations/interactions

Du Toit Loots

North-West University, Potchefstroom, South Africa

Statement of the Problem: Despite the fervent genomic and proteomic based research efforts to date, since its discovery in 1882, TB is still a major global problem, and hence new approaches are necessary to better characterize and diagnose this disease. One such strategy would be to investigate this from a metabolomics research perspective, in order to identify new metabolite markers better characterizing the disease.

Methodology & Theoretical Orientation: A typical metabolomics workflow, including using semi-targeted and untargeted extraction procedures on cell cultures and patient collected sputum and urine, analysis on various LC-MS, GC-MS and NMR based approaches, followed by data clean-up and biomarker identification using various univariate and multivariate statistical approaches, was applied.

Findings: The new TB biomarkers identified in the different sample material shed light on new metabolic pathways and mechanisms associated with growth, virulence, drug resistance, and host and microbe interactions/adaptations.

Conclusion & Significance: Over the past 10 years, metabolomics has led to an exponentially increased number of new biomarkers identified, and subsequently rapid expansion of new knowledge and our understanding of various infectious diseases, including TB, which can ultimately be utilized towards improved diagnostics and treatment approaches.

dutoit.loots@nwu.ac.za