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### **Secreted metabolome of methamphetamine treated human primary macrophages**

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HIV-1 infection combined with the use of illicit drugs such as methamphetamine (Meth) has devastating effects on the function of the entire organism including innate immunity defense. The effect of Meth on the mechanisms regulating human monocyte derived macrophages (MDM) metabolism is not known thus the main goal of this study is to perform mass spectrometry based metabolomic profiling of secreted metabolome of (MDM) to uncover qualitative and quantitative differences due to the exposure to Meth. We applied a multiple reaction monitoring (MRM) based targeted metabolomics approach using ultra-high performance liquid chromatography (UPLC) and QTrap 6500 (Sciex) mass spectrometer with electrospray ionization (ESI). We will present a multistep method of processing and analysis, including the development of a new solid phase extraction procedure. New liquid chromatography (LC) method has been developed and applied in this study. Moreover, we have found novel, previously unreported metabolites of Meth secreted by MDM when treated with this drug. In consequence we have found 12 differentially secreted metabolites made by the MDM (FDR<0.1). All compounds were identified with high resolution mass spectrometry using Orbitrap Fusion (Thermo Fisher) mass spectrometer. We provide mass spectra of precursor ions and fragments for unambiguous identification. A number of internal standards were used for data normalization necessary for proper quantification. A table of approximately 100 metabolites identified but not differentially expressed in MDM secreted metabolome. Results of our studies will be linked to mechanisms of epigenetic regulation providing foundation for more in depth investigations and future collaborations.