

## **Metabolomics to reveal phenotypic diversity in natural *Leishmania* populations**

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Characterising the diversity of pathogen populations is a major key for understanding the clinical polymorphism of infectious diseases. Advances in mass-spectrometry facilitate comprehensive metabolite profiling, hereby providing access to the ultimate expression of an organism's genotype, the closest correlate to the phenotype. In the presented study, metabolome-wide comparison of multiple drug-sensitive and -resistant *Leishmania donovani* clinical isolates was done using ultra high resolution Fourier Transform mass spectrometry (LTQ Orbitrap). The results of this study demonstrate how revealing the diversity on the whole metabolome level in a natural *Leishmania* population can significantly contribute to (i) distinguishing the different phenotypes present in a population, (ii) giving a global overview of all factors involved in drug resistance by highlighting specific metabolic pathways, and (iii) enhancing our understanding of parasite flexibility. The used methodology, from sample preparation to identification of metabolic signatures of drug-resistant parasites, will be presented and discussed in the context of future applications for parasite research.

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