

Publication**A MALDI-TOF MS library for rapid identification of human commensal gut bacteria from the class Clostridia****JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)****ID** 4665709**Author(s)** Asare, P. T.; Lee, C. H.; Hürlimann, V.; Teo, Y.; Cuénod, A.; Akduman, N.; Gekeler, C.; Afrizal, A.; Corthesy, M.; Kohout, C.; Thomas, V.; de Wouters, T.; Greub, G.; Clavel, T.; Pamer, E. G.; Egli, A.; Maier, L.; Vonäsch, P.**Author(s) at UniBasel** [Asare, Paul Tetteh](#) ; [Lee, Chi-Hsien](#) ; [Vonäsch, Pascale](#) ;**Year** 2023**Title** A MALDI-TOF MS library for rapid identification of human commensal gut bacteria from the class Clostridia**Journal** Front Microbiol**Volume** 14**Pages / Article-Number** 1104707

INTRODUCTION: Microbial isolates from culture can be identified using 16S or whole-genome sequencing which generates substantial costs and requires time and expertise. Protein fingerprinting via Matrix-assisted Laser Desorption Ionization-time of flight mass spectrometry (MALDI-TOF MS) is widely used for rapid bacterial identification in routine diagnostics but shows a poor performance and resolution on commensal bacteria due to currently limited database entries. The aim of this study was to develop a MALDI-TOF MS plugin database (CLOSTRI-TOF) allowing for rapid identification of non-pathogenic human commensal gastrointestinal bacteria. **METHODS:** We constructed a database containing mass spectral profiles (MSP) from 142 bacterial strains representing 47 species and 21 genera within the class Clostridia. Each strain-specific MSP was constructed using >20 raw spectra measured on a microflex Biotyper system (Bruker-Daltonics) from two independent cultures. **RESULTS:** For validation, we used 58 sequence-confirmed strains and the CLOSTRI-TOF database successfully identified 98 and 93% of the strains, respectively, in two independent laboratories. Next, we applied the database to 326 isolates from stool of healthy Swiss volunteers and identified 264 (82%) of all isolates (compared to 170 (52.1%) with the Bruker-Daltonics library alone), thus classifying 60% of the formerly unknown isolates. **DISCUSSION:** We describe a new open-source MSP database for fast and accurate identification of the Clostridia class from the human gut microbiota. CLOSTRI-TOF expands the number of species which can be rapidly identified by MALDI-TOF MS.

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