Proteomics is particularly suitable for characterizing human pathogens with high life cycle complexity, such as fungi. Protein content and expression levels may be affected by growth states and life cycle morphs. Identification and typing of fungi by conventional methods are often difficult, time-consuming and frequently, for unusual species, inconclusive. Moreover, substantial changes in medical, intensive care and organ transplantation practices are drastically increasing emerging therapy-refractory/uncommon fungi. Herein we report on proteomic phenotypes from MALDI-TOF MS employed as analytical and typing expression profiling of yeasts, yeast-like species and strain variants in order to achieve fungal proteomics population studies. MS-based dentifications (IDs) can be successfully compared to reference biochemical-based systems (e.g., Vitek-2) and corroborated by genotyping IDs, targeting 25–28S rRNA hypervariable D2 regions. MS IDs show a high analytical performance and profiling heterogeneity which complement or even outclass existing yeast typing tools. This variability reflects the high biological complexity of yeasts and may be properly exploited to provide epidemiological tracing and infection dispersion patterns. Furthermore, filamentous and other fungi (e.g., Aspergillus, Emericella, Fusarium, Geosmithia, Neosartorya, Penicillium, Pseudallescheria, Scedosporium, Talaromyces, Fomitopsis) may be correlated to laboratory-adapted reference “proteomic phenotypes” which extend the diagnostic powerful of basic databases. Growth time-courses at 30°C on Sabouraud agar medium define the 120 hour point as the best peptide extraction condition for full recovery of conidia- or asci-producing multihyphal morph structures and the highest intra- and inter-class profiling correlation, allowing engineered derived libraries. MS mould IDs may be referred to genotyping and to routine morphotyping IDs. Fingerprinting classifiers, selected by Wilcoxon/Kruskal-Wallis algorithm, and computed by different algorithms, allow model construction. Proteomic phenotyping is revolutionizing diagnostic mycology as fully reflecting species/morph varieties but often overcoming taxonomic hindrance. If we are to gain further insights into the description of fungi of relevant medical interest, we need to implement customized fingerprinting databases “ad-hoc” generated. MALDI-TOF MS proteomic phenotyping boosts patient-tailored identification protocols in diagnostic mycology.