**Objectives:**

Matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) provides rapid and reliable mold identification. However, the identification is limited to the molds listed in the commercial filamentous fungi library. In this study, we created an expanded filamentous fungi library (JHH database) by including a number of clinically relevant fungi that are not listed in the current commercial filamentous fungi library. The new main spectra profiles (MSPs) of these fungi were compared to the Bruker MBT Filamentous Fungi Library 2023 to assess if the new expanded database would improve mold identification.

**Methods:**

Spectra for 173 clinical molds (25 Dermatophytes, 69 Hyaline hyphomycetes, 5 Mucorales, 4 Basidiomycetes, and 70 Dematiaceous) were extracted from hyphal mass using the standard liquid cultivation method recommended by Bruker.  The MSPs were generated on the Bruker MALDI Biotyper Sirius BD model using the FlexControl Version 3.4. The spectra were divided into 2 sets, one for database creation (JHH Database) and one for dataset validation.  For species where there were 2 or more strains available, approximately 50% of the spectra were used for the dataset validation.

**Results:**

The spectra from all the mold groups for dataset validation were tested against the i) JHH Database, ii) Bruker MBT Filamentous Fungi library 2023, and iii) JHH Database + Bruker MBT Filamentous Fungi Library 2023. A logarithmic score of ≥ 2.00 indicated species level identification and a logarithmic score of 1.70-1.99 indicated genus/group ID identification (Table). Genus and species level identification in all molds was significantly improved by using the in-house JHH database compared to the commercial MBT filamentous fungi library (92% vs 42%, p<0.05)

**Conclusions:**

The addition of these 173 molds to the existing MBT Filamentous Fungi Library 2023 has made a significant improvement to the genus and species level identification across all the major fungal groups.