Identification of Candida auris and Other Pathogenic Yeasts by MALDI-TOF Mass Spectrometry of Membrane Lipids

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BACKGROUND:
Candida auris represents an emerging global health threat due to the high incidences of multidrug-resistant and healthcare-associated infections; however, accurately diagnosing *C. auris* infections is challenging. Protein-based identification via matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) cannot consistently identify *C. auris*. We developed a novel and complementary platform that utilizes essential membrane lipids as chemical fingerprints for identification of bacterial species. Here we expand this platform to include an extensive fungal library for identification of pathogenic fungi including *C. auris*.

METHODS:
A fungal library of lipid mass spectral profiles was constructed containing fifty-five yeast and fungal species, thirty of which were *Candida* species. Isolates were grown at 30˚C for 48 hours on Sabouraud dextrose agar and harvested by centrifugation. Lipids were extracted by hot ammonium-isobutyrate reaction. Mass spectra were acquired by MALDI-TOF-MS in negative ion mode on a Bruker microflex LRF using the matrix norharmane.

RESULTS:
To evaluate the fungal library for identifying *Candida*, 50% of mass spectra were designated as the testing set from the top five pathogenic *Candida – C. albicans, C. glabrata, C. tropicalis, C. parapsilosis*, and *C. krusei –* and *C. auris*. Using the novel PostalService™ platform, mass spectra were transformed and analyzed to extract unique mass difference features. Testing set isolates were classified using a Support Vector Machine algorithm, and identification rates of accuracy were determined by multiple analyses of different training set iterations. With this novel computational model, we achieved 87-95% mean accuracy for identification of the pathogenic *Candida* with 92% mean accuracy for *C. auris*.

CONCLUSIONS:
Importantly, experiments are ongoing to determine sub-species differences, namely between *C. auris* isolates with different antifungal susceptibilities or within isolates in response to environmental cues, and whether these differences are diagnostic or can offer insight into virulence and drug resistance mechanisms. Overall this study demonstrates the potential of this platform to reduce time and improve accuracy of diagnosis during infection. Our novel diagnostic platform identifies *Candida* species based on their lipid mass spectra including the newly emergent pathogen, *C. auris*.