29th ECCMID Amsterdam, Netherlands 13 – 16 April 2019
The congress of ESCMID

P2158 *Candida auris*: Are we ready for the clones attack?

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Background: Multidrug resistant clonal strains of *Candida auris* have been isolated in the last five years in many countries. The emergence of *C. auris* is alarming, therefore, an accurate and rapid identification at the species-level and differentiation between susceptible and resistant isolates to antifungals drugs is mandatory. Commercial routine systems for yeasts identification commonly misidentify these recently emerged clones and mass spectrometry systems databases lack *C. auris* reference profiles. The aim of the present study has been the implementation of the Bruker MALDI-TOF MS database with *C. auris* mass profiles and the development of a fast and reproducible assay able to rapidly detect *C. auris* resistance to anidulafungin (AFG).

Materials/methods: All the mass measurements below mentioned were performed with a Microflex LT mass spectrometer. Briefly, protein extracts from a panel of *C. auris* isolates from India were obtained with both fast formic acid and long ethanol /formic acid extraction procedures. After the MSPs creation, a score-oriented dendrogram was generated from hierarchical cluster analysis, including *C. lusitaniae*, *C. famata*, *C. guillermondii* and *C. parapsilosis* isolates. To detect *C. auris* resistance to AFG a three hours incubation antifungal susceptibility test (AFST) was developed, after preliminary experiments aimed to find the breakpoint and maximum level of AFG concentrations needed to obtain a correct categorization for the isolates. Spectra obtained at null, intermediate or maximum AFG concentrations were used to create composite correlation index (CCI) matrices for the *C. auris* isolates.

Results: Cluster analysis of MALDI-TOF spectra resulted in the correct grouping according to the five species represented and allowed a correct identification at the species-level for the isolates included in the analysis. Five out of six *C. auris* resistant strains were detected by AFST and among the 12 susceptible strains, eight turned to be susceptible, two resistant and two undetermined.

Conclusions: Given the diagnostic urgency related to the emergence of *C. auris*, our approach would provide a rapid tool for the species-level pathogen identification and speed up the initiation of the appropriate antifungal treatment.