External Quality Assessment pilot study for the detection of *Candida auris*

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Introduction

Candida auris, identified for the first time in 2009, is a multi-resistant emergent yeast that causes nosocomial outbreaks all over the world. This species can be misidentified with other *Candida* species, if the method used for yeasts' identification (biochemical / mass spectrometry (MALDI-TOF-MS) has not been updated in order to contain the profile of this species.

Aiming to raise the awareness about the risk of misidentification associated to this species, the Portuguese External Quality Assessment Program (PNAEQ), in collaboration with the National Reference Laboratory for Parasitic and Fungal Infections of the National Institute of Health Dr. Ricardo Jorge, organized a pilot study in 2020 to evaluate the ability of Portuguese clinical microbiology laboratories to correctly identify *C. auris*.

Methods

On the 15th of November 2019 an email was sent to all PNAEQ microbiology participants with a questionnaire to evaluate the intention of participation in a new quality control scheme and to perceive the available capacity of identifying *Candida auris*. Yeast isolates were previously characterized by molecular methods by PCR sequencing of D1/D2 region and MALDI-TOF-MS. Test samples contained suspensions of three yeast species (*Candida auris, Candida duobushaemulonii, Candida krusei*). Samples were distributed to 18 participant laboratories for the identification of yeasts up to the level of the species, according to the method in use by the participant laboratory, Results were analyzed, and an individual report was sent to the participants.

Results

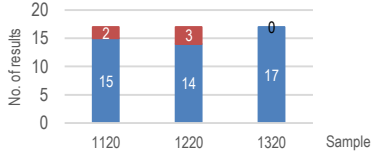
- The participation rate in the detection of *Candida auris* scheme (94%), took into account 18 participants (17/18). Eight of those were Hospital laboratories and nine were ambulatory laboratories.
- Four different methods were used for species identification as seen in table 1: automated biochemical method (10/17), MALDI-TOF-MS (5/17), non-automated biochemical method (1/17) and culture onto chromogenic media (1/17).
- The instruments used by the participants are reported in table 2. Two laboratories used other non-instrumental methods.

Table 1: Methods used for *C.auris* detection

Method	Participants
01 – Automated biochemical	10
02 – Non automated biochemical	1
03 - MALDI-TOF MS	5
06 - Culture - chromogenic media	1

Table 2: Instruments used for *C.auris* detection

Instruments	Participants
01 - Vitek 2	10
03 - Vitek MS	3
04 - Bruker biotyper (MALDI-TOF-MS)	2



Graph 1: Laboratory results per sample (Incorrect answers in red)

- The species *C. auris was* correctly identified by 88% (15/17) of participating laboratories. One laboratory was not able to identify this species and one other identified it as *C. tropicalis*. All the participating hospital laboratories reported the correct species of *Candida*. Participants with incorrect/missing answers used manual methods (non-automated biochemical methods and chromogenic media) (Graph 1 – sample 1120).
- *Candida duobushaemulonii* was correctly identified by 82% (14/17) of participating laboratories the species. One of the participants reported it as *C. auris*, two participants incorrectly identified the sample as *Saccharomyces cerevisiae*/*Candida famata* and as *Candida glabrata*. Again, all hospital laboratories reported the correct identification of this species. Participants with incorrect answers used non-automated biochemical methods, the automated method Vitek 2 and chromogenic media. (Graph 1 – sample 1220).
- All the participants (17/17) correctly identified the sample containing *C. krusei*. (Graph 1 – sample 1320).

Discussion/Conclusion

The identification of yeasts to the species level is of the utmost importance in Hospital units but also in the laboratories that handle ambulatory samples. The results of this pilot study were satisfactory. The majority of the participating laboratories used automated biochemical methods or MALDI-TOF MS, with the updated database for *C. auris.* Participants using non-automated methods such as API and culture in chromogenic media reported incorrect results for the identification of *C. auris* and *C. duobushaemulonii*.

Since *C. auris* is considered an emerge pathogenic agent due to its multi-resistant phenotype, fast identification is mandatory for implementing measures to stop the dissemination.