Comparison between the Vitek2 Yeast Identification and Antifungal Susceptibility testing with the Reference laboratory methods

Sahar Eldirdiri [1], William J Olver[1]
Ninewells Hospital and Medical School, Dundee, UK

Introduction

The decision to identify a yeast to species level is based on a combination of clinical and microbiological factors. Antifungal susceptibility testing remains an area of considerable interest, however there is very little guidance available for yeast susceptibility testing and the evidence base of the guidance currently available is not robust (1). Rapid identification of yeasts provides timely information to physicians for patient management (2)

MALDI-TOF MS was cleared by the FDA for the use in clinical microbiology laboratories. Studies evaluating their performances are promising, showing that this method is able to accurately and rapidly identify *Candida* spp. from positive cultures, with a high concordance consistently {90%} in comparison to conventional methods(3)

EUCAST and CLSI adopt standardized broth microdilution methods for AFST (4,5). Other commercial broth-based MIC systems include Candifast, Intergral systems yeasts and fungitest. A commercial system that includes a colorimetric response is marketed as Sensititre yeast one colorimetric. Besides Etest, Disk-based susceptibility testing and Flow Cytometry (6)

Aim

Yeast identification and antifungal susceptibility testing was performed using Vitek2 (bioMérieux, France) in Ninewells hospital, Dundee. In this study, the Vitek2 system was evaluated by comparing it's results with those obtained by the Mycology reference laboratory in Glasgow (Southern General Hospital)

Methods

Data was collected retrospectively from the microbiology computer system (LabCentre) from April-September 2015. The data covered a sample of 56 specimens.

MALDI from bioMérieux was used for identification of all yeast in the Mycology reference laboratory. Sensititre (Thermo Scientific) was used to test only samples from sterile sites for antifungal susceptibility while all other samples were tested by disc diffusion methods.

Results

The types of specimens investigated in the study were blood cultures, sputum, high vaginal swab, endotracheal aspirate, mouth swab, wound swab, throat swab, line tip and bronchoalveolar lavage(BAL). Samples were received from different clinical specialties including sexual health clinics, GP, paediatrics, haematology, renal, oncology and cystic fibrosis clinics.

Among the 56 specimens included in the study, 57 isolates were identified as *Candida. albicans* (n=23), *C. glabrata* (n=10), *C. krusei* (n=2), *Saccharomyces cerevisiae*(n=2*), C. parapsilosis* (n=2), *C. dubliniensis* (n=3), *C. guilliermondii* (n=3), *C. famata* (n=4), *C.sphaerica* (n=1) *Rhodotorula mucilaginosa* (n=1) and *unidentified fungus*(n=6). One specimen contained 2 isolates (*C. albicans & C. glabrata*).

There was 79% agreement between the vitek2 results and the reference lab results for identification of isolates. A total of 26 (46%) species had the same identification and sensitivity results as the reference laboratory. 6(10.5%) species were misidentified by Vitek2. Additionally, another 6 species (10.5%) were unidentified fungus by Vitek2.

Nineteen (33%) species had different sensitivity pattern compared with the reference lab results. Fluconazole resistant rate was higher by Vitek2 than reference lab results, the rate was calculated as 17.5%.

In this study all the clinical bloodstream yeast isolates had the same identification by both the vitek2 system and the reference lab methods apart from one *C.guilliermondii* misidentified as *C.famata*

Discussion

We have noticed discrepancy in fluconazole sensitivity testing between the Ninewells lab and the reference lab. This overestimated resistance rate may have a major clinical implications as fluconazole considered to be the first recommended antifungal for many infections. Four isolates of *C.glabrata* (n=10) were found to have intermediate sensitivity by both vitek2 and the reference lab methods. The clinical breakpoints have been revised to categorise the entire wild-type population of *C. glabrata* as intermediate, thereby facilitating discrimination between wild-type and isolates with elevated MICs and acquired resistance mechanisms (7)

All *C.famata* (n=4) were misidentified, one sample identified by the reference lab as *C.albicans* and others as *C.guilliermondii*. These disappointing results are due to the fact that *C. guilliermondii* and *C. famata* show similar biopatterns, which could not be sufficiently discriminated by the YST card. Unfortunately we do not have explanation to *C.albicans* misidentified as *C.dubliniensis* from high vaginal swab.

The results of 79% agreement between the vitek2 results and reference lab results for identification of yeast in this study confirmed the result of previous project done in Ninewells lab in 2010 with a rate of 80% agreement

Conclusion

As a result of this study we have changed our practice in Ninewells laboratory. We have started using the MALDI- TOF(Bruker- Germany) for identification of yeasts from all clinical samples. Furthermore, antifungal susceptibility testing are currently all done by Mycology reference laboratory in Bristol

References

1.UK Clinical Mycology Network, Identification and Sensitivity Testing of Yeast Isolates Practice Guide.

2.Giuseppe Valenza et al, Journal of Clinical Microbiology 2008 vol.46 3784-3787 doi: 10.1128/JCM.01318-08

3.Marious Arvanitis et al, Clinical Microbiology rev July 2104 vol 27 nno.3 490-526

4. Manuel Cuenca-Estrella et al, Journal of Clinical Microbiology May 2010,p.1782-1786 Vol.48 No.5

5.EUCAST Definitive document E.DEF 7.3 December 2015

6.John H.Rex et al, Practical Aspects and Current Challenges, Clinical Microbiology Rev 2001 Oct p.643-658

7.EUCAST Technical note on fluconazole, Clinical Microbiology Infect.2008:14:193-195