ESwab for the Collection of Fungal Surveillance Culture from Immunocompromised Patients

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Background

Fungal infections are an important cause of morbidity and mortality in immunocompromised patients especially when they undergo chemotherapy treatment for cancer or are immune suppressed because are bone-marrow or solid transplantation transplant recipients. Candida and Aspergillus species are the most common fungal pathogens responsible for invasive fungal infection (IFI). Unfortunately, the diagnosis of IFIs remains difficult and it is often confirmed late. The value of fungal surveillance cultures (SCs), as predictors of IFIs, is well known and consist of collection of throat, nasal and rectal swabs. Copan ESwab™ is a Liquid Based Microbiology device that we is being used for the collection of all clinical specimens for the diagnosis of infectious diseases including fungal.

Objectives

The objective of this study was to demonstrate the performance of ESwab™ for the collection of clinical specimens for the detection of fungal and yeast in SCs.

Methods

The study was carried out on 21,044 samples received by the laboratory of microbiology of the Polyclinic Tor Vergata starting from 01/01/2010 to 15/11/2015.

All samples were collected in ESwab™ from immunocompromised patients (hematology, oncohematology, Mediterranean institute of hematology and stem cell transplantation).

The SCs for the detection of yeasts and filamentous fungi (Fi) were performed on nasal swabs, throat swabs and rectal swabs.

In particular, 11,339 nasal swabs (53.9%), 8,066 throat swabs (38.3%) and 1,639 rectal swabs (7.8%) were processed (graphic 1).

If positive, isolates were identified by Vitek 2 System cards (YST, bioMérieux) for yeasts and by microscopic exam (using lactophenol cotton blue stain) as well as MALDI-TOF System (Bruker Daltonics) for filamentous fungi (FI).

In some occasion FI required identification by gene sequencing, which was carried out by performing amplification and nucleotide sequencing of 18s rDNA partial gene (using ABI 310 genetic analyzer; Applera).

The identifications were achieved by sequence alignment (searching the best consensus sequences) to the universal databases in the NCBI data bank.

Results

The positive samples were 237 (1.12%), namely: 80.1% throat swabs, 8.1% rectal swabs and 11.8% nasal swabs.

The yeasts were mainly represented by Candida spp. (90.7%). Candida albicans was the most common specie (59.5%) followed by Candida tropicalis (15.8%), Candida glabrata (9.7%) and Candida parapsilosis (5.1%) (graphic 2). Penicillium was isolated in 3.2% of specimens, while 3.2% of the isolates was Aspergillus (especially niger, fumigatus and nidulans) (Figure 1).

The remaining 3% were other genera of Fi and other Candida species (Sporotrichum pruinoseum, Cryosporium parvum, Geotrichum capitatum, Cryptococcus laurentii, Candida krusei, Candida lusitaniae and Candida dubliniensis).

Conclusions

Both Candida and Fi were easily detected (in an elapsed time ranging from 24-48h and 48h-5 days for yeast and fungi, respectively) from all clinical specimens submitted in Copan Eswab, demonstrating that is a good system for preserving the viability of yeasts and fungi.

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