

P0033

Poster Session I

How to improve fungal diagnosis

CANDIDA COLONIZATION OF THE LOWER RESPIRATORY TRACT INVESTIGATED BY CONVENTIONAL CULTURE AND FUNGAL MICROBIOME ANALYSIS

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Objectives

Antibiotic therapy and treatment at intensive care units (ICU) have been considered as risk factors for Candida colonization of the lower respiratory tract (LRT). We investigated the presence of Candida colonization of the LRT with conventional culture and culture-independently by internal transcribed spacer (ITS) -based microbial community analysis using next generation sequencing (NGS) in the following groups: 1a, healthy individuals (n=8); 1b, patients with healthy lungs but with antibiotic therapy for treatment of extrapulmonary infections (n=7); 2a, mechanically ventilated patients at the ICU without antibiotic therapy (n=7); 2b, mechanically ventilated patients at the ICU with antibiotic therapy for extrapulmonary infection (n=6) and 3, mechanically ventilated patients at the ICU with pneumonia and antibiotic therapy (n=26).

Methods

In patients from group 1 endobronchial secretion (EBS) was aspirated during general anesthesia performed for routine surgical procedures. For group 2 and 3 patients bronchoalveolar lavage (BAL) was bronchoscopically performed via orotracheal tubes or tracheostomas. EBSs and BALs were quantitatively cultured on Candida CHROMagar (Becton Dickinson, Heidelberg, Germany) and chocolate agar and incubated for 48h. Isolates were counted and subsequently identified by API Aux (biomerieux, Marcy-l'Etoile, France) and MalDI-TOF-mass-spectrometry. EBSs and BALs were also submitted to NGS for characterization of fungi using panfungal ITS primers. For 10 samples, the PCR did not produce any amplicons; these samples were excluded from analysis (4 in group 1a, 2 in group 1b, 4 in group 3). After denoising and removal of contaminant sequences phylogenetic analysis of the ITS dataset was done using the advanced BLAT approach of the phylotyping pipeline SnoWMAAn (<http://SnoWMAAn.genome.tugraz.at>).

Results

Candida species were cultured in 0/8 (group 1a), 0/7 (group 1b), 1/7 (group 2a), 3/6 (group 2b), and 11/26 (group 3) patients. By culture-independent analysis the lower respiratory tract of group 1a, 1b, 2a, 2b, and 3 patients contained 36, 199, 104, 29 and 129 fungal genera. By molecular analysis Candida species were detected in group 1a, 1b, 2a, 2b, and 3 in 0,1%, 0,2%, 50%, 62% and 72% of total fungal genera, respectively. Principal component analysis revealed a distinct clustering of groups 1a, 2a, and 3 compared to groups 1b and 2b indicating a difference in fungal microbiota composition between groups.

Group	1a	1b	2a	2b	3
positive Candida culture	0/8 patients	0/7 patients	1/7 patients	3/6 patients	11/26 patients
fungal genera (by NGS)	36	199	104	29	129
Candida species (by NGS); % of total fungal genera	0,1%	0,2%	50%	62%	72%

Conclusions

This study describes the fungal microbiome of the lower-respiratory tract (with focus on Candida species) in different patient groups, including ventilated ICU patients with antibiotic therapy. Data show that treatment on intensive care wards and not antibiotic therapy shifts lung fungal microbiota to Candida species dominated fungal profiles.