Mycobiota analysis of samples from different body regions in ICU patients

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Introduction

Infections due to Candida spp. are increasing worldwide. Invasive Candida infections are serious complications in immunocompromised patients and in patients undergoing treatment for cancer but occur also in patients treated in ICUs. Risk factors for invasive candidiasis include multicolonization with Candida spp., prior or concomitant exposure to antibiotics, neutropenia, vascular access, long ICU stay, surgical procedures, renal failure, and use of steroids. Candida colonization (determined by conventional cultures) as well as Candida infection rate increase with length of ICU stay. Previously, mycobiota analysis showed that admission to and treatment on ICUs shifted lower respiratory tract fungal microbiota to Candida spp. dominated fungal profiles but antibiotic therapy did not. However, time dependent mycobiome profiles from various body sites at given time points are missing. We therefore aimed to analyze mycobiota in samples from different body regions of ICU patients and to investigate potential factors for shifts in mycobiome composition.

Methods

Fourteen medical ICU patients were prospectively investigated and 128 samples from different locations collected: 31 fecal, 29 gastric, 33 tracheal, 35 pharyngeal samples. Samples were refridgerated until mycobiota analysis was performed by next generation sequencing as previously described (ITS 1 and 2 PCR, sequencing using IonTorrent, sequence analysis using qiime with open reference otu picking and UNITE database. Linear effect size (LEfSe) analysis was performed using the default parameters to identify features that discriminated our groups of interest). Samples below 2000 sequences per sample were excluded from further analysis, therefore 94 of 128 samples were used for results (24 fecal, 21 gastric, 25 tracheal, 24 pharyngeal samples). Samples were categorized in early (day 1-5 of ICU treatment), indermediate (6-14 days), and late collected samples (later than day 14). Number of antimicrobials used prior to sampling were categorized into: none, one, 2-3 antibiotics (few) and more than 4 antibiotics (many).

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Results

Overall, Candida dominated mycobiota in fecal, gastric, pharyngeal and tracheal samples. Time dependent Candida sp. abundance are depicted in table 1, Candida sp. abundance and antibiotic treatments (few=2-3 antibiotics, many=more than four antibiotics) is depicted in table 2. Figures show LDA (Linear discriminant analysis) plots and cladograms.

Table 1: Time dependent Candida sp. abundance

	early (day 1-5) ICU stay	intermediate (day 6-14) ICU stay	late (day 15+) ICU stay
fecal samples	41,6 %	86,9 %	86,3 %
gastric samples	58,5 %	90,3 %	74,7 %
pharyngeal samples	32,5 %	95,2 %	91,3 %
tracheal samples	59,6 %	88,3 %	86,5 %

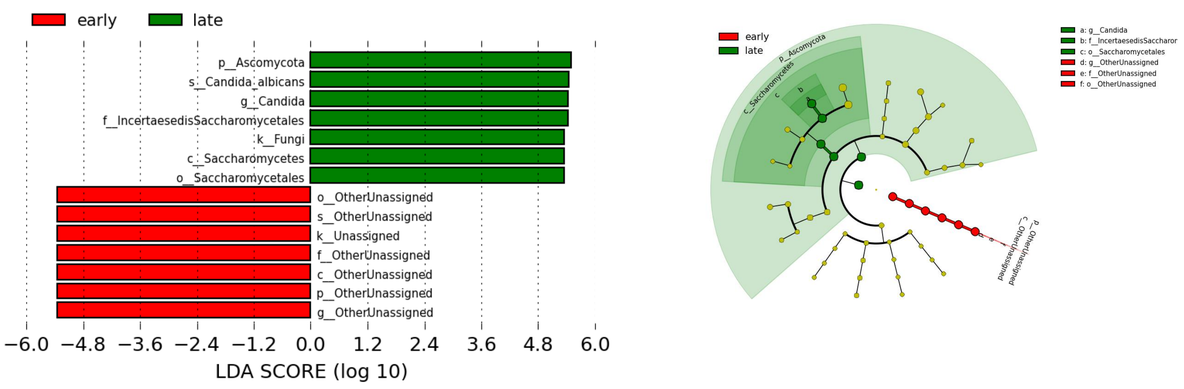

Figure 1: Linear discriminant analysis effect size (Lefse Plot) and cladogram of fecal samples, early (day 1-5 days ICU) versus late (day +15)

Table 2: Candida sp. abundance and antibiotic treatments

	none	one	few	many
fecal samples	0 %	52,8 %	85,5 %	82,3 %
gastric samples	95,2 %	54 %	81,2 %	91,4 %
pharyngeal samples	81,4 %	57 %	96,5 %	93,3 %
tracheal samples	92,5 %	75,3 %	83,1 %	94,2 %

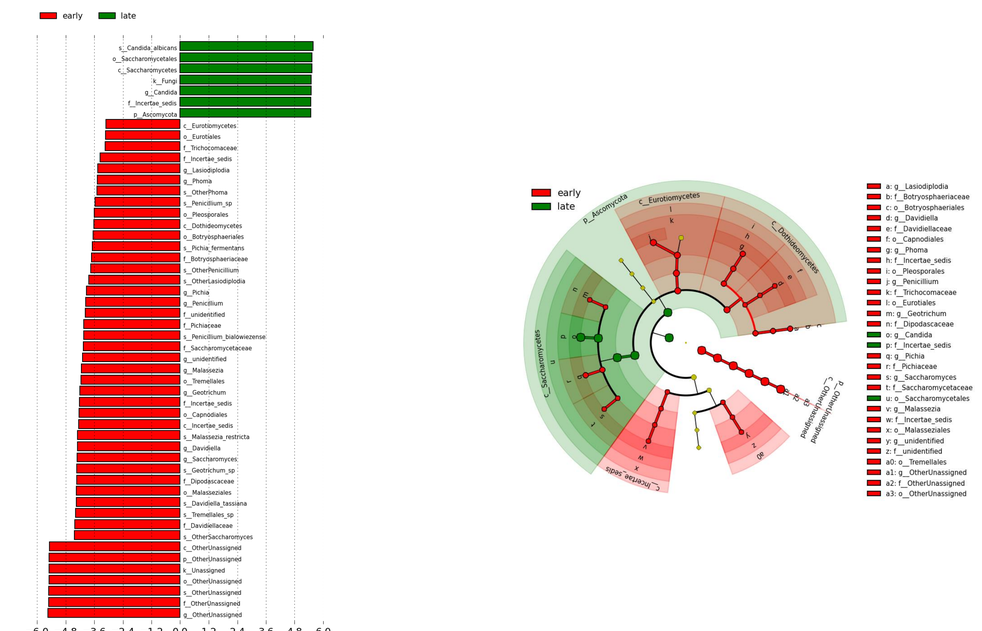

Figure 2: Linear discriminant analysis effect size (Lefse Plot) and cladogram of pharyngeal samples, early (day 1-5 days ICU) versus late (day +15)

Conclusions

Treatment on ICUs shifted fecal, gastric, pharyngeal and tracheal fungal microbiota to Candida spp. dominated fungal profiles. Antibiotic therapy affected fecal mycobiota but had no influence on mycobiota in samples from other locations.

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