Prolonged mechanical ventilation support was associated with the development of nosocomial candidiasis and bacteremia. Parallel to the development in the field of diagnosis and treatment, an increase in the incidence of fungal infections and the number of patients who are in the risk group for the development of opportunistic fungal infections have been observed in recent years. Among the hospitalized patients, those most at risk in terms of fungal infections are intensive care unit (ICU) patients. The rate of Candida infections amongst critical care patients is very low and may serve as useful surrogate if not diagnostic, treated, and handled effectively, and promptly.

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Bacterial and fungal infection in COVID-19 diagnosed cases in a tertiary care ICU setting in the wake of second wave in Kolatka, India

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Poster session 3, 23rd December 2021, 12:30 PM - 1:30 PM

Background: During the second wave of COVID-19, we aimed to study the development of bacterial and fungal infections in COVID-19 positive intensive care unit patients in our center.

Methods and Methods: All COVID-19 positive intensive care unit patients admitted during the second wave of COVID-19 were recruited. Results: A total of 221 patients were included in the study. The median age was 55 years (range: 18-85). Males constituted 70% of the patients. 219 patients were symptomatic. 77 patients were admitted for intubation and were either on mechanical ventilation or high flow nasal cannula oxygen. Bacterial and fungal infection were seen in 168 (76%) patients and in 64 (30%) patients respectively. The most common bacterial pathogens were S. aureus (11%), Acinetobacter baumannii (11%), and Pseudomonas aeruginosa (9%). The most common fungal pathogens were Candida albicans (11%) and Candida krusei (9%). The most common comorbidities were diabetes (34%) and chronic obstructive pulmonary disease (COPD) (30%). Conclusion: The incidence of bacterial and fungal infection in COVID-19 positive intensive care unit patients was high.

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Detection of causative agents of infectious keratitis in patients from western rajasthan

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Objective: To determine the spectrum of causative agents, the related risk factors, and their association in patients of infectious keratitis.

Design: It was a prospective study conducted over a period of 10 months from August 2018 to January 2019, which included 100 patients attending the Ophthalmology OPD with features of keratitis. Ophthalmological examination was followed by corneal scrapings collection, which were subjected to culture, microscopy, and molecular diagnostic tools. Bacterial isolates were identified by conventional methods and Multispecies WalkAway system while the fungal isolates were identified conventionally. Pap-fungal stains were used to detect fungal elements directly from the sample.

Results: Out of 100, 41 cases were positive by culture, of which 12 (28.76%) held fungal and 29 (68.29%) held bacterial keratitis. Paasman spp. accounted for 53.52% of fungal and Pseudallescheria boydii accounted for 55.52% of the bacterial isolates. Fungal keratitis was detected in 45% using pan fungal primers. Cases were maximally recorded during July-October. Traumatic history was present in 78% patients caused by vegetative matter (48%). A male predominance (67%) was also observed. Four patients underwent keratoplasty in spite of rigorous management.

Conclusion: Poorer prognosis emphasizes the need for better diagnosis, which can detect the causative agents from the clinical specimen itself, reinforcing the concept of clinical instigations.

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Molecular identification, genotyping, and antifungal susceptibility of Trichosporon species isolated from clinical samples of patients at various parts of the Indian subcontinent

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Objectives: (1) To study mycological characteristics of strains belonging to Trichosporon and its related genera obtained from clinical samples of patients from India. (2) Molecular identification by intergenic spacer (IGS) region 1 sequencing of the rDNA locus. (3) Genotyping of the major causative agent, T. asahii, and its in-vitro drug susceptibility testing. Materials and Methods: A total of 15 clinical isolates of Trichosporon species were collected from NCUP (National culture collection of pathogenic fungi) PMGER, Chandigarh along with different health institutions of India. These isolates were recovered from urine, blood, sputum, nail, tissue biopsy, pleural fluid, brain abscess, and wound discharge over a period of 12 years (2006-2018). The isolates were molecularly characterized and genotyped using IGS-1 region sequencing. In vitro drug susceptibility testing of the isolates was performed against amphotericin-B, fluconazole, voriconazole, and posaconazole according to the CLSI M27-A3 guidelines (CLSI 2008). Results: Predominant underlying risk factors identified were presence of an indwelling catheter, use of broad-spectrum antibiotics, and presence of comorbid conditions such as diabetes, hypopituitarism, and asthma. A total of 47 (93.8%) of the 55 isolates were identified as T. asahii, 6 were T. candida (11%), and 2 were Caninum Trichosporonum (3.4%). Trichosporon asahii genotype III (22, 41%) was the most common type, followed by genotype IV (12, 22%), II (9, 15%), and VI (2, 4%). In addition to the 15 known Trichosporon species, one novel genotype was identified from one isolate showing high MRC ranges to amphotericin-B (0:04-4 mg/L) and fluconazole (0:24-64 mg/L). Relatively low MRC ranges were found in the case of voriconazole (0:05-5 mg/L), Posaconazole (0:06-1 mg/L), and itraconazole (0:06-5 mg/L). Voriconazole appeared to be the most active drug against T. asahii isolates. The MRC for all the drugs were comparatively lower in the case of non- T. asahii strains. Conclusion: Trichosporon asahii remains the most common etiology of Trichosporon in India and presents a challenge for both diagnosis and treatment. With increasing drug resistance, therapeutic options are limited, and antifungal regimens with triazoles especially voriconazole appear to be the best. Accurate timely identification, removal of indwelling catheterisation venous lines, and voriconazole-based treatment along with control of underlying conditions were associated with favorable outcomes. Identification of the novel genotypes has epidemiological implications and requires further work up.