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Purpose: COVID-19 has emerged as the "first pandemic of the 21st Century" and continues to pose challenges to global health. Currently, the most common symptomatic management of COVID-19 patients involves isolation and oxygen therapy. However, present protocols are still deemed insufficient; hence, other treatment options are being considered and tested. This includes convalescent plasma therapy (CPT), which involves a strategy of passive immunization.

With this, the primary objective of this systematic review/meta-analysis is to collate, systematically compare, and synthesize available clinical trials involving convalescent plasma (CP), more specifically, high-titer CP, as adjunctive therapy in the treatment of patients with severe COVID-19.

Methods & Materials: This was accomplished by comparing the effect of high-titer CP with standard treatment alone, in terms of mortality rate and viral clearance, by reviewing selected studies based on an inclusion-exclusion criteria and synthesizing selected studies through qualitative analysis and meta-analysis.

Results: A total of five studies were included, which consist of: three randomized clinical trials (RCTs); one retrospective trial; and one single arm trial. Four studies were subjected to meta-analysis for mortality rate. For instance, it was determined that the overall incidence mortality rate of patients who received high-titer CP is 11.59% of the experimental group, while the incidence mortality rate of patients who only received standard care is 20.25% of the control group (Risk Ratio (RR), 0.71; 95% confidence interval (CI), 0.46-1.09; P-value = 0.46). Moreover, three of the included trials were subjected to qualitative analysis, all of which depicted undetectable viral levels in some patients as early as 3 days, while others exhibited a steady decline.

Conclusion: Treatment of COVID-19 with the use of high-titer convalescent plasma as an adjunctive therapy, compared with standard care or treatment, was not significantly associated with reduction of all-cause mortality. High-Titer CPT also shows potential in increasing COVID-19 viral clearance, which indicates an antiviral effect; however, controlled clinical trials with comparator or placebo groups are needed to further support these findings.

https://doi.org/10.1016/j.ijid.2021.12.088

OP05.04 (367)
Investigation of SARS-CoV-2 RNAemia in the convalescent plasma of COVID-19 patients
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Purpose: The novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), is responsible for the ongoing global COVID-19 disease pandemic. Convalescent plasma therapy (CPT) is one of the promising therapies being tried for COVID-19 patients. However, the presence or disappearance of SARS-CoV-2 RNA (RNAemia) in convalescent plasma is unclear and the prognostic implication of viral RNA detection in these samples is not fully understood. Hence, we aimed to investigate SARS-CoV-2 RNAemia in the convalescent plasma of COVID-19 patients.

Methods & Materials: Convalescent plasma samples from donors with a previous laboratory-confirmed SARS-CoV-2 infection were included in the study. Samples were screened for the presence of Anti-SARS CoV-2 IgG antibodies using a commercially available enzyme-linked immunosorbent assay targeting the whole-cell antigen of SARS-CoV-2. Then plasma samples were pooled by the mixing of five samples. RNA extraction and realtime RT-PCR for SARS-CoV-2 specific gene targets was performed for pooled plasma samples.

Results: A total of 250 convalescent plasma samples of COVID-19 patients with different disease severity were included in the study; of these, 149 (59.6%) were found to have anti-SARS-CoV-2 antibodies using serological tests. SARS-CoV-2 RNA was not detected in any of the convalescent plasma samples.

Conclusion: SARS-CoV-2 RNAemia was not found in individuals with a previous laboratory-confirmed SARS-CoV-2 infection at least 28 days after the resolution of their symptoms. All RT-PCR positive COVID-19 patients subsequently may not develop antibodies. Our study showed that screening for neutralizing antibody titres is more important rather than SARS-CoV-2 RNA detection in convalescent plasma samples for therapeutic use.

https://doi.org/10.1016/j.ijid.2021.12.089

OP05.05 (448)
Emerging COVID-associated mucor-aspergillosis – A Need of Separate Definition
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Purpose: During COVID pandemic, several cases of isolated COVID-associated mucormycosis and COVID-associated pulmonary aspergillosis have been reported. There is no data regarding both infections in same patients. Herein, we present series of ten consecutive cases with dual invasive molds in patients infected with SARS-CoV-2.

Methods & Materials: Among patients hospitalized with diagnosis of COVID in May 2021 at a tertiary care center in North India, ten microbiologically confirmed dual/mixed COVID-associated mucor-aspergillosis (CAMA) were analysed. We hypothesised case definition for Covid-associated mucormycosis and aspergillosis infection derived from EORTC/MSG, as possible, probable, and proven CAMA.

Results: Six men and four women had a mean age of 49.2 ± 8.8 years. All patients were diabetic with history of COVID pneumonia. Patients presented with headache, fever, altered sensorium, decreased vision, nasal obstruction, periorbital swelling, nasal stuffiness, nasal discharge. Rhizopus arrhizus was isolated in all, Aspergillus flavus in seven and Aspergillus fumigatus in three patients. Patient 2,5,6,8,9 were histopathologically proven dual infections with patient 3 & 7 having only angiinvasion. Patients received amphotericin B and all except 3 were managed by surgical debridement, the remaining 3 succumbed.
**Conclusion:** These findings may help towards a better insight into the clinical profile of invasive CAMA and thus we propose a definition in connotation with EORTC/MSG for IFD.

| Invasive Fungal Disease (IFD) (EORTC/MSG Criteria) | Corresponding Present case series as per new definition CAMA | Proposed definition of CAMA |
|--------------------------------------------------|---------------------------------------------------------------|-----------------------------|
| POSSIBLE: Immunocompromised                       | -                                                             | Concurrent or recently treated COVID-19 (<6 weeks) |
| PROBABLE IFD: Possible plus                       | Cases 1,4,10                                                   | Corresponds |
| Mycological evidence: Cytology, direct microscopy, or culture | i. Corresponds, but additional host factors for Aspergillosis to be included: Uncontrolled DM ii. Asthma iii. Cystic Fibrosis iv. Environmental factors v. Colonizer vi. Additional host factors for Mucormycosis to be included: Uncontrolled DM vii. CKD viii. Iron overload ix. Trauma x. Antifungal prophylaxis xi. Intravenous drug use |
| PROVEN IFD: Probable plus Confirmed with Histopathology Host factors: Immunocompetent also | Cases 2,3,5,6,7,8,9 | Corresponds, but in combination of IFD cases such as CAMA one IFD may be proven and another probable type. |

https://doi.org/10.1016/j.ijid.2021.12.090

**OP05.06 (350)**

**Trends of a syndromic approach based respiratory PCR during the second wave of the COVID 19 pandemic in a tertiary care center in Mumbai**

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**Purpose:** The clinical presentation of COVID 19 disease caused by Severe Acute Respiratory Syndrome Related Coronavirus – 2 (SARS-CoV2) is similar to other causes of upper respiratory viral infections caused by influenza, epidemic corona viruses, Parainfluenza virus etc. This study was undertaken to study the presence of different pathogens in the nasopharyngeal samples of symptomatic patients visiting the COVID OPD or the Emergency services over six month duration.

**Methods & Materials:** This was a prospective study from Dec 2020 to May 2021 conducted in a 220 bed tertiary care hospital in Mumbai. We are a designated COVID care hospital with 55 isolation beds including 16 beds in the COVID ICU, a dedicated OPD for symptomatic patients and Emergency services (EMS). The test was performed on a syndromic approach based respiratory PCR with 22 targets inclusive of SARS-CoV2. Nasal and a pharyngeal swab samples (NPS) were collected and the results of the test were available in 1.5 hours from sample receipt to the lab.

**Results:** A total of 335 patient samples were received during the study period for the syndromic approach based PCR. 133 (39.7%) of the symptomatic patients had a positive test result. 87(26%) SARS-CoV2 and 27(8.05%) Rhinovirus/Enterovirus (RHV/EV) were the two common viruses that were identified during the study duration. Other viruses, like Parainfluenza 3 (PIV3), Coronavirus 229E (229E), Coronavirus HKU1 (HKU1), Influenza AH3 (AH3), H1N1, Coronavirus OC43 (OC43) and Adenovirus were also identified. We observed co-infections 1 each of RH/V/E- AH3, RH/V/E-OC43, SARS-CoV2 +PIV3 and 2 cases of SARS-CoV2+HKU1. The trend indicated the appearance of the 2nd wave of SARS-CoV2 infection that Mumbai experienced between 1st March to 15th May 2021. Other pathogens were mostly seen in the symptomatic population especially before and after the 2nd wave.

**Conclusion:** Our study documented the appearance of the second wave in Mumbai between 1st March to 15th May 2021. Approximately, 34.5% of patients had other respiratory pathogens detected in the syndromic PCR. This is the 1st study from Mumbai documenting the types of respiratory pathogens and co infections seen during the 2nd wave of the COVID 19 pandemic in Mumbai.

https://doi.org/10.1016/j.ijid.2021.12.091

**OP05.07 (995)**

**SARS-CoV-2 variants detection using TaqMan SARS-CoV-2 mutation panel molecular (genotyping) assays**

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**Purpose:** For rapid detection and tracking of SARS-CoV-2, alternative method for screening in few hours is highly desirable. Here, we evaluated performance characteristics of TaqMan SARS-CoV-2 mutation panel genotyping molecular assay for detection of most common published SARS-CoV-2 variants using specific RT-PCR assays targeting single nucleotide polymorphisms (SNP).

**Methods & Materials:** A total of 150 SARS-CoV-2 positive samples from March to July were included for this study. In addition, five controls comprised of synthetic RNA B.1.1.7_601443, B.1.351_678597, B.1.351_678597, P.1_792683, B.1.617.1_1662307 and MN908947.3-Wuhan-hu-1 from Twist bioscience and B.1.1.7 (England/204820464/2020) and B.1.351 (South Africa/KRISP-K005325/2020) from (Zeptrometrix, NY, USA) were used for validation. RNA from all specimens were extracted using Omega Bio-Tek Mag-Bind Viral RNA Xpres Kit and tested for known SARS-CoV2 variants using ThermoFisher TaqMan SARS-CoV-2 mutation panel molecular assay on the Quant Studio 12K Flex. Nine representative samples have been compared with sequencing. Data were analyzed by genotype calling using QuantStudioTM design and analysis software v2.5 with the genotyping analysis module.

**Results:** All validation controls were tested in triplicate and repeated in singlet on three different days and all reported variants were matching as expected. Out of 150 SARS-CoV-2 positive specimens, 69 (46%) were B.1.617.2, 49 (32.7%) were B.1.1.7, P1 and P2 were 4 (2.7%) each and B.1.351 and B.1.427/B.1.429 were 2 (1.3%) each. 3 (2%) were B.1.526 and 17 (11.3%) have mutation in D614G. Genotyping results from present study showing B.1.617.2, B.1.1.7 and B.1.526 variants and their mutation genes were concordant with sequencing results.

**Conclusion:** Our study indicates that TaqMan SARS-CoV-2 mutation panel molecular (genotyping) assays detects and differentiates all published common variants B.1.617.2 (Delta), B.1.1.7 (Alpha), B.1.526 (Iota), B.1.351 (Beta), P1 (Gamma), B.1.617.1 (Kappa) and B.1.427/ B.1.429 (Epsilon) that can be used for surveillance and epidemiological prevention.

https://doi.org/10.1016/j.ijid.2021.12.092