Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

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) (EORCT/MSG Criteria)	Corresponding Present case series as per new definition	Proposed definition of CAMA
	CAMA	Concurrent or recently treated COVID-19 (≤6 weeks)
POSSIBLE: Immunocompromised	-	Corresponds
PROBABLE IFD: Possible plus Mycological evidence: Cytology, direct microscopy, or culture	Cases 1,4,10	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 approached based respiratory PCR during the second wave of the COVID 19 pandemic in a tertiary care center in Mumbai

A. Poojary*, A.K. Bari

Breach Candy Hospital Trust, Dept of Pathology & Microbiology, Mumbai, India

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 RhV/EV+AH3, RhV/EV + 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 has 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

P. Neopane*, J. Nypaver, R. Shrestha, S.S. Beqaj

Patients Choice Laboratories, Indianapolis, United States

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 (Zeptometrix, NY, USA) were used for validation. RNA from all specimens were extracted using Omega Bio-Tek Mag-Bind Viral RNA Xpress Extraction 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 QuantStudio™ 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, P.1 and P.2 were 4 (2.7%) each and B.1.351 and B.1.427/B.1429 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 concordance with sequencing results.

Conclusion: Our study indicates that TaqMan SARS-CoV-2 mutation panel molecular (genotyping) assays detects and differentiate all published common variants B.1.617.2 (Delta), B.1.1.7 (Alpha), B.1.526 (Iota), B.1.351 (Beta), P.1 (Gamma), B.1.617.1 (Kappa) and B.1.427/ B.1.429 (Epsilon) that can be used for surveillance and epidemic control and prevention.

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