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.

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AAGTAAGTACTGGGTGAGCG-3. Results obtained in the format of multiple band sizes and analyzed using Gel Analyzer Software.

**Results:** Clonal diversity has been determined for 22 Acinetobacter baumannii, 15 different patterns were obtained from ERIC-PCR analysis including 2 patterns as common ERIC pattern and 13 patterns were unique. Most common ERIC pattern was designated as ERIC type-1 and on the basis of relatively low frequency, ERIC patterns were designated as ERIC type 2, 3 and so on. ERIC type-1 was identified in 6 isolates and ERIC type-2 was identified in 3 different isolates. Similarities have been identified in 4 ERIC patterns i.e. between type-1 and 3. Low levels of similarities have been identified in type 4 and 5. Total 50% isolates representing ERIC type-1 pattern were from pleural fluid and 33.3% from cerebrospinal fluid.

**Conclusion:** The presence of different ERIC patterns categorized isolates into groups and implies that the spread of some of the circulating strains from a common source. Isolate with almost similar pattern indicates the emergence of diverging strain in the patient and environment. This information will also be helpful in identification of clones in different areas.

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**Topic 02: Big Data, Genomics and Outbreaks**

**PS02.01 (875)**

**Surveillance for molecular and biological properties of HIV strains**

D. Kolpakov, S. Ivanova, A. Suladze, A. Matuzkova, A. Ryndich, N. Dolgova, T. Tverdokhlebova, L. Ermakova

Rostov Scientific Research Institute of Microbiology and Parasitology, Rostov-on-Don, Russian Federation

**Purpose:** The rate of spread of HIV pandemic requires study of the genetic variability of the infectious agent. This study allows us to optimize epidemiological investigations and improve the quality of surveillance. The regional features of the HIV epidemic were studied taking into account the genetic characteristics of the pathogen.

**Methods & Materials:** We examined 468 sample of biological material (patients with HIV infection blood from 15 subjects of Southern and North Caucasian Federal Districts) from 2014 to 2019. The nucleotide sequences were determined with the ABIPRISM 3500 sequencer, Applied Biosystems (USA). DEONA v1.2.3 (MAG, Russia) software was used to assemble the nucleotide sequences. HIV-1 subtypes were determined using the on-line resources Comet HIV-1 v2.0 and the Stanford University database.

**Results:** We established, that the A1 subtype of HIV-1 still dominates in the Southern and North Caucasian Federal Districts (80.1% of all new strains researched in the laboratory). Subtype B was much less common (6.9%), Since 2009, isolated detection cases of subtype G (3.6%) have been found, but all strains identified at this time had no epidemiological connection with nosocomial outbreaks in southern Russia in the 90s of the 20th century. Also, the recombinant forms of CRF02_AG, CRF03_AB, which previously had a predominant distribution in West Africa, Southeast and Central Asia there, were detected. In 2010, a recombinant subtype, CRF63_02A1 (6.5%), has been registered in the south of Russia. Such regions as Krasnodar Krai, Rostov Oblast and Volgograd Oblast have the greatest variety of HIV-1 variants. It is proven that the majority of carriers of these subtypes of the HIV-1 strain moved to the south of Russia from the Siberia, the Urals and the Kaliningrad region.

**Conclusion:** The study and monitoring of molecular and biological properties of circulating virus strains make it possible to identify the main chains of introduction and spread of the pathogen to different territories, both within the country and in the global migration process.

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**PS02.02 (887)**

**Hybrid de novo Whole-Genome Assembly and Annotation of SARS-CoV-2 Virus from Nosocomial Infection in Pahang, Malaysia**

U.A. Zainulabid 1,*, N. Kamardin 1, R. Mohd Rus 2, S.N. Sofian 3, A.S. Mat Yassim 4, S.H. How 5, H.F. Ahmad 6

1International Islamic University Malaysia (IIUM), Internal Medicine, Kuantan, Malaysia
2International Islamic University Malaysia (IIUM), Pathology and Laboratory Medicine, Kuantan, Malaysia
3International Islamic University Malaysia (IIUM), Community Medicine, Kuantan, Malaysia
4Universiti Malaysia Pahang, Faculty of Industrial Sciences and Technology, Gambang, Pahang, Malaysia

**Purpose:** SARS-CoV-2 virus is highly contagious and spreads easily that it is difficult to detect in elucidating the pattern of infection for contact tracing purposes. The advent of high-throughput sequencing techniques has improved diagnosis in detection the viral lineages especially involving sporadic infection. The combination of short- and long-reads greatly improved the assembly of the SARS-CoV-2 genome and marked as a new approach to correct erroneous frame-shifts from single sequencing effort.

**Methods & Materials:** The samples were recovered from nasopharyngeal and oropharyngeal swab specimens of symptomatic health-care worker. The viral RNA was extracted for RT-qPCR and constructed for genomic library according to the ARTIC ncov-2019 protocol. We performed whole-genome sequencing using hybrid approach combining both short and long-read sequencing approaches, respectively. The raw reads were reconstructed using a combination of bioinformatic tools for trimming, assembly and annotation. Finally, the consensus sequence was mapped with Geneious mapper using default parameters.

**Results:** The hybrid approach resulted in a 29,782bp complete whole-genome with GC content of 38%. The product was deposited to GISAID as hCov-19/Malaysia/IIUM316/2020, and was identified to be originated from B.6 lineage of clade O. Besides, we observed several mutational points such as M153I (spike), P13L (N), T198K (NSP3), L37F (NSP6), and A97V (NSP12), which may representing the major contributor to early pandemic transmission in Malaysia.

**Conclusion:** The present study highlights the utility of whole-genome sequencing as a diagnostic tool of evaluating sporadic pattern of infection that can help to provide information regarding viruses relatedness, mutational rate, geographical spread and host adaptation. High-quality genome data can be used to assist in epidemiological investigation particularly when combined with other types of data.

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