Research Article

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SARS CoV-2 Pandemic conference report: Azerbaijan Medical University educational therapeutic Clinic, March 4th, 2022 Baku-Azerbaijan

Abstract

The Covid 19 infections started in the last days of 2019, and its effects keep continuing. Since March 2022, the number of cases and deaths has also decreased. The first case in Azerbaijan was reported on February 28th, 2020. According to the World Health Organization (WHO) report on May 4th, 2022, comparing the previous week's reports, a decrease in new cases and deaths was reported as total as 17% and 3%, respectively. To date, 792 638 cases and 9709 deaths were reported in total. No new cases have been reported in recent days In Azerbaijan. The mask restriction within the country has been lifted as of May 1st, 2022, but all measures continue to be taken. Only PCR test is accepted for diagnosis in the country. About 50 laboratories in Azerbaijan are actively working on Covid-19 PCR tests, and the results are reported through a single system. A very successful campaign is managed in the fight against coronavirus. This conference was held to provide information exchange among diagnostic laboratories in the country.

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Introduction

Corona viruses, belonging to the *Coronaviridae* family, cause upper respiratory tract infections in some animals, especially mammals such as bats, camels, and birds. Signs and symptoms include respiratory symptoms and include fever, cough, and shortness of breath. The infection can cause pneumonia, severe acute respiratory syndrome, and sometimes death in more severe cases.[1–3] According to the hosting species, the symptoms and tissue damage of coronavirus infection may change. In humans, coronavirus infections may be asymptomatic or accompanied by fever, cough, shortness of breath, and gastrointestinal irritation.[4] There have been three known major Coronavirus outbreaks. These are SARS CoV, MERS CoV, and SARS COV-2. Among them, the most common cause was SARS CoV-2. The electron microscope assessment of SARS CoV-2, which has a 29-30 kB RNA genome showed that this virus is a member of the beta coronavirus group.[5]

Most researchers do not accept that SARS-CoV-2 was created in the laboratory, but argue that the virus originated in nature with some evidence (I). Given the similarity between SARS-CoV-2 and SARS-CoV, bats are likely to have a reservoir for the SARS-CoV-2 progenitor.[6] Currently, the closest virus to SARS-CoV-2 is RaTG13 which isolated from *Rhinolophus affinis* bat and RaTG13 is 96.2% similar to the entire SARS-CoV-2 genome.[6,7] Nevertheless, such a low level of similarity requires the existence of an intermediate host, but intermediate host of SARS-CoV-2 has not yet been identified, and this has led to conflicting discussions about the origin of SARS-CoV-2. According to another hypothesis, the progenitor of SARS-CoV-2 may have jumped to humans long before the pandemic and acquired new features (especially the furin cleavage sites) during undetected transmission in humans.[6–9]

Based on the high similarity of the RBD domains of the spike protein of SARS-CoV-2 and Pangolin CoV, it has been hypothesized that the RBD domain of SARS-CoV-2 added by pangolins in the recombination events and this suggests pangolins as an intermediate host.[6,7] In the other hand, the fact that bats and pangolins live in different ecosystems contradicts this hypothesis.[10] However, the total genetic identity between the SARS-CoV-2 sequence and the pangolin CoV sequence is 90.7%, which contradicts the criterion of being an intermediate host of pangolins.[11] Early facts of COVID-19 were known to be linked to the Huanan Seafood Market in Wuhan, and it is believed that the animal source of the virus was in this market.[6] However, between December 1, 2019 and January 2, 2020 there were 41 SARS-CoV-2 facts in China, of which 14 facts, including the first COVID-19 case on December 1, 2019, were no contact to Huanan seafood market.[12]

According to some researchers, the hypotheses that the virus originated from nature do not fully explain the origin of the new unique genome features of SARS-CoV-2 (IX). According to these researchers, switching non-human-infected bat coronavirus to an infectious form for humans is possible by selectively passage in cells that express human ACE2 receptors.[13,14] In the other hand, all amino acids in the RBD domain of the spike protein have been extensively analyzed, and new models are available to predict affinity for the ACE2 receptor. Even Modern technologies based on synthetic genetic platforms allow to reconstruct viruses according to their genome sequencing without the need for natural isolates.[15]

However, it should be noted that the hypothetical generation of SARS-CoV-2 in cell culture or animal models requires isolation of a progenitor virus with high genetic similarity, and this virus has not yet been detected (I). Generation of a new furine cleavage site requires sequential passage of the virus in cell cultures or in animal models

with receptors similar to the human ACE2 receptor, but no such study has been performed before.[6]

As a result, the detection of similar viral sequences from animal sources will be the most accurate way to detect the origin of the virus and will be of great help in viral functional studies.[6] Although CoVs are still being obtained from bats to determine the origin of SARS-CoV-2, it is not yet possible to say for sure whether the virus originated in the laboratory or in nature.

In the last days of December 2019, an epidemic of pneumonia with an unknown origin was reported, and later it was reported that the causative agent was coronavirus. WHO declared an international emergency on January 31st, 2020, and a pandemic was declared on March 11th, 2020. As of May 11th, 2022, there were 515.7 million overall cases and 6.2 million deaths.[2] During the week of April 25th through May 1st, 2022, over 3.8 million cases and over 15000 deaths were reported, decreases of 17% and 3%, respectively, compared to the previous week.

WHO has been tracking the mutations of Covid-19 since January 2020. With the decision taken on May 1st, the Greek alphabet letters for nomenclature of the variants, except for the names indicated with letters and numbers will be used. The WHO has defined five variants of concern (VOC=Variants of concern) and eight variants to be followed up so far. The WHO warned that mutations, defined as VOCs, can "increase the contagiousness and risk of spreading the virus, change its lethality or symptoms, and reduce the effectiveness of prevention and control measures." Alpha, Beta, Gamma to the five variants designated as "Worrying Variant." Delta and Omicron the eight variants categorized as "Variants to Watch" were Epsilon (2 variants), Zeta, Eta, Theta, Iota, Kappa, and Lambda. Although Delta and Omicron variants have been seen more frequently in recent years, new variants are also likely to occur.[16–17]

Venue and conference Info

This conference, under the name of "Current Approaches and Problems in the Diagnosis of SARS-COV-2 (COVID 19)", was held on March 4th, 2022, between 12:00-19:00 with the participation of 120 people in the Conference Hall of Azerbaijan Medical University Therapeutic Education Clinic. Eight presentations and a panel where current diagnoses and problems were discussed were held at the conference.

Results and discussion

The Omicron variant and current diagnostic methods were widely discussed at the conference. Although it is emphasized that the PCR test must be used in the diagnosis of Covid-19, based on the decisions of the Council of Ministers of Azerbaijan, it was emphasized that antigen test could also be used because it is practical and fast, but a PCR test must confirm it. It is recommended for rapid isolation of patients with positive antigen tests. However, positive cases must be confirmed by a PCR test. In this way, it is aimed to apply unnecessary treatments to possible false positives. Again, the results obtained as antigen-negative in patients with symptoms in favour of Covid 19 must also be confirmed.

In PCR tests, the RdRp gene region was found in the kits produced at the beginning. In addition, the N gene region was added. The success of these two gene regions was quite good, but as the sensitivity started to decrease with the increasing variants, it became necessary to include the ORF1ab gene region. Especially with the omicron variant, the ORF1ab gene region was required. For this reason, it is recommended that N/RdRp/ORF1ab genes be found together in PCR kits. Since the sensitivity of each PCR kit is different from each other, interlaboratory differences may arise from time to time.[18]

Omicron or other variants do not need to be known for treatment, but it should be done for each country to determine its distribution. The distribution of VOC variants should be particularly monitored. A combined nose and throat swab were taken as a sample worldwide. In addition, it has been seen that saliva and mouthwash have recently started to be accepted. It is stated that the sensitivity of PCR studies performed on mouthwash is higher, mainly because it is easy to sample, reduces the risk of infection transmission, and is less complicated for the patient, so concentrated mouthwash can also be used.[19]

Serological tests can be broadly divided into two categories: rapid diagnostic tests and nonrapid tests. Rapid diagnostic tests are lateral flow assay tests that detect antibodies against SARS-CoV-2 antigens within 30 minutes. Non-rapid serological test methods include solid-phase immunoassays (ELISA, CLIA, ECLIA, ELFA), viral neutralizing tests, bead-based flow cytometry-based methods, and immunofluorescence microscopy tests.[9]

Potential antigens for COVID-19 serodiagnosis are different; some use a recombinant N protein, while others use a recombinant spike (S) protein. Different targets such as spike protein, RBD and spike S1 subunit can also be used. In serological diagnosis, IgG, IgA, IgM antibodies can be measured alone or in combinations of different immunoglobulin classes (IgG / IgM).[20]

There are two types of antibodies against SARS-CoV-2: binding and neutralizing antibodies. The level of neutralizing antibodies can be an important indicator of protection. Previously published studies have shown that S-specific antibodies decline more slowly than N-specific antibodies.[21]

Studies have evaluated the dynamics and duration of antibody responses for SARS-CoV-2. These findings are not uniform due to different group's measuring different antibodies and most studies were done at an early stage of the convalescent phase. Because of this, some researches claiming a rapid reduction in antibody titters, while others show antibody persistence.[21]

The majority of patients appeared to have seroconversion at day 14 following symptoms. Approximately 94% of infected individuals had detectable levels of IgM against the RBD of the SARS-CoV-2 S protein and 88% had detectable levels of IgM against the N protein (III). IgM antibodies decline rapidly in about 20 days following symptoms and become undetectable after an average of 60 days following symptoms. Median time to IgG detection ranges from approximately 7 days to 14 days.[22] Different commercial serological tests are available to monitor antibody response following SARS-CoV-2 infection.[21] Enzyme-linked Immunosorbent assay (ELISA), chemiluminescent immunoassay (CLIA), and enzyme-linked fluorescence assays (ELFA) are the main methodologies available for automated analytical systems.[20]

However, current anti-S protein assays are highly variable in clinical practice with different neutralizing activities, possibly due to the lack of reference materials. The Centers for Disease Control and Prevention (CDC) has recently emphasized the need for standardization in SARS-CoV-2 quantitative IgG and neutralization assays. Improvements in the comparability of antibody assay results have been made possible by the recent introduction of WHO's first International Standard (IS) for anti-SARS-CoV-2 immunoglobulin (NIBSC code 20/136) to harmonize assessment of immune response after natural infection or vaccination. Insufficient clinical data were

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available to assign an IU for antibody binding activity and it was recommended to report results with the BAU for comparison of assays detecting the same class of immunoglobulins with the same specificity.[23]

However, when the WHO 20/136 IS was first released, manufacturers did not adopt the new standardization on existing tests and provided a conversion factor for AU/mL to BAU/mL to create a harmonization between different assays.[23]

The countries with the highest number of new cases reported recently are Germany (558, 958 new cases; -24%), followed by Italy (384, 825 new cases; -8%), France (382 208 new cases; -30%), the Republic of Korea (380 455 new cases; - 35%) and the United States of America (372 167 new cases; +27%).[2]

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Conflicts of interest

The author declares no conflicts of interest.

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