CORONAVIRUSES AND DETECTION
FOR SARS-CoV-2 VIRUS CAUSING COVID-19 INFECTION

Antonio E. Lim, Jr.
Department of Medical Laboratory Science
St. Scholastica’s College Tacloban, Palo, Leyte, Philippines
Virology & Bacteriology Laboratories, Department of Pathology, Divine Word Hospital
Tacloban City, Leyte, Philippines
antonio_lim55@yahoo.com

Abstract

COVID-19 infection caused by a newly discovered virus SARS-CoV-2 has already reached a pandemic state involving 190 countries seven months after it was first reported in Wuhan province, China, before the end of 2019. The first aim of this paper is to describe (a) the general characteristics of viruses, (b) the coronaviruses, and (c) SARS-CoV-2 virus. The second aim is to discuss the diagnostic tests used for the detection of SARS-CoV-2 and COVID-19. Since the virus is new, there is a need to disseminate information about viruses in general and SARS-CoV-2 in particular. The laboratory tests for the detection of the virus and the disease are likewise presented. Altogether, the pieces of information provided here can help various stakeholders make sound and prudent decisions to contain the disease and prevent further spread of the virus so that everybody will be able to live once again a normal life.

Keywords: COVID-19, RT-PCR, rapid test kit, SARS-CoV-2

Introduction

Viruses have been changing the course of human history. Although invisible to the naked eye, they have caused several pandemics and killed millions of people worldwide (Weyer & van Bergen, 2014; Krause, 1992). More than 200 virus species are now known to cause human infections (Woolhouse et al., 2012). Many species have emerged and re-emerged since the yellow fever virus; the first human pathogenic virus was described in 1901 (Levine & Inquist, 2007). The main purpose of this paper is to present an overview of viruses and provide some updates on the coronaviruses where SARS-CoV-2 belongs. The laboratory tests used for the detection of the SARS-CoV-2 virus and COVID-19 infection are also discussed.

General Characteristics of Viruses

The viral particle and genetic composition

Viruses are the smallest agents of infectious diseases with sizes ranging only from 20 to 300 nanometers (1 nm = 1 x 10⁻⁹ m). They are so small that some 50 or more bacterial viruses (bacteriophages) can infect at the same time a single bacterium. While bacteria, other unicellular and multicellular organisms contain both nucleic acids - deoxyribonucleic acid (DNA) and ribonucleic acid (RNA) in every cell, viruses are distinct in that each viral particle from a certain group contains only DNA or RNA. In viruses, the genetic material used to transmit hereditary traits from the parent virus to its progeny is DNA or RNA. In contrast, in other types of cells mentioned earlier, the genetic material is always DNA.

The genetic material of viruses is protected by an inner protein layer called a capsid, and an outer layer of protein called the envelope. Some viruses contain a lipid envelope and glycoprotein spikes. These spikes recognize a receptor on the host cell surface, enabling viral attachment and entry to the host, a characteristic of Coronaviruses. Like in Coronaviruses, the lipid envelope is sensitive to organic solvents like alcohol and ether (Brooks et al., 2013).

Viral multiplication and effects on the host

Viruses are non-metabolic, non-reproducing, and crystallizable outside the host cell, which are characteristics of non-living things. But as the viral particle successfully infects a suitable host, the viral genome (DNA or RNA) gains control of the host cell’s metabolic activities to synthesize new viral particles in a very complex manner. Once completed, newly made viral particles exit from the host cell, ready to infect the nearby cells or be transmitted to a new host. The previously infected cells may die, and severe and
extensive conditions were resulting in the death of the entire host. The host cells may survive, but changes in genetic traits or mutations can occur, which leads to cancer development (MacLachan and Dubovi, 2017; Wessner, 2010).

**Evolution and emergence of viruses**

Evolutionists have shown that DNA viruses evolved and diversified millions of years ago (Simmonds, 2011), while most RNA viruses evolved more recently in the last century, trying to adapt to human hosts (Kitchen et al., 2011; Wolfe et al., 2007).

Some viruses are emerging or re-emerging pathogens. These have caused human diseases in the past and have reappeared in recent times (Parvez and Parveen, 2017) as pathogens cause epidemic or pandemic but disappear after some time. Intensive contact tracing and isolation of cases were used as effective strategies to shorten the presence of the pathogens in the human population and contain their spread to others (Cheng et al., 2020).

**Detection of viruses**

Unlike bacteria and other types of organisms where smears of specimens can be stained followed with brightfield microscopy, viruses cannot be easily detected routinely because of their very small size. Instead, they require the use of cell lines for the culture and detection of their pathogenic potential. Likewise, an electron microscope is used to see the morphology of the viral particles. These two approaches are very expensive and tedious. Many laboratories cannot afford it. As will be presented later, antibody-based and nucleic acid-based methods are most often used to detect viruses and the diseases they cause.

**Characteristics of Coronaviruses**

Coronaviruses are present in animals causing diseases of the lungs, intestines, liver, and nerves. Some species can cause epidemics and pandemics in humans (Lau et al., 2011). These viruses contain an RNA genome between 26-32 kilobases (1 kilobase = 1000 bases or nucleic acids such as adenine, guanine, cytosine, and uracil). Their unsegmented genomes have similar arrangement of genes (Forni et al., 2017). They are classified based on the appearance of the viral particles seen under the electron microscope, replication strategy of the RNA genome, organization of the genes within the RNA, and sequence of nucleic acids in every gene inherited by the viral progeny from the parent virus (Cheng et al., 2007). Currently, Coronaviruses are classified as follows: Phylum Riboviria, Order Nidovirales, Family Coronaviridae, Subfamily (main) Orthocoronavirinae, Genera Alpha (α), Beta (β), Gamma (γ), and Delta (δ) coronaviruses. Alpha and Beta Coronaviruses are transmitted by bats to wild and domestic mammalian hosts and eventually to humans. Once they are stable in the human host, human to human transmission can occur (Lu et al., 2020b).

Betacoronaviruses cause pulmonary diseases in humans. Some of the more commonly known species include the Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV), H5N1 influenza A virus, H1N1 2009 virus, and the Middle East Respiratory Syndrome Coronavirus (MERS-CoV). The latest among Coronaviruses to cause human disease is the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), which has reached a pandemic state in 190 countries (Shereen et al., 2020).

Coronaviruses undergo natural recombination in a host wherein two distinct RNA genomes exchange their genetic materials resulting in new strains of genetically different RNA genomes. This process explains the appearance of mutant strains of the virus at a later time. In Coronaviruses, the rate of recombination is faster than in other groups of microorganisms. This phenomenon influences the severity of disease produced and the immune response of the infected human host (van der Most et al., 1992; Makino et al., 1986).

**SARS-CoV-2 and COVID-19**

In December 2019, medical doctors from Wuhan City, Hubei province, China reported a cluster of patients suffering from a certain type of pneumonia (Huang et al., 2020; Lu et al., 2020). Early symptoms included cough, fever, sore throat, and shortness of breath (Chan et al., 2020; Riou et al., 2020). Soon after, the disease was associated with a new coronavirus (Zhu et al., 2020) similar to the one that caused severe acute respiratory syndrome (SARS-CoV) reported some years ago (Ksiazek et al., 2003; Peiris et al., 2003). The virus was initially called 2019-nCoV with the “n” to mean novel or new Coronavirus (Coronaviridae Study group 2020). Others named the virus SARS-CoV-2 to mean the second version of SARS-CoV. Pictures taken with an electron microscope showed spherical particles with petal-like extensions
characteristic of a crown or corona (Wu et al., 2020). When the RNA genome of this virus was sequenced (Wu et al., 2020), it was finally known that the agent belongs to the Coronaviruses. The World Health Organization officially named it SARS-CoV-2, and the disease was called Coronavirus Infectious Disease of 2019 or COVID-19 (WHO, 2020a).

Based on the RNA sequence of the viral genome obtained from bronchoalveolar lavage of a patient in Wuhan, China (Wu et al., 2020), the SARS-CoV-2 contains 29,903 nucleotides (nt). Sequence alignment in the database showed that it belongs to genus Betacoronavirus and is highly related to SARS-CoV Tor2, a coronavirus in humans and SL-CoVZC45, a Coronavirus in bats. If we have to see the viral RNA genes from left (5' end) to the right (3' end), they are arranged consecutively to include replicase ORF1a/b (21,291nt), spike (S) (3,822 nt), ORF3a (828 nt), L (228 nt), M (669 nt) and N (1,260 nt). Knowledge of these gene sequences made it possible for biotechnological companies to develop a variety of nucleic acid-based Reverse Transcriptase Polymerase Chain Reaction (RT-PCR), the gold standard the confirmation of COVID-19 infection in suspected patients (Yang and Wang, 2020).

Development of Diagnostic Tests for SARS-CoV-2 and COVID-19

Sensitivity and specificity

Before discussing the tests used to detect SARS-CoV-2 and COVID-19, it is important to present the topic of sensitivity and specificity because, in medical science and clinical research, these two are crucial in deciding whether to use a test or not. Biotechnological companies are also concerned about the sensitivity and specificity of the test they developed because they would determine whether the product is marketable.

Sensitivity is the ability of a test to correctly identify patients with the disease, abnormality, condition, or causative agent. Specificity is the ability of the test to identify accurately those patients who have no disease, abnormality, condition, or causative agent. For instance, in our discussion, the disease is COVID-19; the abnormalities are the clinical signs and symptoms present; the condition is the appearance of antibodies in the blood. At the same time, the causative agent is the virus SARS-CoV-2. The formula used is:

\[
\text{Sensitivity} = \frac{\text{No. of True Positives}}{\text{No. of True Positives} + \text{No. of False Negatives}} \times 100 \\
\text{Specificity} = \frac{\text{No. of True Negatives}}{\text{No. of True Negatives} + \text{No. of False Positives}} \times 100
\]

True Positives are those patients who are confirmed positive while True Negatives are those who are confirmed negative using a standard gold test. In contrast, False Positives are those patients who become positive despite their being negative using the gold standard test, while False Negatives are those who are harmful to the test despite their being positive in the standard gold test. For practical reasons, a 100% sensitivity test is better than one with a 100% specificity. However, in actual situations, the extent of sensitivity and specificity of an inspection varies depending on its method or product. Thus, for instance, a technique or product that has 90% sensitivity will detect correctly 90% of patients with the disease, abnormality, condition, or causative agent, but 10% of these patients are undetected (Lalken & McCluskey, 2008; Altman, 1991). In situations where facilities or supplies for testing are limited, even the test or product with low sensitivity can be used because it is better than none. However, reservations have to be considered in interpreting the results because of the possibility of false positives and false negatives. Such tests can be regarded as only for screening or medical surveillance (Maxim et al., 2014). Confirmation is still needed by getting a sample from the patient and submitting it to a more complex laboratory where a test with high sensitivity and specificity is performed. The standard gold test is available.

In clinical virology, the gold standard in virus culture. Thus, when a test is developed to detect the virus's presence, it is compared with culture.

Antibody-based detection

Nature of humoral immune response

When an infectious agent enters a human host, it carries with its proteins and other bio-molecules that are foreign to the host’s immune system. These can serve as antigens that stimulate the immune system to mount an immune response. Part of this immune response is humoral, characterized by the production of antibodies by B lymphocytes and later on by memory B lymphocytes that proliferate to become plasma cells. Plasma cells are capable of producing antibodies that can be protective to the host. Likewise, these
antibodies can be detected to determine the host's history of exposure to the infectious agent (Turgeon, 2014). (The cellular immune response will not be discussed.)

The humoral immune response is characterized by the production of five classes of antibodies, namely, IgM, IgG, IgA, IgE, and IgD, that can specifically react against the antigen or microorganism caused their production. IgM and IgG play very important roles in protecting the infected host (Sela-Culang et al., 2013). These antibodies can also be detected to check if the host was exposed to the microorganism in question.

The incubation period of SARS-CoV-2 in infected persons is about 5-7 days. By around 10th day, IgM already appears in the blood, but the amount depends upon the extent of the immune response mounted by the person. Thus, a rapid test for IgM alone may give a weak or strong signal. IgM does not persist for long in the blood. By the 20th day from infection, the level will already start to go down, but another antibody, IgG, will start to appear in the blood and persists for several weeks, even months or years (Gunther et al., 1982). Since IgG can be a neutralizing antibody, viruses in the body that have caused its production will be neutralized, rendering the viral particles non-infectious. If the virus mutated and changed its antigenic property, the IgG may be rendered non-neutralizing. Thus, even if this antibody is detected in the rapid test, there might be viral particles in the host that are still infectious.

**Rapid test for SARS-CoV-2 or COVID-19**

The test is called rapid because results can be obtained in about 15-30 minutes, and the most common approach used is the lateral flow assay. The kit is rectangular, measuring 70 mm long, 22 mm wide, and 5 mm thick. Blood is extracted from the patient by venipuncture and clotted to get the serum. A drop of serum is placed on the well located near the left end of the kit. Then, a drop of the buffer is added to the well. The diluted serum migrates on the nitrocellulose membrane that is embedded in the kit. If there is IgM and/or IgG in the serum, these will react with the recombinant SARS-CoV-2 gold-labeled antibody located on the path where the serum and buffer are moving towards the right end of the kit. As the antigen and antibody continue to move to the right, an embedded rat anti-human IgM and/or rat anti-human IgG react correspondingly to the antigen-IgM and/or antigen-IgG complex, manifesting as the grayish line on the window of the kit. The non-reacted gold-labeled antibody continues to move to the extreme right and reacts with the embedded sheep anti-mouse polyclonal antibody that corresponds to the positive control. Results can be interpreted as follows: (a) if the grayish line appears only for the positive control, it means the patient has no COVID-19 infection because the patient was not exposed to SARS-CoV-2 or the serum was collected very early during the infection; (b) if the lines appear on the positive control and IgM, it means the patient has a current COVID-19 infection and may have one or more of the clinical signs and symptoms; (c) if the lines appear on the positive control and IgG, it means the patient has a history of COVID-19 infection but may or may not manifest the clinical signs and symptoms anymore; and (d) if three lines appear on the IgM, IgG, and positive control, it means the patient has still COVID-19 infection, and may or may not have clinical signs and symptoms. If the control line does not appear, the test is invalid and must be repeated using a new test kit.

The rapid test has some limitations. It does not identify the virus, timing in the collection of blood specimen influences the reactivity of the serum, and cross-reaction may occur. But still, its usefulness cannot be discounted, especially for mass testing. Although several brands are available in the market utilizing a similar principle, there is a need to evaluate them. In one study, the sensitivity was only 69% for IgM and 93.1% for IgG using RT-PCR positivity as a reference due to the absence of a gold standard for serology (Hoffman et al., 2020). The portability of the test kit and the comparatively lower cost makes it more commonly used in health centers and the field.

**Nucleic acid-based detection**

**Basics of PCR**

Polymerase chain reaction (PCR) was developed to multiply or amplify the gene of interest in a target DNA (Mullis, 1990). The nucleic acid sequence of the gene of interest in a DNA molecule must be known to facilitate the design of primers. In principle, a PCR test can be developed once the gene sequence is determined. The reactants in a usual PCR are shown in Table 1.
Table 1. Characteristics and functions of reactants in a regular Polymerase Chain Reaction.

<table>
<thead>
<tr>
<th>REACTANT</th>
<th>CHARACTERISTIC &amp; FUNCTION</th>
</tr>
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<tbody>
<tr>
<td>Target DNA</td>
<td>Contains the gene to be amplified; must be made single-stranded by heat denaturation</td>
</tr>
<tr>
<td>Primers P₁ and P₂</td>
<td>Short single-stranded oligonucleotides of around 20 bases; P₁ hybridizes with the 3’ end of the single-stranded target DNA, P₂ hybridizes with the 5’ end of the single-stranded target DNA, synthesized upon the order in a molecular biology laboratory or biotechnology company.</td>
</tr>
<tr>
<td>Taq DNA polymerase</td>
<td>Enzyme extracted from the bacterium <em>Thermus aquaticus</em> for the synthesis of complementary DNA strand starting from the primer on the target DNA; the enzyme is resistant to heat, available commercially.</td>
</tr>
<tr>
<td>Magnesium chloride</td>
<td>Divalent cation that activates the enzyme can be prepared in the laboratory or ordered commercially.</td>
</tr>
<tr>
<td>Potassium chloride</td>
<td>Monovalent cation for optimal hybridization of the primer to target DNA can be prepared in the laboratory or ordered commercially</td>
</tr>
<tr>
<td>Deoxynucleotide phosphates (dNTPs): dATP, dGTP, dTTP and dCTP</td>
<td>Each one binds complementary to the sequence of the nucleotides in the gene found in the target DNA while extending the primer’s length, available commercially.</td>
</tr>
<tr>
<td>Tris (tris-hydroxymethyl aminomethane) buffer</td>
<td>Maintains the pH for optimal reaction, can be prepared in the laboratory or ordered commercially.</td>
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There are three steps involved in PCR repeatedly performed in about thirty to forty cycles using a programmable thermocycler or PCR machine. The first step is denaturation. High temperature, usually between 92°C to 96°C, is applied to the target DNA (gene) for 1 min, which causes the double-stranded DNA to separate longitudinally into two single strands. When the temperature of the reaction goes down between 50°C to 60°C, the second step, which is annealing, occurs for another 1 min. During this step, the short, single-stranded DNA primers bind correspondingly to the 5’ or 3’ ends on the target DNA. Since the primers were synthesized with sequences complementary to the gene of interest in the target DNA, specific binding takes place.

As the temperature rises between 70°C to 75°C, Taq DNA polymerase catalyzes dNTPs complementary to the nucleotide sequence in the target DNA, thus achieving the third step, which is the extension. Once the three steps are done, the thermocycler will repeat these until the desired cycles are
completed. In the process, a logarithmic increase in the number of copies of the target gene is obtained. Theoretically, a single DNA molecule is enough for the amplification of the target gene into millions of copies. The resulting DNA product (amplicon) is added with DNA loading buffer and resolved using agarose gel electrophoresis. By running side-by-side a DNA molecular weight marker, the estimated size in base pairs of the amplified gene can be determined later when the gel is added with a DNA stain and visualized using an ultraviolet transilluminator. The DNA marker will show several bands in decreasing molecular sizes from the top to the bottom of the agarose gel. In contrast, the amplicon will show one band of a particular molecular size. The DNA bands will show fluorescence over the UV transilluminator. A photograph can be taken to document the result (De Vos et al., 1993). It is also possible to amplify two or more genes present in the target DNA, and this is called multiplex PCR. Every specific gene to be amplified will require a pair of primers. If two genes are amplified from a target DNA, it is expected that two bands of the amplicon will be seen fluorescing on the stained agarose gel. Certainly, the two bands will have different molecular sizes. Multiplex PCR is useful for the rapid detection of two or more genes and for determining if any of the genes of interest has undergone mutation (De Vos et al., 1997).

**Specimen(s) used and timing of collection**

There has been a debate on the best specimen to be collected when performing RT-PCR for the SARS-CoV-2 virus. No matter how sensitive the test is, proper collection, timing, and collection site or source of the specimen are essential components for the successful detection of the virus. The Centers for Disease Control and Prevention, USA recommends a collection of the nasopharyngeal swab (NPS) after clearing the nostrils with a single sneeze on to a paper towel (CDC, 2019). After collection, the swab is placed in a tube containing a liquid virus transport medium, sealed with the screw cap, labeled with the full name, birth date, date, and time of collection and wrapped with absorbent material. The tube is then placed in a zip-lock plastic pouch and, finally, in a thermocol box containing a frozen gel pack or ice. The patient information sheet is placed in a separate zip lock, attached outside of the thermocol with adhesive tape, and brought to the COVID-19 or virology laboratory without delay (WHO, 2020b). Other specimens may include oropharyngeal swab (OPS), nasal mid-turbinate swab, anterior nares swab, bronchoalveolar lavage, sputum, stool, urine and blood in varying percentages of positivity but lower than OPS and dependent on the clinical course of COVID-19 (Mathuria et al., 2020; Wang et al., 2020). Some claim of higher positivity rate by combining NPS and OPS in one viral collection tube. By experience, the OPS has contaminants like food particles and hamper in the micro-pipetting procedure. The patient is advised to gargle with water to remove contaminants before swabbing is done.

Studies on the timing show that 5-7 days from the onset of signs and symptoms would be best for specimen collection. But since many who are infected are asymptomatic, the same number of days from the suspected day of exposure would suffice (Adhikari et al., 2020).

**RT-PCR for SARS-CoV-2**

The detection of nucleic acids in the RNA genome of SARS-CoV-2 is the preferred approach for the diagnosis of COVID-19. This is made possible by performing real-time polymerase chain reaction commonly known as RT-PCR (Chu et al., 2020a; Loeffelholz et al., 2020; Corman et al., 2019).

Unlike the PCR procedure for specimens containing DNA, the SARS-CoV-2 genome is a single-stranded RNA that cannot be easily used as a target for PCR since the reaction happens with a double-stranded DNA as the target molecule. An initial step is done in the process whereby the enzyme reverse transcriptase in the presence of dNTPs, oligo dT primer or random hexamer primer synthesizes a single-stranded DNA (cDNA) using the RNA genome as template resulting in a hybrid RNA: DNA. Once done, the RNA is cleaved and destroyed by another enzyme, RNase, leaving the cDNA single-stranded, which serves as a subsequent template for the synthesis of the complementary DNA strand. In the end, a double-stranded DNA molecule contains now the genetic information found in the RNA. Then, PCR can now proceed, amplifying the target gene(s) of the RNA; thus, the name RT-PCR (Buckingham and Flaws, 2007). Depending on the product kit used for the RT-PCR, one, two or even three of the following genes in the SARS-CoV-2 virus is/are amplified: Hel (helicase), N (Nucleocapsid), M (Transmembrane), E (envelope), S (envelope glycoprotein spike), ORF1a and ORF 1b (Open reading frame 1a/b), and RdRp (RNA-dependent RNA polymerase).

In the current protocol for RT-PCR (i.e., for Coronavirus), the RNA from the specimen is extracted using an RNA Extraction kit sold commercially. The RNA extraction process may be done manually or with an automated machine. A master mix, which is also available commercially containing
the Taq DNA polymerase, RNAses, primers, electrolytes, dNTPs, and buffer, is added to the RNA template. RT-PCR is performed in one of the new editions of thermocyclers. Since there is no more agarose gel electrophoresis after the RT-PCR is done, a novel method based on the 5' nuclease activity of Taq DNA polymerase is used (Holland et al., 1991). Two types of primers bind to the target sequence in the single-stranded DNA in a so-called dual-labeled hybridization (Heid et al., 1996; Livak et al., 1995; Lee et al., 1993c). The first primer binds close to the 3' end of the target DNA and serves to synthesize the complementary strand from 5' -- 3'. The second primer, which is the probe binds to the same DNA some sequences away downstream from the first primer. This probe is labeled with two fluorogenic dyes. The first one serves as a reporter at the beginning of the probe (FAM: 6-carboxyfluorescein), with its emission spectrum being quenched by a second fluorescent dye (TAMRA: 6-carboxy-tetramethyl rhodamine) found at the other end of the probe. When the extension of the first primer occurs, the complementary DNA lengthens displacing the fluorescent-labeled probe. Due to the 5' nuclease activity of Taq DNA polymerase, the probe is degraded, releasing the FAM. Since the quenching effect of TAMRA is no longer effective, FAM being excited by UV light in the thermocycler absorbs that energy and emits it in the form of visible light that is detected by a built-in spectrophotometer at 518 nm. As the PCR cycle continues, more DNA molecules are synthesized exponentially in real-time.

Correspondingly, the amount of light detected increases resulting in a sigmoid curve when plotted. A thermocycler can accommodate a total of 96 wells, with most of the testing for the SARS-CoV-2, while the rest is for the positive and negative controls. For each run of RT-PCR, a cycle threshold (CT) value is set at 40, which is the number of cycles required for the fluorescent signal to go beyond the threshold and be detected. Thus, a sigmoid curve less than 40 is considered positive, meaning, the RT-PCR amplified the SARS-CoV-2 gene(s). A negative result is a straight line below the CT. Although the RT-PCR can have a 100% sensitivity, error in the collection of specimens and transport, as well as inappropriate timing of collection, can give false-negative results. Care in the manipulation of the specimens and reactants is hugely needed to avoid contamination of the reaction tubes, which may give a false-positive result. Since the SARS-CoV-2 virus is highly infectious, the laboratory analysts should wear full personal protective equipment.

Until when will the virus be detected? This will depend on the specimen used for RT-PCR. In a study conducted to detect Severe Acute Respiratory Syndrome (SARS), the range time for conversion from positive to negative was between 2 – 81 days or a mean of 30 days. This has implications on adopting a 14 days quarantine after the first NPS became positive, especially on people without clinical signs and symptoms (Chu et al., 2005a). Studies on this aspect for SARS-CoV-2 are needed involving a large sample size. Limited data from our COVID-19 laboratory show that there are persons who are still RT-PCR positive after 14 days of quarantine. Others remained positive even after 21 days or more from the first positive test. Whether the SARS-CoV-2 virus is still infectious or not is not known because we do not have the facilities for viral culture.

**Radiologic tests for COVID-19**

There are claims that radiologic techniques such as chest x-ray and computerized tomography (CT scan) can be used for the diagnosis of COVID-19 (Long et al., 2020; Xu et al., 2020). However, it was argued that radiologic techniques have limited use compared to RT-PCR, especially among asymptomatic patients and those who are screened early in the disease. It was suggested that chest radiology be used only as a supplemental diagnostic procedure, especially for symptomatic patients (Waller et al., 2020).

**Conclusions**

SARS-CoV-2 is a newly discovered Coronavirus that causes COVID-19. It started in China just before the end of 2019 and has affected 190 countries already in a pandemic state. Understanding of the nature of viruses, Coronaviruses, and SARS-CoV-2 is critical since correct information guides decision-makers and the general public on the actions that can be taken to prevent, control and contain the spread of viruses that infect humans.

While rapid tests using antibodies provide immediate information on the state of persons suspected of COVID-19, several limitations are involved. The nucleic acid-based RT-PCR, commonly called the "swab test" is the preferred test to determine the presence of the SARS-CoV-2 virus specifically. It is a powerful test recommended by health authorities worldwide.
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