rates BAL, which has the highest reported sensitivity (3) but may aerosolize infectious particles. (The sensitivity of sputum obtained from intubated patients by deep tracheal suctioning through a closed ventilator circuit has not been reported, but it may present a practical alternative to BAL.) Sensitivity and FOR can be optimized by employing proper techniques for collecting, handling, and testing of clinical specimens, but clinicians who feel an individual patient has very high pretest probability might reasonably decide not to completely rule out COVID-19, even after negative results using the best diagnostic strategies we modeled.

Our analysis relates to patients admitted with a clinical–radiographic syndrome consistent with pneumonia and is not generalizable to outpatients. Significant variation between patients in day-to-day viral shedding has been observed, and our model does not account for the possibility that COVID-19 patients with initial false-negative results may be more likely to have repeated false-negative results. Despite limitations, our modeling should help clinicians recognize that FOR increases with disease prevalence and make more objective decisions about how to interpret COVID RT-PCR test results when considering the discontinuation of infection control precautions in patients suspected of having COVID-19.

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Viral Transportation in COVID-19 Pandemic: Inactivated Virus Transportation Should Be Implemented for Safe Transportation and Handling at Diagnostics Laboratories

To the Editor.—The potential for a laboratory-acquired SARS-CoV-2 infection, causing COVID-19 disease, from accidental exposure grows as the pandemic progresses, making the biosafety of samples during transportation and laboratory diagnosis vital. Therefore, the Centers for Disease Control and Prevention’s (CDC) recommendation to transport diagnostic specimens in viral transport media (VTM) that preserve viability and infectivity of the SARS-CoV-2 virus is unexpected. Additionally, some health care professionals and transport personnel may not be aware that they are handling specimens with live viruses collected in CDC-recommended media.

Modern molecular nucleic acid (NA) tests, unlike traditional virology tests, do not require viable virus, but rather only intact NA particles of the viral genome. These tests also have improved test performance with better turnaround time, sensitivity, specificity, precision, and reproducibility compared with traditional tests. Indeed, the majority of currently approved SARS-CoV-2/COVID-19 tests in the world are NA-based molecular tests. A variety of transport media have previously been shown to effectively inactivate/kill viral, bacterial, and fungal pathogens while preserving stability of the released DNA and RNA for diagnosis.2–4 These media include ones with a surfactant (eg, guanidine thiocyanate) or molecular-grade ethanol.2–4 One such medium has been extensively analyzed and is approved by the US Food and Drug Administration.2–4 Moving to virus-inactivating VTM at collection allows risk mitigation from transportation and handling of bio–specimens for diagnosis and can potentially reduce the need for special packaging and transportation measures for SARS-CoV-2/COVID-19 test samples.

Although current CDC recommendations classify SARS-CoV-2/COVID-19 test samples in media that keeps virus intact as International Air Transport Association (IATA) Category B (UN3373—for diagnostic testing), some have raised concerns that these specimens should be classified as IATA Category A (UN2814—potential to cause severe harm).3 In addition, CDC recommendations impose additional burdens on aircraft carriers, as alcohol-based hand sanitizers, recommended by CDC for use by transportation staff, are in themselves dangerous goods and specifically not permitted by IATA, requiring special authorization by the civil aviation authority. Furthermore, even the lower IATA-B rating imposes significant packing and cold-chain requirements, which may be difficult to maintain in low-resource settings. Use of traditional VTM also leaves open the possibility of an accidental population outbreak from a vehicular accident, which could release large amounts of viral particles into the atmosphere.

The CDC’s recommendation for using virus-preserving VTM may have been intended to allow for identification and tracking strain evolution for epidemiologic studies. However, as the approved molecular NA tests do not inform on strain identification, this goal cannot be met. Therefore, the current VTM requirements only end up imposing unnecessary risk on transportation and laboratory professionals without any epidemiologic benefits. The CDC should therefore
rconsider its recommendation for transportation of SARS-CoV-2/COVID-19 specimens in virus-preserving VTM to reduce the risk to laboratory and transportation professionals who are battling this pandemic.

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Using an R Program to Monitor Pathology Reports for Omissions in Reporting Ancillary Tests and Errors in Test Names

To the Editor.—A key aspect of standardizing pathology reporting is to include all the necessary elements in the reports, including reporting the results of all the billable ancillary tests. Despite care exerted by pathologists, occasional omissions or wrong test names in reports do occur. We have been using a computer program written in the R programming language (https://www.r-project.org, accessed December 25, 2019) to continually monitor the newly finalized cases to detect reports with such omissions or errors.

The pathology information system was PowerPath 10.0.0.19 (Sunquest Information Systems, Tucson, Arizona), with Microsoft SQL server as the database management system. A computer program (see supplemental digital content at www.archivesofpathology.org in the August 2020 table of contents) written in R (version 3.5.1) was hosted on a virtual Microsoft Windows server and ran once every 5 minutes to retrieve and analyze data on cases finalized during the preceding 5 minutes. The process by which the program obtains data from the database was described previously.1

To detect the possible omission of billable ancillary tests (special stains, immunostains, and others), a list of tests that had been ordered and billable to the patient was retrieved from a table in the database for each case. The final report text for the same case was parsed to see if every test was mentioned in the report text. The program used a conversion text file to link the single way the test was designated in the data table to multiple ways that pathologists would refer to a test in the reports. Taking cyclin D1 as an example, it was designated as “CYCLIN D1” in the data table, but 10 variations such as “cyclin d1,” “cyclin D1,” “D1,” or “Cyclin D-1” were seen in the report texts. Additional acceptable variations were added to the conversion file periodically to reduce the number of false alarms over time. If the immunostain for cyclin D1 was performed but the corresponding report text did not contain any of the above variations, the program considered the interpretation of this test not included in the report. If one or more tests for a given case were not detected in the report text by the program, such an omission would be brought to the attention of the pathologist via an email.

For a 23-month period from August 2017 through June 2019, 547 emails were sent to the pathologists. In 42 cases, the pathologists intended to finalize the reports first and add the interpretations of ancillary tests as addenda subsequently. They were excluded from the analysis. The remaining 505 reports were classified into 3 categories: false alarms (149), test name errors (47), and omissions (309).

The false alarms belonged to 2 subcategories. First, there was no error or omission. The reason an email was sent was because the test name conversion file had not contained the acceptable variation of the test name used in that particular report, so that the R program did not know the test was already mentioned in the report. The second category contained either a slightly vague description of the test or the use of unconventional uncapsulation of the letters or unconventional spacing between the characters for the test names. The examples include reporting Ki-67 as proliferation rate, CK5 as high molecular weight keratins, CDX-2 as CDx-2, and CD1a as CD1-A.

Because the test name errors and omissions constituted the real deficiencies, the specificity of the alerting emails was 70% ([47 + 309]/505).

During the same period, there were 13 890 cases where billable ancillary tests were performed. In 97.4% (13 534 of 13 890) of the cases, the tests were reported without error or omission when initially finalized. The computer program detected 2.6% (356 of 13 890) of reports with either omissions or test name errors that required remedial actions (averaging 15.5 reports/mo). Of these cases, remedial actions were taken in 298 reports (84%; 298 of 356). Computational monitoring made a difference in 21.2% (298 of 13 890) of the cases, increasing the percentage of reports with no error or omission from 97.4% (13 832 of 13 890) to 99.6% (13 832 of 13 890).

The computer program was designed to detect inadvertent omissions in reporting ancillary tests; its ability to identify reports with test name errors was an unexpected benefit. These included nonsensical (Table 1) and potentially misleading test name errors (Table 2), together constituting 13.2% (47 of 356) of the deficiencies. In the latter category, some of the tests performed and the tests in the initial reports had very different diagnostic implications. Examples include CK5 versus CD5, CD30 versus CD38, CD117 versus CD34, BCL-2 versus BCL-6, and p63 versus p16.

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