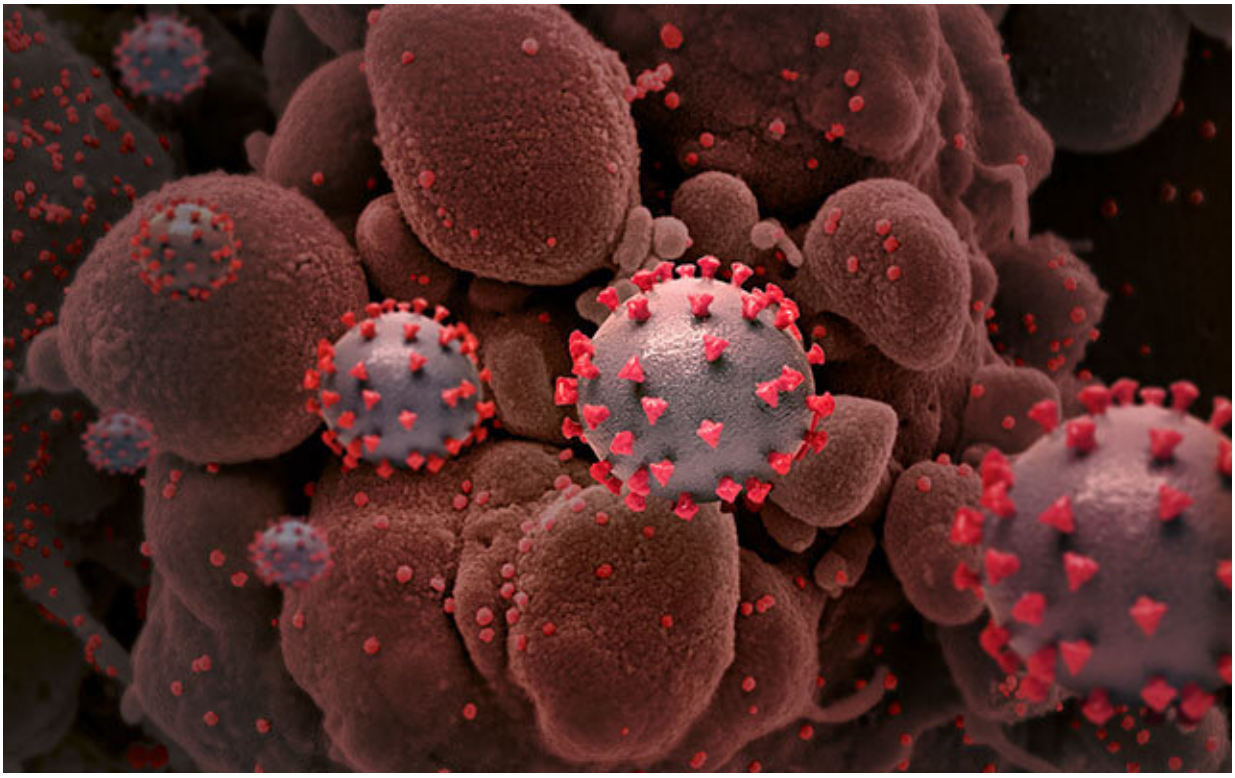
MedicalXpress

New review article outlines potential of SARS-CoV-2 genetic sequencing in patient care

November 12 2021



Creative rendition of SARS-CoV-2 particles (not to scale). Credit: National Institute of Allergy and Infectious Diseases, NIH

The rise of more transmissible variants of SARS-CoV-2 has spurred growing interest in harnessing information about the genetic sequences of these variants to help treat patients. A new joint consensus review

from the American Society for Microbiology (ASM) and the Infectious Diseases Society of America (IDSA) outlines the potential role of SARS-CoV-2 sequencing in clinical care and the challenges in implementing this process in laboratories. The review is published in *Journal of Clinical Microbiology* and *Clinical Infectious Diseases*.

"Although clinical uses of SARS-CoV-2 sequencing are currently limited, rapidly changing technology and the ability to interpret variants in near real-time suggests a growing role for SARS-CoV-2 genotyping in caring for patients as data emerge on vaccine and therapeutic efficacy," said Francesca M. Lee, M.D., an author of the review and a member of IDSA's Diagnostic Committee. Dr. Lee is also an associate professor in the Division of Infectious Diseases and Geographic Medicine in the Departments of Pathology and Internal Medicine at the University of Texas Southwestern Medical Center in Dallas.

With more than 2 million SARS-CoV-2 genomes sequenced so far during the pandemic, this testing has provided critical information about the lineages and evolution of the virus that has supported the public health response. The new review publishing today describes several potential clinical applications of this testing process, including for screening immunocompromised COVID-19 patients being considered for monoclonal antibody therapy and for infection prevention efforts in health care facilities using whole genome sequencing.

The new IDSA-ASM article also outlines related issues, from assay validation and regulatory requirements to clinical reporting for laboratories and emerging challenges in clinical SARS-CoV-2 sequencing. Key considerations for implementing whole genome sequencing, including clinical/epidemiological and laboratory issues, such as accuracy and reproducibility, quality control, workflow and ordering decisions, and billing and reimbursement, are also summarized.

The consensus review, "Clinical Applications of SARS-CoV-2 Genotyping," is available online now. In addition to Dr. Lee, authors of the review include Alexander L. Greninger, M.D., Ph.D., M.S., MPhil; Jennifer Dien Bard, Ph.D.; Robert C. Colgrove, M.D.; Erin H. Graf, Ph.D.; Kimberly E. Hanson, M.D., M.H.S.; Mary K. Hayden, M.D.; Romney M. Humphries, Ph.D.; Christopher F. Lowe, M.D., M.Sc; Melissa B. Miller, Ph.D.; Dylan R. Pillai, M.D., Ph.D.; Daniel D. Rhoads, M.D.; and Joseph D. Yao, M.D.

More information: Alexander L. Greninger et al, Clinical and Infection Prevention Applications of SARS-CoV-2 Genotyping: an IDSA/ASM Consensus Review Document, *Journal of Clinical Microbiology* (2021). DOI: 10.1128/JCM.01659-21