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Commentary

# Implications for the Clinical Microbiology Laboratory

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## DESCRIPTION

Society Clinical microbiologists interact with other staff members and doctors to help in the identification, control, and treatment of infectious diseases. Information from direct smears and stains; cultures, molecular analysis, serological testing, and antibiotic susceptibility testing can be given to the doctor by the microbiology laboratory. The majority of visible qualities, such as morphology, metabolic traits, and antigenic connections, have been the basis for classification historically.

DNA base composition and ratio classification are two aspects of genetic homology. As a measure of relatedness, the ratio of total base content to Cytosine and Guanine content (CG) is utilized. Parallel to this, Machine Learning (ML), a subfield of artificial intelligence, has established itself in numerous clinical medical specialties.

We actually have ML-driven tools that can diagnose, assist clinicians in difficult decision-making situations like the selection of a certain medication, and even provide patients the ability to manage their own healthcare. Clinical microbiology laboratories are in charge of not only identifying pathogens but also supplying details regarding the pathogens' antibiotic susceptibility to aid in choosing the best pharmacological regimen.

First of all, automation improves sample processing capabilities with greater documentation and traceability. Second, there is a quicker diagnosis due to improved cost management and shorter turnaround times. Thirdly, complete automation enables the laboratory to remain open later, greatly enhancing patient care. Adoption of point-of-care testing, extended automation, and new technologies, such as mass spectrometry for colony identification, real-time genomics for isolate characterization, and adaptable and permissive culture methods, have all contributed to this crucial role.

The expanding number of newly discovered pathogens makes it challenging for doctors to recall the precise list of bacteria that cause each infectious disease and to recommend all necessary diagnostic microbiology tests. By employing diagnostic kits that are standardized for the syndrome or disease, sampling can be performed to cut down on the delays caused by resampling or retesting.

However, it's likely that the higher laboratory expenses will be offset by shorter hospital stays as a result of early diagnosis and beginning of the necessary antibiotic medication, as well as by avoiding over-treating viral illnesses. It may be possible to track outbreaks and characterize new infections by conserving clinical isolates, which could be useful for both scientific and public health objectives.

This approach might provide quick and thorough access to the genotypes of rare or challenging-to-grow bacterial strains isolated from clinical specimens, antibiotic resistance indicators, or virulence determinants. Investigations into hospital outbreaks of *A. baumannii*, *S. aureus*, and *Clostridium difficile* infections, as well as the identification of the virulence determinants of a Staphylococcus epidermidis strain that was the etiological agent of native valve endocarditis are examples of whole-genome sequencing in clinical microbiology that have recently been used.

Multi Locus Sequence Typing (MLST), multi spacer sequence typing 2, and genome sequencing are DNA sequence-based techniques that are discriminatory and repeatable but time- and money-consuming. The majority of genotyping techniques are not commonly used, with the exception of the identification of specific clones of certain diseases, even though genotyping all the pathogenic isolates from all cultures would likely have a considerable impact on infection control policies and their execution.

### Transformation of clinical sample

**Direct investigation:** Microorganisms may be recognized *via* microscopy. Specific microbial antigens may be found *via* immunofluorescence, immuno-peroxidase staining, and other immunoassays. Species- or genus-specific DNA or RNA sequences are found using genetic probes.

**Clinical sample culture:** The first method is based on empiricism and employs current media or media that has

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enrichment components added to it. This method has historically been the most effective. A similar strategy might be used to cultivate the fastidious pathogens *Mycobacterium leprae* and *Treponema pallidum*, as well as two more purely intracellular bacteria, *Coxiella burnetii* and *Chlamydia trachomatis*. Even substances that are not strictly intracellular have been isolated using this technique, which has proven to be quite effective.