TABLE 87-2 RAPID IDENTIFICATION METHODS FOR A POSITIVE CULTURE BROTH OR COLONY

METHOD*	ORGANISMS DETECTED	TIME	COST	TECHNICAL EXPERTISE
PNA fluorescent smear	Bacteria, fungi (yeast)	1-2 hr	$$	+
MALDI-TOF	Bacteria, fungi, mycobacteria	Minutes	$	+
Hybridization probes	Bacteria, dimorphic fungi, mycobacteria	1-4 hr	$$	++
Amplification†	Bacteria, viruses, mycobacteria	1-4 hr	$$$	++
16s/18s sequencing	Bacteria, fungi	1-12 hr	$$$	+++
HPLC	Mycobacteria	24 hr	$$$	+++

MALDI-TOF, Matrix-assisted laser desorption ionization–time of flight mass spectrometry; PLC, high-pressure liquid chromatography; PNA, peptide nucleic acid; $, relative cost; +, relative level of required expertise.

*Rapid methods require 2 to 24 hours. Methods presented are U.S. Food and Drug Administration cleared or have had test performance validated in the clinical laboratory. Due to required technical expertise and cost, some of these assays may not be available in the routine laboratory, and providers should inquire about availability

†Includes many different technologies, such as polymerase chain reaction (PCR), transcription-mediated amplification (TMA), and isothermal loop amplification (LAMP).

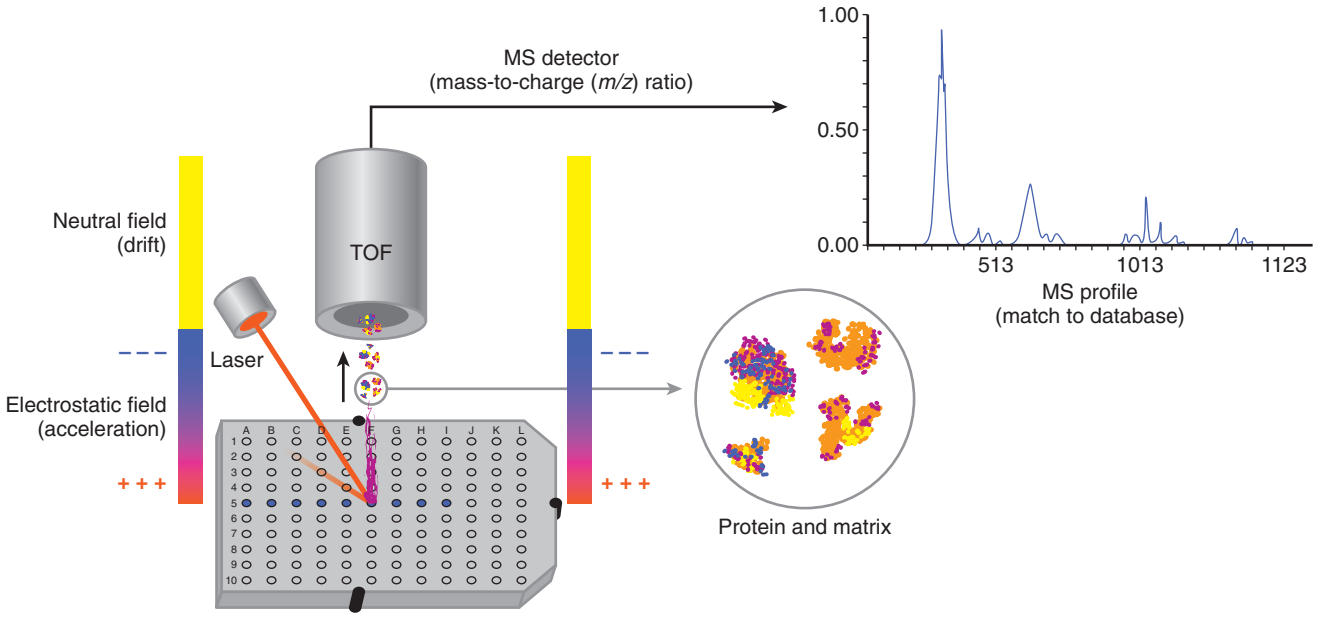

FIGURE 87-4 Matrix-assisted laser desorption–time of flight mass spectrometry (MALDI-TOF MS). Bacterial or fungal growth is selected from a culture plate and applied directly onto a MALDI slide. Samples are overlaid with a matrix and dried. Samples are then bombarded by a laser, which results in sublimation and ionization of the sample and the matrix. The ions are separated based on their mass-to-charge ratio in a tube that measures the time it takes the ions to travel. A spectral representation of these ions is generated and analyzed by software that generates a profile that is subsequently compared with a database of reference MS spectra and matched, generating identification. The process takes only minutes. Although the instrumentation is expensive, the technology is U.S. Food and Drug Administration cleared, and it yields rapid, robust, and reliable identification.

traditional screening tests for the detection of MRSA, vancomycin-resistant enterococci (VRE), carbapenem-resistant organisms, and rifampin-resistant *Mycobacterium tuberculosis*. However, the medical implications of detecting a resistance gene sequence and its expression are not fully understood.

TRENDS IN THE DIAGNOSIS OF INFECTIOUS DISEASES

Evidence-based guidelines exist for specimen work-ups in an effort to standardize reporting and interpretation of microbiologic results. They are especially useful for specimens submitted from sites potentially contaminated with normal commensal flora (e.g., urine, surface wounds, respiratory sources).

There are limitations on which microbes and how many different microbes should have full identification and susceptibility testing according to the specimen type submitted. For instance, a clean catch urine specimen is called *mixed* if three or more organisms are present in equal amounts (even if they are potential pathogens) because the significance of any one organism cannot be determined. The specimen must be recollected. Likewise for other specimen types, listing every organism present is not considered helpful.

Other trends include limiting test ordering and the use of algorithms that may be disease or health care system based; continued efforts between microbiologists, pharmacists, and practitioners to optimize the stewardship of anti-infectives; use of multiplex testing to streamline the diagnosis of complex entities such as acute gastroenteritis; developing data on the relevance of a positive molecular result; and the increasing use of metagenomics and sequencing data to perform direct testing (e.g., blood, orthopedic specimens) and to identify infectious disease outbreaks.

SUGGESTED READINGS

Balcl C, Sungurtekin H, Gürses E, et al: Usefulness of procalcitonin for diagnosis of sepsis in the intensive care unit, Crit Care 7:85–90, 2003.