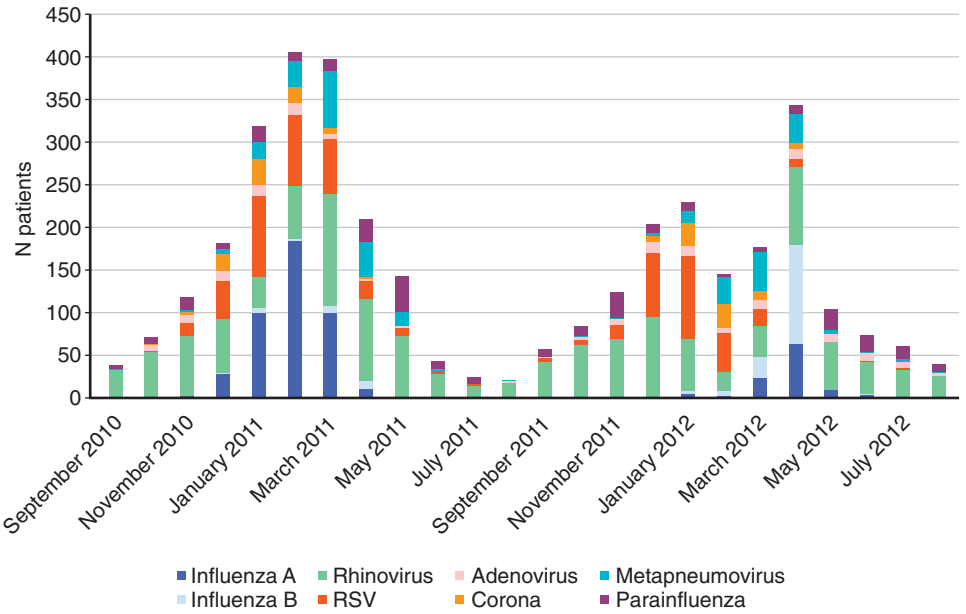

FIGURE 87-2 The graph represents the respiratory viruses detected from hospitalized patients who had influenza-like illness over a period of two respiratory seasons. Viral epidemiology was determined using a multiplex respiratory viral assay for 14 viral pathogens. The viral epidemiology provides helpful information for decreasing antibiotic use and discussing the likely cause of illness with patients.

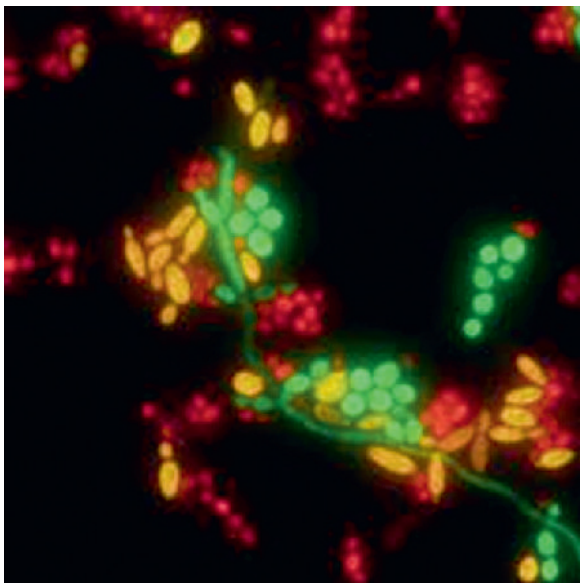

FIGURE 87-3 A protein nucleic acid (PNA) hybridization probe can be used to identify yeast from a positive blood culture. The Yeast Traffic Light PNA FISH assay identified *Candida albicans* and/or *Candida parapsilosis (green)*, *Candida tropicalis (yellow)*, and *Candida glabrata* and/or *Candida krusei (red)*.

amplification and detection occurring simultaneously, enabling the analyte to be detected more quickly. Amplification assays can detect a single analyte (e.g., enterovirus from CSF) or a group of pathogens for a disease entity from a single specimen, such as sexually transmitted infections (e.g., *Chlamydia trachomatis*, *Neisseria gonorrhoeae,* and *Trichomonas vaginalis*).

These assays can detect numerous pathogens from a single specimen in a multiplex amplification testing format (i.e., FDA-cleared multiplex assays for 14 to 24 targets exist for respiratory or acute gastroenteritis pathogens). They also allow quantification of the viral load for purposes of long-term treatment and assessment of clearance (i.e., human immunodeficiency virus, hepatitis B virus, and hepatitis C viral loads).

Culture

Despite advances in rapid direct and molecular diagnostics, culture is still a mainstay for infectious disease diagnosis of most specimen types, but techniques for rapid identification of cultures have been enhanced with updated technology. Blood and AFB specimens are incubated in continuously monitoring incubator cabinets that signal when a specimen is positive based on algorithmic growth curves. A positive specimen can be identified at any time of day, pulled and stained immediately after signaling positive, and tested for definitive identification and susceptibility.

Table 87-2 lists the most common identification methods used from positive broth cultures (e.g., blood) and from colony growth on a culture plate. They include several molecular hybridization methods that have become standard practice for many laboratories (see Fig. 87-3).

Although most laboratories still rely on biochemical and enzymatic phenotypic methods for identification, 16s and 18s sequencing of microbial genomes has demonstrated that the biochemical methods lack specificity. In addition, they require growth for reactions to take place, resulting in further delay of organism identification. The increased use of matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) represents a significant methodologic change. This technique relies on the protein spectral analysis of the organism for identification and takes only minutes rather than days. The technique is described in Figure 87-4.

Susceptibility testing typically requires growth of an organism in the presence of the antibiotics that are appropriate for treatment of the organism. Molecular technology has improved