methicillin and those for resistance to macrolides and streptogramin have been amplified by this method (Misawa et al. 2007; Mu et al. 2016). A LAMP-based assay has been automated to detect the β-lactamase genes that confer resistance to cephalosporins and carbapenems in Gram-negative bacteria in 15 minutes (García-Fernández et al. 2015). Similar to other target amplification and detection methods, the LAMP method provides information about the presence or absence of specific resistance genes rather than whether they are involved in resistance to a particular drug.

21.6 Mass Spectrometric Methods

Mass spectrometry (MS) has both high sensitivity and high specificity. Applications of MS for the detection of antimicrobial resistance in bacteria generally require growing pure cultures first to simplify the MS profile (Lay and Liyanage 2006). MS methods are based on the measurement of a discrete and reproducible set of molecular biomarkers in these cultures that may be correlated with specific attributes (Lay 2001). These biomarkers may be nucleic acids or lipids, but are most often proteins or peptides. Generally, each class of biomarkers requires a different method (Drissner et al. 2016). Bacterial species identity, virulence, and resistance can all be probed at the molecular level and addressed in terms of chemical profiles. Identification of bacteria based on the detection of specific chemical species by MS has been referred to as MS-based chemotaxonomy (David et al. 2008). To the extent that antibiotic-resistant bacterial strains can be distinguished from their sensitive counterparts, chemotaxonomy can be applied to address resistance properties as well as identity. Some of the MS methods that have been developed thus far allow the rapid determination of antibiotic resistance in previously identified bacteria, but not in real unknowns.

The prospect of rapidly and directly detecting identification markers from whole bacterial cells by *pyrolysis MS* with little or no sample treatment was investigated first by Anhalt and Fenselau (1975). Pyrolysis MS methods were adapted for clinical applications (Morgan et al. 2006) and initially were successful under controlled experimental conditions, but the small spectral differences and problems with spectral reproducibility hindered the development of libraries for routine microbial identification. A recent improvement in pyrolysis MS, called plasma jet ionization, may allow better evaluation of small differences between bacterial cultures (Alusta et al. 2015). *Electrospray ionization (ESI) MS* (Yamashita and Fenn 1984) was developed to allow the characterization of nonvolatile but biochemically important compounds, such as proteins. The development of *matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) MS* of proteins (Karas and Hillenkamp 1988) made possible the first practical method for rapid identification of intact bacteria (Lay 2001; Lay and Liyanage 2006; Singhal et al. 2015).