resistance (Zou et al. 2009). Commercially available microarray systems have been shown to detect genes for different β-lactamases and carbapenemases in clinical and reference strains of bacteria with high sensitivity and specificity (Bogaerts et al. 2011; Naas et al. 2011). Microarrays have been used for analysis of resistance genes in some impure samples, such as positive blood cultures (Buchan et al. 2013; Han et al. 2015). However, microarray results do not show whether bacteria are phenotypically resistant, nor do they show MICs (Khan et al. 2011b). Microarrays cannot recognize resistant strains that use novel mechanisms of resistance other than the genes included in the assay (Pulido et al. 2013).

In *whole genome sequencing (WGS)*, the whole bacterial sequence is screened for known antimicrobial resistance genes using publicly available websites for comparison (e.g. www.genomicepidemiology.org). Because of the availability of technology to rapidly sequence the whole bacterial genome economically and bioinformatics tools that facilitate the analysis of data, resistance genes can be detected by WGS in a relatively short time (Dunne et al. 2017). Experiments performed to detect resistance genes from bacteria that have been determined by antibiotic susceptibility testing to be phenotypically resistant have shown correlations in many cases, but not all, between data obtained by both methods. Although the use of WGS for routine clinical testing and detection of resistant strains is not currently practical, this method has epidemiological applications for surveillance and tracking of outbreaks (Osei Sekyere et al. 2015). As with most genetics-based detection techniques, this method shows the presence of resistance genes but not their expression, and it does not identify unknown resistance mechanisms.

Loop-mediated isothermal amplification (LAMP) uses a single temperature for target gene amplification rather than the temperature cycling used for PCR (Mori et al. 2004; Tomita et al. 2008; Mu et al. 2016). A set of four especially designed primers is used to amplify a target gene. The DNA polymerase used for amplification uses the different primers to synthesize DNA, displaces the single-stranded DNA downstream of the synthesis point during amplification, and generates multiple copies of the selected genes. The copies of newly synthesized DNA fragments are connected via stem loops (Fu et al. 2011). The LAMP assay has high specificity and produces a large number of DNA copies in a short time. The amplification can be followed by measuring fluorescence or turbidity (magnesium pyrophosphate is produced in large amounts), and the products may be analyzed by gel electrophoresis (Mori et al. 2004; García-Fernández et al. 2015; Mu et al. 2016). To avoid amplification of nontarget genes and formation of primer dimers, it is important to design specific primers using LAMP primer designing software, such as PrimerExplorer V4 (http://primerexplorer.jp/e). Commercial kits are available that have been shown to be efficient for the detection of resistance genes from phenotypically resistant bacterial strains. For instance, in *S. aureus*, the genes for resistance to