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Parallel Analysis of Antimicrobial Activities in Microbial Community using Single-Strand Conformation Polymorphism

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High-throughput analyses for biologically active molecules are the limiting step for discovery of new drug. Antibiotics are categorized as one of the most market-sharing product in the pharmaceutical industry and searching for new antibiotics is considered as the most critical due to the natural adaptation process developing the mutants resistant to antibiotics such as "super bug." Several studies show that antimicrobial peptides (AmPs) have activity against pathogens that are resistant to traditional antibiotics including penicillin, tetracycline, and vancomycin and other interesting clinical applications: they act as adjuvants for the adaptive immune system and may be useful in treating certain cancers. Recently, a number of works suggested that combinatorial generation of antibiotic candidates can be the most achievable way for the new antibiotics discovery. Antimicrobial activity assay, however, is very labor-intensive procedure and known as the major hurdle for high-throughput AmP discovery system. In this study, we present a new antimicrobial activity assay method capable for parallel analysis in the microbial community using single-strand conformation polymorphism (SSCP) and 16S rRNA gene. Also, its potential in multi-dimensional assay for antimicrobial assay and pharmacokinetic assay for clinical application will be illustrated