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Conventional methods and future trends in antimicrobial susceptibility testing

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Abstract:

Antimicrobial susceptibility testing is an essential task for selecting appropriate antimicrobial agents to treat infectious diseases. Constant evolution has been observed in methods used in the diagnostic micro-biology laboratories. Disc diffusion or broth microdilution are classical and conventional phenotypic methods with long turnaround time and labour-intensive but still widely practiced as gold-standard. Scientists are striving to develop innovative, novel and faster methods of antimicrobial susceptibility testing to be applicable for routine microbiological laboratory practice and research. To meet the requirements, there is an increasing trend towards automation, genotypic and micro/nano technology-based innovations. Automation in detection systems and integration of computers for online data analysis and data sharing are giant leaps towards versatile nature of automated methods currently in use. Genotypic methods detect a specific genetic marker associated with resistant phenotypes using molecular amplification techniques and genome sequencing. Microfluidics and microdroplets are recent addition in the continuous advancement of methods that show great promises with regards to safety and speed and have the prospect to identify and monitor

resistance mechanisms. Although genotypic and microfluidics methods have many exciting features, however, their applications into routine clinical laboratory practice warrant extensive validation. The main impetus behind the evolution of methods in antimicrobial susceptibility testing is to shorten the overall turnaround time in obtaining the results and to enhance the ease of sample processing. This comprehensive narrative review summarises major conventional phenotypic methods and automated systems currently in use, and highlights principles of some of the emerging genotypic and micro/nanotechnology-based methods in antimicrobial susceptibility testing. (c) 2023 The Author(s). Published by Elsevier B.V. on behalf of King Saud University. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

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