

Bacterial metabolomics reveals the evolution of antibiotic resistance.

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Summary

The present world crisis to the bacteria enhance towards antibiotic tolerance and the evolution of resistance acquisition. However, it is utmost important to identify novel metabolite reactivity with known drugs effectively enhancing the resistant strains. Monitoring the changing environmental adaption of microbes and the prevalence of Multi-Drug-Resistant (MDR), novel antibiotics that target distinct cellular functions are needed. The new drugs are frequently entering into the market along with the existing drugs. The antibacterial agents can be discussed in five major classes, i.e. classification based on the type of action, source, and spectrum of activity, chemical structure and function. Multi drug resistance of bacteria (*Pseudomonas aeruginosa* and *Staphylococcus aureus*.) to antibiotics is an urgent problem of the human race, which leads to the lack of therapy for infectious diseases. Development of new / old drugs has almost ceased in the last decades-even when a new antibiotics is launched, very soon the resistance of bacteria appears. Many clinicians recommend alternative approaches of using antimicrobial substances. However, the misuse and mishandling of drugs lead to microbial, resistance as well as result in the difficulty of treating multidrug resistance organisms. Metabolites are the driving force to rapid adaption on unexpected environmental changes such as stresses and nutrient shifts. The Whole cell metabolite profiling approaches would give rise to a more complete mechanistic insight [1] Recent reports say the metabolite plays emergence of multidrug resistance. Metabolism is the central role in mediating the early response to antibiotics [2-3]. The metabolites [4] Involved in the stress response may confer an advantage during infections regulations in response to environmental conditions and also mortality due to bacterial infections is underestimated. Those bacterial responses to environmental factors are related to metabolism. in contrast, the metabolome refers to a complete set of small-molecules with diverse metabolic activity found within a biological sample and can be a very sensitive measure of an organism's phenotype because metabolites are the final products of enormous genome-wide or proteome-wide interactions [5]. Since, more efforts had focused on target-based discovery leading to an era of screening chemicals for inhibitory activity against protein targets.

It is crucial to understand the detailed mechanisms of antibiotic action and resistance with metabolome scale level [6]. The network express the functionality of biological systems, through observation of changes in the concentration of metabolites as

low-molecular weight (<1 kDa) compounds [7]. The end products of the organisms to monitor the gene function and the biochemical status of an organism the interplay between natural selection of resistance mutations and the environment remains unclear. However, the bacteria has been shown to acquire resistance to antibiotics is a very short time period; *Escherichia coli* was shown to gain resistance to ciprofloxacin in a matter of 10 hours [8]. Novel metabolites such as Gepotidacin [9], cathelicidin [10], Rhodethrin [11], Rubrivivaxin [12] etc. were discovered by Ranjith Kumavath and his group in the recent past showing promising antimicrobial activity and also enzymes associated with bacterial metabolism of aromatic compounds [13-14]. However, as discussed previously, resistance to any antibiotic is only a matter of time. Hence, there is an urgent need to tackle the current multidrug resistant pathogens.

The promising field of metabolomics, and the closely related areas of metabolomics and metabolite profiling, involve the quantitative detection of multiple small molecule metabolites in biological systems [15]. The mechanisms behind the opportunity to gain a system of cellular biochemical networks under defined conditions and has been increasingly employed in bacterial physiology and drug discovery to elucidate the mechanism of drug action. The metabolisms of cellular lipids, nucleotides, amino sugars and energy are common pathways involved in the bacterial physiology and regrowth occur in a differential time-dependent manner the metabolome of bacterial cells can potentially lead to innovative strategies for effective antibacterial therapy [16]. The opportunistic pathogens influenced by intracellular and extracellular metabolic processes and modulate antibiotic susceptibility in bacteria a deeper understanding of these environmental processes may prove crucial for the development of new antibacterial therapies [17]. The clearer understanding is needed to acquire comprehensive insights into the pathogenesis and antibiotic resistance. A primary issue is our incomplete knowledge of the metabolome; extensive effort is still required to characterize the metabolome from all organisms. The above report provides better understanding the important of the secondary metabolites leads to have high efficacy on virulence and high chances of sustainable antibiotic resistance.

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