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The Eternal Battle between Microbes and Humans

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Introduction

In 1950s, practitioners believed that the age-old battle of mankind with microbes was finally stopped. Shortly thereafter that concept has been completely changed following the occurrence of major outbreaks caused either by new pathogens or traditional resurging agents with a potential global spread [1]. Depending on their evolutionary dynamics, the ability of microorganisms to cause diseases is rapidly changing and increasing over time [2]. One potential example is the pathogens of animal origin (i.e. zoonotic diseases) that have accounted for more than two thirds among of emerging human infections, and therefore constitute a serious human health hazard [3,4]. Disease emergence involves the appearance of new pathogens as well as re-emergence of already known ones [5]. The transfer of diseases to humans from food animals is a particular problem and the situation is aggravated by the spread of pathogens carrying resistomes (i.e. antimicrobial resistant genes) such as Salmonella, E. coli and Staphylococcus aureus in food-producing animals owing to the overuse of antimicrobials which present a public health risk by the transfer of such resistant pathogens eventually to humans [6,7].

Additionally, recent research has suggested that certain microbes which have known as strictly human or animal pathogens for a long time may be changing their epidemiology, underscoring the urgent need for careful source tracking. An example is Clostridium difficile which has been known since 1970s as a nosocomial pathogen in health care facilities affecting elderly and hospitalized patients worldwide [8] and producing diarrhea, pseudomembranous colitis, toxic megacolon, and death, especially after antibiotic therapy [9]. In recent years, C. difficile has alarmed public health officials by emerging as a community acquired pathogen outside the healthcare settings among young and relatively healthy individuals without known predisposing factors or classified as a low risk e.g. children and pregnant women [10]. The zoonotic origin of C. difficile is possible especially with the increasing reports of its isolation from various animals such as pigs, calves, horses, poultry, and pet animals [11]. On the other hand, the host range of another zoonotic pathogen, hepatitis E virus, (the natural reservoir is swine) has expanded to involve more species such as cattle, and such expanded host selection may constitute an additional zoonotic risk to human [12]. Early detection of zoonotic pathogens and description of their associated resistomes will be a priority in controlling unprecedented outbreaks in the coming decades especially with the continuous evolution of pathogens as a result of environmental changes and medical interventions [13]. Traditionally, microbes and their associated resistomes can be identified by a wide range of conventional and molecular techniques however, given their capability in rapid and simultaneous detection of multiple pathogens in a single test, detection of pathogens at a very low numbers, and identifying novel pathogens as well as detection of the transmission events, the culture-independent approaches (such as 16S ribosomal RNA and metagenomics) hold a future promise as alternatives to the traditional methods in pathogen detection and characterization [14].

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