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Emerging antibiotic resistance: A threat to modern medicine

Global consumption of antibiotics has increased nearly 40% in the last decade. The incredible rapid resistance of antibiotic resistance which is taking place worldwide is not only a serious threat to the practice of modern medicine, but equally important, a threat to global public health. This urgent issue is so alarming that it caught the attention of G-20 Summit in both China (2016) and Germany (2017), let alone the U.N. Assembly in 2016 had called for a special meeting of “superbugs” which focused on the escalating drug resistance with respect to the sexually transmitted disease gonorrhea and carbapenem resistant Enterobacteriaceae. While the causes of antibiotic resistance are complex, certainly human behavior play a significant role in the spread of antibiotic resistant genes. In addition to the human behavior, the drivers of resistance include agriculture sector, animal husbandry, household and industry – these factors contribute significantly to the spread of the resistant genes within the ecosystem. Such resistant mechanisms are continuously emerging globally, which threatens our ability to treat common infections, resulting in increased death, disability and costs. Since the development and clinical use of penicillins, nearly 1000 resistant-related beta-lactamases that inactivate various types of antibiotics have been identified. There is also a global concern about the emergence of antibiotic resistant carried by the healthy individuals, the commensal bacteria. The CDC and WHO surveillance data shows that the resistance in *E. coli* is generally and consistently the highest for antibacterial agents in both human and veterinary medicine. Within communities, resistant bacteria circulate from person to person or from animals and environment to person, or vice versa. With 1 billion people travelling each year, bacteria is becoming more mobile. The bacterial resistance can kill 700,000 worldwide each year and it's been estimated to kill 10 million by 2050. The WHO estimates 78 million people a year get gonorrhea, an STD that can infect the genitals, rectum and throat - there is a widespread resistance to the first-line medicine ciprofloxacin as well as increasing resistance to azithromycin. The emergence of resistance to last-resort treatments known as extended-spectrum cephalosporins (ESCs) is now eminent. The five riskiest superbugs are recognized as (1) the original one: *Staphylococcus Aureus* (MRSA), (2) the hospital lurkers: *Clostridium Difficile* and *Acinetobacter*, (3) the food borne pathogens: *Escherichia Coli* and *Salmonella*, (4) The sexually-transmitted infections: Gonorrhea and Chlamydia, and (5) TB. India is a typical example of encountering the deadly bacterial resistance. The discovery of the *New Delhi metallo-beta-lactamase-1* (NDM-1) which disables almost all antibiotics directed against it, was turning point in the rapid emergence of *bla*_{NDM-1} gene which was first identified in 2008 in people who had traveled in India or sought medical care in South Asia. The gene for NDM-1 travels on a plasmid, an extra-chromosomal loop of DNA that can be traded freely among bacteria. So far, it has been found a variety of bacterial species that carry NDM-1 particularly in the gut bacteria, can cause serious infections in vulnerable hospital patients in India, South Asia, South Africa and the UK. There are two major routes of spread for the bacteria; hospital and the community. In hospital infections, bacteria carrying NDM-1 move from person to person when patients who have received many antibiotics, develop diarrhea and traces of feces contaminate surfaces, equipment and healthcare workers' hands. In community infections, the bacteria carrying the enzyme passes from person to person when traces of feces contaminate municipal water supplies – and with a large percentage of the population lacking any access to sanitation. Public Health Foundation of India believes that 60,000 infants per year are dying of drug-resistant infections due to NDM-1. In addition, tourists can pick up antibiotic-resistance genes in just 2-3 days. Currently, India is facing with two antibiotic resistant genes what carry NDM-1; *E. coli* and *Klebsiella*. The discovery *mrc-1* gene in China which is being transferred between *Klebsiella pneumoniae* and *E. Coli* further compounded the global burden of antibiotic resistance, which has already spread to the neighboring countries. In the animal husbandry and agricultural sectors of China, the demand for the antibiotics to reach almost 12,000 tons per year. The high prevalence of the *mrc-1* gene in *E. Coli* samples both in animals and raw meat, with the number of positive-testing samples are increasing each

year in China. On average, more than 20 percent of bacteria in the animal samples and 15 percent of the raw meat samples carried the *mrc-1* gene. Numerous European countries have reported the existence of *mrc-1* gene in the isolates from human, isolates from animals used for food, isolates from food, and isolated from the environment. In conclusion, pathogens rapidly develop mutations that render current treatments ineffective – resistance to carbapenems, one of the ‘last lines’ of antibiotics, is widespread and has been observed in numerous countries. Therefore, there is an urgent need between research universities and industry aimed at developing novel antimicrobial agents to save the practice of modern medicine.

Biography

Reza Nassiri is a former Associate Dean of Global Health at the Michigan State University (MSU). He also served as MSU director of Institute of International Health. He is currently Professor of Pharmacology and Toxicology, Professor of Family and Community Medicine, and, lecturer in Global Health, Infectious Diseases and Tropical Medicine. He currently works on international public health issues relating to chronic diseases and has expertise in global health. He has made contributions in various fields of medical sciences including clinical investigation and health education. On the basis of his extensive experience and expertise in chronic infectious diseases including HIV/AIDS, TB as well as antimicrobial resistance and human gut microbiome, he developed clinical research programs in Brazil, South Africa, Haiti, Dominican Republic and Mexico.

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