

Antibiotic resistance—the need for global solutions



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The causes of antibiotic resistance are complex and include human behaviour at many levels of society; the consequences affect everybody in the world. Similarities with climate change are evident. Many efforts have been made to describe the many different facets of antibiotic resistance and the interventions needed to meet the challenge. However, coordinated action is largely absent, especially at the political level, both nationally and internationally. Antibiotics paved the way for unprecedented medical and societal developments, and are today indispensable in all health systems. Achievements in modern medicine, such as major surgery, organ transplantation, treatment of preterm babies, and cancer chemotherapy, which we today take for granted, would not be possible without access to effective treatment for bacterial infections. Within just a few years, we might be faced with dire setbacks, medically, socially, and economically, unless real and unprecedented global coordinated actions are immediately taken. Here, we describe the global situation of antibiotic resistance, its major causes and consequences, and identify key areas in which action is urgently needed.

Part 1: Global epidemiology of antibiotic resistance and use

The rise of resistance

The decreasing effectiveness of antibiotics in treating common infections has quickened in recent years, and with the arrival of untreatable strains of carbapenem-resistant Enterobacteriaceae, we are at the dawn of a postantibiotic era.¹ In high-income countries, continued high rates of antibiotic use in hospitals, the community, and agriculture have contributed to selection pressure that has sustained resistant strains,² forcing a shift to more expensive and more broad-spectrum antibiotics. In low-income and middle-income countries (LMICs), antibiotic use is increasing with rising incomes, high rates of hospitalisation, and high prevalence of hospital infections.

Resistance arises as a consequence of mutations in microbes and selection pressure from antibiotic use that provides a competitive advantage for mutated strains. Suboptimum antibiotic doses help stepwise selection of resistance. Resistance genes are borne on chromosomal, and increasingly, on transmissible extrachromosomal elements. The resulting resistant clones—eg, methicillin-resistant *Staphylococcus aureus* (MRSA) USA 300, *Escherichia coli* ST131, and *Klebsiella* ST258) are disseminated rapidly worldwide. This spread is facilitated by interspecies gene transmission, poor sanitation and hygiene in communities and hospitals, and the increasing frequency of global, travel, trade, and disease transmission.

Resistance is spreading worldwide

Even before penicillin was introduced, resistant strains of bacteria had been detected.³ The selection pressure caused by the use of millions of tonnes of antibiotics over the past 75 years since antibiotics were introduced has made almost all disease-causing bacteria resistant to antibiotics commonly used to treat them. The rapid evolution of bacterial resistance is clear in the case of β -lactamases class of antibiotics. Nearly 1000 resistance-related β -lactamases that inactivate these antibiotics have been identified, a tenfold increase since before 1990.⁴

Resistance has spread worldwide. Antibiotic-resistant gonorrhoea emerged in Vietnam in 1967,⁵ then spread to the Philippines, and finally the USA.⁶ NDM enzymes, first reported in 2008, are now found worldwide.⁷ The distribution of resistance genes, such as Enterobacteriaceae-

Panel: Contributions to the Commission

The Commission is a single document, each group of authors take responsibility for the text and views expressed in their individual parts.

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Lancet Infect Dis 2013; 13: 1057–98

Published Online
November 17, 2013
[http://dx.doi.org/10.1016/S1473-3099\(13\)70318-9](http://dx.doi.org/10.1016/S1473-3099(13)70318-9)

This online publication has been corrected.

The corrected version first appeared at thelancet.com/infection on Nov 21, 2013

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