

Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active. Contents lists available at ScienceDirect

Clinical Microbiology and Infection

journal homepage: www.clinicalmicrobiologyandinfection.com

Commentary Are we living in an antibiotic resistance nightmare?

C. Abat, D. Raoult, J.-M. Rolain*

Aix Marseille Univ, IRD, APHM, MEPHI, IHU-Méditerranée Infection, 19-21 boulevard Jean Moulin, 13005 Marseille, France

A R T I C L E I N F O

Article history: Received 6 December 2017 Received in revised form 30 December 2017 Accepted 3 January 2018 Available online 11 January 2018

Editor: L. Leibovici

Keywords: Antibiotic resistance Bacteria MDR Mortality Predictions

There is a growing disconnect between catastrophic information and observed reality. This catastrophism has taken over the popular and scientific press at even the highest levels and is fueled by predictive models the value of which has never been confirmed [1]. Thus, for 30 years we have been lurching from one infectious disease health warning to another—including H7N9, Middle East respiratory syndrome and Ebola—while the actual record of infectious disease evolution shows a significant decrease.

Over recent decades, antibiotic resistance has become the new worldwide fear, and multidrug-resistant (MDR) bacterial strains have been assumed to cause thousands of human deaths every year around the world [2]. A report from 2015 estimated that MDR infections will lead to ten million extra human deaths worldwide by 2050 [2]. However, we observed that the antibiotic resistance of clinical bacterial strains isolated in our hospitals, which belonged to 11 bacterial species of clinical interest, did not significantly change from 2001 to 2015 [3]. Given the aforementioned predictions, estimations and our observations, we recently decided to perform a 7-year analysis of the antibiotic-resistance test results obtained in

* Corresponding author. J.-M. Rolain, URMITE, UMR CNRS 7278, IRD 198, INSERM U1095, Faculté de Médecine, 27 boulevard Jean Moulin, 13385 Marseille CEDEX 5, France.

E-mail address: jean-marc.rolain@univ-amu.fr (J.-M. Rolain).

our hospitals to determine the true impact of extensively drugresistant (XDR) bacterial strains (those susceptible to fewer than two generic antibiotics) on the mortality of patients hospitalized in our facility [2]. Focusing our analysis on ten bacterial species and genera of particular interest, we finally concluded that no human deaths were attributable to XDR bacterial infections over the 7-year period, and that only one human death was due to an XDR bacterial strain in our hospital in 2002 [2]. Comparing our observations to the estimations and predictions mentioned above [2], we clearly identified that the reality in terms of antibiotic resistance is totally different to that which is reported, and that empirical data are urgently needed, as recently supported by Abat et al. [2]. Empirical observations that would truly enable us to quantify the number of deaths due to therapeutic impasses and a lack of antibiotic solutions are currently nonexistent.

According to the 'Alice's living croquet' theory, which states that it is impossible to predict the future amongst living things [1], we strongly believe that it is not possible to predict antibiotic resistance epidemiology. The first example proving this is that of methicillin-resistant Staphylococcus aureus (MRSA). Although methicillin and oxacillin are still used to treat patients infected with S. aureus, we are currently facing an unexplained worldwide decrease in the levels of MRSA strains, which is clearly not the result of screening and isolation strategies developed to control MRSA in hospital settings [3]. Another good example is that of Streptococcus pneumoniae infections. Pneumococcal infections have long been treated using penicillin, which has resulted in the dramatic decrease of worldwide mortality from pneumococcal pneumonia, dropping from 20-40% to only 5% over the last few decades, and was part of the reason for the dramatic decrease in the number of deaths due to lower respiratory infections over the years. However, only a very small proportion of the pneumococcal strains that are currently isolated worldwide are resistant to penicillin [3], and the reason for this phenomenon remains unclear. Moreover, predicting the number of deaths directly attributable to MDR bacterial strains is more complex than expected. Firstly, the definition of MDR remains unclear and changes depending on the author [2]. Secondly, extra MDR deaths are directly related to the time patients spend in hospital and the departments to which they were admitted. Indeed, a patient hospitalized for a long stay in an intensive care unit (ICU) is more likely to be infected by MDR bacterial strains, but will also have more chance of dying in hospital





because of the comorbidities that brought them to the ICU [3]. Hence, if a patient infected by an MDR dies in an ICU, it is clearly impossible to determine whether or not the MDR bacterial strain is responsible for the death.

For all these reasons, we think that it is crucial to urgently collect and analyse clinical antibiotic resistance data to determine the real increases and decreases in antibiotic resistance, and to use this information to make good public health decisions. Inadequate prescriptions should thus be evaluated, as it is expected that prescribing a compound considered inactive in vitro is less likely to be efficient on patients [4]. By doing so, a huge amount of money could be saved and allocated to better purposes, including the development of new antibiotic drugs, improved management of patients infected with antibiotic-resistant bacterial strains and implementation of laboratory hospital data-based antibiotic resistance monitoring systems to detect and monitor antibiotic resistance in hospital settings [2,3]. Finally, antibiotic stewardship programmes must be implemented to adapt prescriptions to the local epidemiology and to the microbiologic results [4,5] in order to avoid the predicted disasters.

Transparency declaration

All authors report no conflicts of interest relevant to this commentary.

References

- [1] Raoult D. Alice's living croquet theory. Int J Antimicrob Agents 2016;47:249.
- [2] Abat C, Rolain JM, Dubourg G, Fournier PE, Chaudet H, Raoult D. Evaluating the clinical burden and mortality attributable to antibiotic resistance: the disparity of empirical data and simple model estimations. Clin Infect Dis 2017;65: S58–63.
- [3] Rolain JM, Abat C, Jimeno MT, Fournier PE, Raoult D. Do we need new antibiotics? Clin Microbiol Infect 2016;22:408–15.
- [4] Gutiérrez-Gutiérrez B, Salamanca E, de Cueto M, Hsueh PR, Viale P, Paño-Pardo JR, et al. Effect of appropriate combination therapy on mortality of patients with bloodstream infections due to carbapenemase-producing *Enterobacteriaceae* (INCREMENT): a retrospective cohort study. Lancet Infect Dis 2017;17:726–34.
- [5] Pulcini C, Mohrs S, Beovic B, Gyssens I, Theuretzbacher U, Cars O, et al. Forgotten antibiotics: a follow-up inventory study in Europe, the USA, Canada and Australia. Int J Antimicrob Agents 2017;49:98–101.