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EDITORIAL

Bacterial resistance in enterobacteria

Cecilia Godoy Carvalhães

Universidade Federal de São Paulo (UNIFESP), São Paulo, Brazil.

The increase on antimicrobial resistance rates worldwide is a fact that has received great emphasis, not only in the scientific community, but also within the governmental, economic and social scope. In 2013, at the World Economic Forum in Davos, bacterial resistance was described as one of the problems that threats the human existence. In that same year, the Center for Disease Control and Prevention (CDC) published a document classifying the risk of multi-resistant bacteria and alerting people to mortality rates and associated hospital costs[1]. Every year 23 thousand deaths are estimated to happen due to drug-resistant bacteria in the United States. In April 2014, the World Health Organization (WHO) warned against the risk of lack of available antimicrobials for the treatment of infections caused by multidrug-resistant bacteria[2]. In both publications, by CDC and by WHO, Gram-negative bacteria, notably enterobacteria, are considered a serious threat to public health.

Surveillance studies are essential to understand, monitor, and guide the empirical treatment of bacterial infections. Few are the surveillance studies that include Brazilian bacterial isolates, among them, we can cite the SENTRY Antimicrobial Surveillance Program, the Surveillance and Control of Pathogens of Epidemiological Importance (SCOPE)-Brazil, and more recently, the Brazilian National Program for Monitoring the Prevalence of Bacterial Resistance conducted by the National Health Surveillance Agency (Anvisa)[3-5]. In these studies, the Gram-negative bacteria were responsible for approximately 50% of the isolates, distributed among species of enterobacteria, *P. aeruginosa* and *Acinetobacter* spp. Among the species of enterobacteria, *K. pneumoniae* stands out, followed by *Enterobacter* spp., *Serratia* spp., *E. coli* and *Proteus* spp. The study conducted by Soares *et al*. (2016) published in this issue also shows high frequency of *Enterobacter* spp. and *E. coli* isolated from pressure ulcers, including isolates resistant to diverse antimicrobials[5].

By means of the Brazilian National Program for Monitoring the Prevalence of Bacterial Resistance, Anvisa delivered epidemiologic reports with data on primary bloodstream infections (BSI) confirmed by laboratory exams obtained in all the 27 Brazilian states[6,7]. More than 900 medical centers sent collected data in 2012 and 2013, where isolates of *Klebsiella* spp. reached 35% resistance to broad-spectrum cephalosporins and 33% resistance to carbapenems. Confirming these data, also in this issue, the study by Flores *et al*. (2016) assessed the genetic relationship and the presence of beta-lactam resistance genes in isolates of *K. pneumoniae* from surveillance cultures at an intensive care unit (ICU) in Rio de Janeiro. The study reflects the national reality concerning genetic diversity and clonal variability[8].

Since the discovery of the first antimicrobial agent of the class, beta-lactams are the therapy of choice for several infections, due to their favorable clinical properties, such as broad-spectrum activity, good tissue penetration, and low toxicity. The serious infections caused by Gram-negative bacteria are frequently treated with broad-spectrum cephalosporins. However, with the appearance and dissemination of extended-spectrum beta-lactamases (ESBL)-producing isolates, there was a marked increase in carbapenem use. Bacterial response occurred with the emergence and dissemination of carbapenemases, enzymes capable of hydrolyzing all the compounds of the group, including carbapenems, definitely restricting the use of this class of antimicrobials in clinical practice[9].

The great variety of carbapenemases produced by pathogens of clinical importance, and their different kinetic characteristics, makes it difficult for a single test to detect them. Several methods were proposed and assessed, but there is not a single available method in clinical practice, so far, that is rapid, practical, low-cost and that presents 100% sensitivity in detecting all classes of carbapenemases. This diagnostic difficulty contributes to the rapid dissemination of these enzymes in the hospital setting, as well as to the delayed adoption of an adequate treatment, what consequently influences the high mortality rates[10].

Unfortunately, we observe the extention of bacterial resistance beyond the limits of beta-lactams, also affecting the use of aminoglycosides, fluoroquinolones, and more recently, polymyxins – these last ones presenting growing resistance rates – . In Brazil,

with the objective of warning against the emergence of plasmid-mediated polymyxin resistance (*mcr-1* gene), Anvisa published a risk communication (nº. 01/2016 – Health Surveillance and Monitoring Management/General Technology Management in Healthcare Services [GVIMS/GGTES]/Anvisa) for microbiology laboratories, central public health laboratories, and infection control teams (CCIH)[11].

Several strategies are considered fundamental to contain antimicrobial resistance. Among them, we can cite, in socioeconomic and veterinary scopes, the protection of food supplies, and the judicious use of antimicrobials in agriculture, animal husbandry and veterinary practice. In the scope of human medicine, both the rational use of antimicrobials and the control of person-to-person dissemination by means of adequate detection, treatment and prevention are fundamental. The understanding of the dimension of antimicrobial resistance in Gram-negative bacteria in each medical center, as well as the mechanisms involved in their dissemination, is the departure point to draw up detection strategies, effective therapy and control, and that is what the two articles published in this issue discuss. Have a great time reading!

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