

You can teach old pathogens new tricks: the zoonotic potential of *Escherichia coli*, *Clostridium difficile*, *Staphylococcus aureus*, and enterococci, or from Noah's Ark to Pandora's Box

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Think of your typical infectious disease agent of major morbidity and mortality today: you will probably think of *Escherichia coli* and other *Enterobacteriaceae*, methicillin-resistant *Staphylococcus aureus* (MRSA), *Enterococcus faecium* and *Enterococcus faecalis*, *Klebsiella* spp., *Pseudomonas aeruginosa*, or *Acinetobacter baumannii*. You will probably think of antimicrobial resistance, of hospital-acquired infections, of intensive-care or surgical units, of the need for implementation of strict institutional measures for avoiding the spread of resistance, of resistance genes and plasmids travelling around the world and necessitating the urgent development of novel antimicrobials, or the ideal public health policies for avoiding resistance becoming entrenched in a healthcare setting. From this perspective, you will rarely think of a community-acquired infection, except perhaps for MRSA. But are we missing the whole picture?

Random, but consistent, evidence has been accumulating in recent decades, constructing a complex framework, and underlining the existence of an overlooked infectious disease reservoir of uncertain significance: animals. The extent and burden of typical zoonotic infections has been the subject of a past theme issue in this journal, but the zoonotic nature of MRSA, *E. coli* and enterococci is increasingly being recognized.

On the other hand, *A. baumannii* has not been implicated in zoonotic transmission: there have been observations of an increased prevalence of *A. baumannii* in the human body louse [1], but whether the pathogen utilizes the humans as reservoirs for the infection of lice or vice versa has not been adequately clarified.

The present issue hosts four reviews that discuss the zoonotic potential and significance of three of the classic pathogens (*E. coli*, MRSA, and enterococci), as well as of an emerging public health infectious threat, that of *Clostridium difficile*. These exhaustive reviews summarize the diverse epidemiological, clinical and experimental knowledge that is gradually accumulating: the zoonotic gene transfer risks of *Enterococcus faecium* and the potential zoonotic nature of *Enterococcus faecalis* are highlighted

in the review by Annette Hammerum [2]; the importance of the zoonotic MRSA reservoir, referring both to companion animals and to the food-chain industry, and the characteristics of the human–animal interaction are discussed by Iris Spiliopoulou and Efthimia Petinaki [3]; the significance for humans of the circumstantial presence of a *C. difficile* type in pigs and calves is reviewed by Marjolein Hensgens and colleagues [4] in a Netherlands–Australia collaborative work; and the extremely complex situation of the presence of extended-spectrum β -lactamase (ESBL)-producing *E. coli* strains is thoroughly presented by Christa Ewers and colleagues [5].

These reviews tell us that we are far from fully understanding the complete extent of the actual zoonotic nature of these pathogens, but also that we are obliged to investigate this nature in detail. A recent research article published in this journal [6] demonstrated persuasively that a percentage of the ESBL-producing *E. coli*-related human disease in The Netherlands can be attributed directly to an ESBL-producing strain of animal origin. Similar observations are being continuously published; in some studies, methodology may be an issue, regarding the need to exclude the possibility that humans may serve as reservoirs for animal colonization. However, there is a need to see the big picture, and to understand that our close relationship with animals, directly in our Noah's Ark, or indirectly through the food chain, may actually open a Pandora's Box with hitherto non-quantified consequences.

Transparency Declaration

No conflict of interest.

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