Reply to Bonten and Mevius

To the Editor—We thank Bonten and Mevius for their interest in our systematic review [1]. In their letter, they disagree with our finding that whole-bacterium transmission (WBT) of expanded-spectrum cephalosporin-resistant (ESCR) *Escherichia coli* between food-producing animals and humans likely contributes to the burden of human extraintestinal infections. We respectfully argue against 2 assumptions that underlie their assertion.

First, the conclusions from our systematic review are derived from the analysis of 6 publications that supported WBT [1]. Three of these studies were conducted in the Netherlands. The correspondence by Bonten and Mevius refers to 1 of these studies [2]. The additional studies by Kluytmans et al [3] and Overdevest et al [4] also support the hypothesis of WBT of ESCR *E. coli* using high-quality sampling and molecular epidemiological methods, including pulsed-field gel electrophoresis (PFGE) and amplified fragment-length polymorphism typing.
Second, we do not believe that the findings by de Been et al [5] refute the findings of Leverstein-van Hall et al [2] insofar as they relate to the hypothesis of WBT. The conclusions that can be drawn from de Been et al’s findings [5] are constrained by methodological and inferential limitations. In particular, only 24 isolates, from a pool of >200 ESCR E. coli isolates in Leverstein-van-Hall et al, were analyzed. Furthermore, to some extent, these isolates were selected for on the basis of similarities among mobile genetic elements, such as those identified through plasmid polymerase chain reaction–based repilon typing, plasmid multiclocus sequence typing, and ESCR genetic environment similarities, rather than high-resolution whole-bacterium genetic similarities, such as PFGE.

We thus argue that there remains evidence supporting the hypothesis that WBT transmission of ESCR E. coli between poultry and humans contributes to extraintestinal infection, especially in the Netherlands. However, we do acknowledge that there are few studies in this area and that further work is required to conclusively answer the question of WBT from poultry to humans.

As mentioned in our review, we strongly agree with and welcome the use of whole-genome sequencing as a means of conducting further analyses in this area of research [1]. Going forward, we also agree that the potential mechanisms of transmission warrant further investigation. In particular, the possibility of direct transfer of ESCR E. coli between animals and their caretakers is of significant interest. During our systematic review, we identified 2 other studies supportive of this phenomenon [6, 7].

We would again like to thank Bonten and Mevius for their interest in the topic and raising some important points for discussion.

**Note**

Potential conflicts of interest. All authors: No potential conflicts of interest. All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest.

Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

Benjamin Lazarus,1 David L. Paterson,1 Joanne L. Mollinger,2 and Benjamin A. Rogers1,3
1The University of Queensland Centre for Clinical Research, Royal Brisbane and Women’s Hospital, Herston, 2Biosecurity Sciences Laboratory, Biosecurity Queensland, Department of Agriculture, Fisheries and Forestry, Coopers Plains, and 3Monash Infectious Diseases, Monash Health, Clayton, Victoria, Australia

References


Correspondence: Benjamin A. Rogers, MBBS, FRACP, UQ Centre for Clinical Research, The University of Queensland, Level 8, building 71/918, Royal Brisbane Hospital, Herston, Brisbane 4003, Australia (ben.rogers@monash.edu).

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