

Less Evidence for an Important Role of Food-Producing Animals as Source of Antibiotic Resistance in Humans

TO THE EDITOR—In their systematic review on the role of food-producing animals as a source for human extraintestinal *Escherichia coli* infections resistant to expanded-spectrum cephalosporins, Lazarus et al conclude that there is evidence for whole-bacterium transmission [1]. This evidence is almost exclusively coming from studies from the Netherlands. Indeed, the study of Leverstein-van Hall et al provides the most detailed molecular analysis supporting this transmission route [2]. Based on the similarity of extended-spectrum β -lactamase (ESBL) genes, plasmid multilocus sequence typing

(MLST) results, and bacterial MLST results for *E. coli* isolates derived from poultry, poultry meat, and human infections, it was concluded that 11% of *E. coli* bacteremia episodes in the Netherlands might have originated from poultry. Yet, a subsequent analysis with whole-genome sequencing by de Been et al [3] of those sets of *E. coli* from poultry meat and human infections with identical sequence types in the Leverstein-van Hall study demonstrated that these isolates were not phylogenetically related. Therefore, in contrast to what was stated by Lazarus et al, we conclude that there is currently no evidence of whole-bacterium transmission of cephalosporin-resistant *E. coli* from poultry meat to humans. Yet, the whole-genome sequencing data did demonstrate the possibility of direct transfer of *E. coli* between animals and animal caretakers and the predominance of identical ESBL-carrying IncI-plasmids in cephalosporin-resistant *E. coli* derived from human and animal sources. The latter finding suggests the possibility of mobile genetic element-mediated transmission originating from food-producing animals. Yet, given the complexity of the epidemiology of mobile genetic elements and the lack of inclusion of all possible sources in existing studies, the role of this transmission between food-producing animals and humans remains unknown.

Note

Potential conflict of interest. Both authors: No potential conflicts of interest.

Both 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.

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