



International 58th Meat Industry Conference “Meat Safety and Quality: Where it goes?”

Spread of antibiotic resistant bacteria from food of animal origin to humans and vice versa

Andrej Kirbis^{a,*}, Manja Krizman^a

^a*Institute of Food Hygiene and Bromatology, Veterinary Faculty, University of Ljubljana, Gerbiceva 60, Ljubljana 1000, Slovenia*

Abstract

Food-related bacteria are a very diverse population. They can be found in environment where food and feed is produced and handled. Nowadays, the foodborne zoonoses of greatest concern are campylobacteriosis, salmonellosis and Verotoxigenic *Escherichia coli*, and antibiotic resistance in these pathogens is an emerging health issue. Studies have been published about antibiotic resistant bacteria in different ecological niches. In our study, we found 40% of samples from food of animal origin contained bacteria resistant to one or more antibiotics. Without the interdisciplinary concept “one world one medicine one health”, bacteria will continue to produce offspring that are multiresistant to antibiotics.

© 2015 The Authors. Published by Elsevier Ltd. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Peer-review under responsibility of scientific committee of The 58th International Meat Industry Conference (MeatCon2015)

Keywords: resistant bacteria; food of animal origin; food safety

1. Main text

Food-related bacteria constitute a heterogeneous group, with their original habitats extending to all ecological niches where food for human consumption is produced and handled. Such environments may be soil, plants, husbandry, animals, fresh water, marine ecosystems, fish, wild birds and other wild animals, or areas with human impact related to the people handling the food, e.g. food production industry or restaurants, or the effluent from

* Corresponding author. Tel.: +386-1-4779-101; fax: +386-1-4779-174.
E-mail address: andrej.kirbis@vf.uni-lj.si

human sewage¹. In the past decades, campylobacteriosis, salmonellosis and Verotoxigenic *Escherichia coli* (VTEC) infection have largely replaced tuberculosis, brucellosis and parasitic diseases as the most common sources of foodborne zoonoses in humans in the EU². However, an emerging health issue that poses a serious threat to public health worldwide is antibiotic resistance in these bacteria. Nowadays, effort has been directed into the study of antibiotic resistance of the nonpathogenic bacteria, most often *E. coli*. *E. coli* is a normal inhabitant of the warm blooded animal intestine, including human intestine, and can easily contaminate food products during animal evisceration at slaughter or during food manipulation³. In addition, *E. coli* can transfer their resistant genes to other pathogenic bacteria in the intestine. For this reason, industrialized animal food and food of animal origin is a potential source of antimicrobial resistant and virulent bacteria. Consequently the question remains: are resistant bacteria brought to food from the animal gut or from human carriers handling the food?

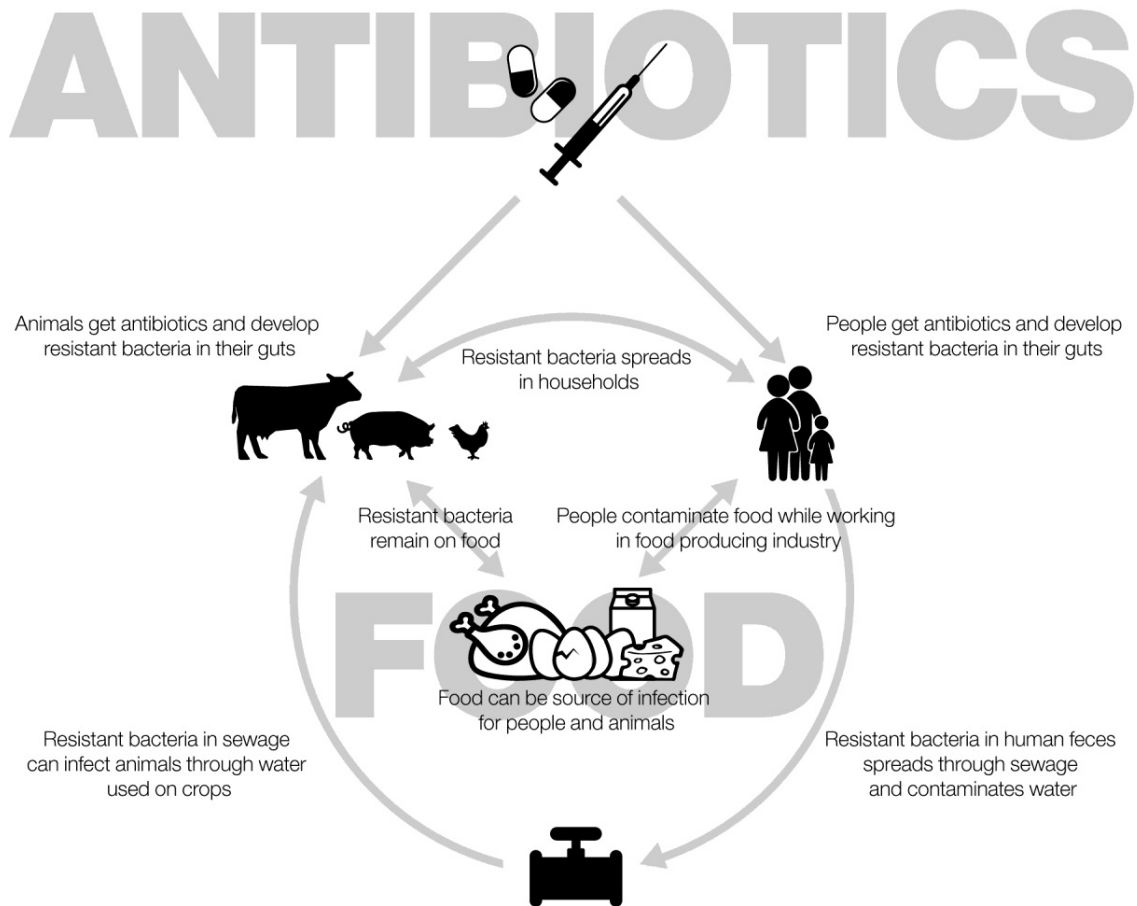


Fig. 1. The occurrence of resistance in bacteria and transfer via humans, animals and foodstuffs.

In past years, many studies have been published on antibiotic resistant bacteria. They were found in food of animal origin^{4,5,6,7}, livestock^{5,6,8}, companion animals^{7,9} and in humans^{7,9}. However, different studies yielded different results. Jouini et al.⁴ discovered that 26% of *E. coli* isolates from food contained extended spectrum β -lactamases (ESBL) enzymes; while on the other hand, none of the faecal samples from animals had ESBL producing *E. coli*. In this study, the contamination during the transformation or commercialization processes of food cannot be excluded. In contrast, Geser et al.⁶ found ESBL producing *Enterobacteriaceae* in 15.3% porcine, 13.7% bovine, 8.6% sheep and 63.4% chicken faecal samples and none in minced meat and milk samples. In contrast, Leverstein van Hall et al.⁵ found the same ESBL genes in retail chicken meat and in poultry isolates. Overdeest et al.¹⁰ found ESBL *E. coli* in

chicken, beef, pork and mixed or ground meat and also in rectal swabs and blood cultures from humans. Furthermore, results from Ambrožič-Avguštin et al.⁷ showed also ESBL producing *E. coli* in diseased companion animals and poultry meat; however, preliminary study showed that these isolates were genetically diverse (unpublished data). In our study, we screened 249 *E. coli* isolates from food of animal origin and we found 6% were *E. coli* ESBL producing isolates. In addition, 40% of isolates were resistant to one or more antibiotics. Twenty-six were multi drug resistant (MDR), which means they were resistant to at least 3 groups of antibiotics. Isolates were assigned to 4 phylogenetic groups by Cleromont et al.¹¹ and 80% of strains belong to group A and B1 which means they were commensal strains (unpublished data). These studies show resistant bacteria in a variety of ecological niches. Resistance in food-related bacteria reflects the resistance situation in bacteria from all the various environments from which food for human consumption originates¹. So the big question is: who is infecting who? In past years, much has been done about usage of antibiotics, with the main goal to minimize the application of antibiotics in human and veterinary medicine. World Health Organization (WHO) and others are raising awareness on wiser usage of antibiotics. As a result, most doctors prescribe antibiotics only for bacterial infections and not for viral ones. The patients are now more aware about antibiotics, their effects and usage. The Federation of Veterinarians of Europe (FVE) is emphasizing that the prudent use of antibiotics is an integral part of good veterinary practice. A big part of responsibility in transferring resistant bacteria also lies in the hands of companies and individuals that deal with food. Educating workers who work in production, processing, manufacturing, preparation and trade with foodstuffs is of the utmost importance. We must be aware that human health is multidisciplinary and involves a large number of professions responsible for human, animal and environmental health. New sense in health care for the 21st century the “one world one medicine one health” concept is being adopted.

Much has been done in studying resistant bacteria in different ecological areas. Data show that multiresistant bacteria have spread from hospitals, nursing homes and livestock animals to healthy humans, food and companion animals. This type of multiresistant isolates can cause serious infections and their multiresistance is a challenge for treatment. WHO, FVE and others are making an effort in raising awareness about how important prudent use of antibiotics actually is. However, since we can find resistant bacteria in industrially-produced food, the question of new rules suitability, majority of all support processes and the level of hygiene awareness of individuals involved in the food supply chain is raised. What is left to do? We must be aware that we are all connected in the same world and so we are all more or less in trouble. Smart usage of antibiotics nowadays will leave better options for next generations in fighting bacterial infections while bacteria have ancient gene intelligence, which they advantageously use.

References

1. Sørum H, L'Abée-Lund TM. Antibiotic resistance in food-related bacteria—a result of interfering with the global web of bacterial genetics. *Int J Food Microbiol* 2002;**78**:43-56.
2. Scientific report of EFSA and ECDC. The European Union Summary report on trends and Sources of Zoonoses, Zoonotic Agents and Food-borne Outbreaks in 2011. *EFSA Journal* 2013, **11**(4):3129.
3. Ben Slama K, Jouini A, Ben Sallem R, Somalo S, Saenz Y, Estepa V. Prevalence of broad-spectrum cephalosporin-resistant *Escherichia coli* isolates in food samples in Tunisia, and characterization of integrons and antimicrobial resistance mechanisms implicated. *Int J Food Microbiol* 2010;**137**:281-86.
4. Ahlem J, Vinué L, Ben Slama K, Sáenz Y, Klibi N, Hammami S, Boudabous A, Torres C. Characterization of CTX-M and SHV extended-spectrum β -lactamases and associated resistance genes in *Escherichia coli* strains of food samples in Tunisia. *J Antimicrob Chemother* 2007;**60**:1137-41.
5. Levertin-van Hall MA, Dierikx CM, Cohen SJ, Voets GM, Munckhof van den MP, Essen-Zandbergen van A, Plateel T, Fluit AC, Sande-Bruinsma van de N, Scharinga J, Bonten MJM, Mevius DJ. Dutch patients, retail chicken meat and poultry share the same ESBL genes, plasmids and strains. *Clin Microbiol Infect* 2011;**17**:873-80.
6. Geser N, Stephan R, Hächler H. Occurrence and characteristics of extended- spectrum β -lactamase (ESBL) producing Enterobacteriaceae in food producing animals, minced meat and raw milk. *BMC Vet Res*. 2012;**8**. doi: 10.1186/1746-6148-8-21.
7. Ambrožič-Avguštin J, Zdovc I, Strumbej I. *Escherichia coli* producing extended spectrum beta-lactamases: genotypes of isolates from diseased animals and food of animal origin compared with genotypes of human clinical isolates. *Medicinski razgledi* 2012;**51**:219-25.
8. Ramos S, Igrejas G, Silva N, Jones-Dias D, Capelo-Martinez JL, Caniça M, Poeta P. First report of CTX-M producing *Escherichia coli*, including the new ST2526, isolated from beef and sheep in Portugal. *Food Cont* 2013;**31**:208-10.

9. Ewers C, Bethe A, Semmler T, Guenther S, Wieler LH. Extended-spectrum β -lactamase-producing and AmpC-producing *Escherichia coli* from livestock and companion animals, and their putative impact on public health: a global perspective. *Clin Microbiol Infect* 2012;**18**:646-55.
10. Overdeest I, Willemsen I, Rijensburger M, Eustace A, Xu L, Hawkey P, Heck M, Savelkoul P, Vandenbroucke-Grauls C, Van der Zwaluw, Huijsdens X, Kluytmans J. Extended-Spectrum β -Lactamase Genes of *Escherichia coli* in Chicken Meat and Humans, the Netherlands. *Emerg. Infect Dis* 2011;**17**:1216-22.
11. Clermont O, Bonacorsi S, Bingen E. Rapid and simple determination of the *Escherichia coli* phylogenetic group. *App Environ Microbiol* 2000;**66**:4555-58.