

Zoonotic pathogens and antimicrobial resistance in 'animal-friendly' pig production systems in Switzerland

O 43

U. Ledergerber¹, G. Regula¹, J. Danuser¹, B. Bissig¹, R. Stephan², K.D.C. Stärk¹

¹ Swiss Federal Veterinary Office, Schwarzenburgstr. 161, CH-3003 Bern, Switzerland, Phone: +41-31-323 9550, Fax: +41-31-323 9543, E-mail: Ursula.Ledergerber@bvvet.admin.ch. ² Institute for Food Safety and Hygiene, University of Zürich, Switzerland

Keywords: Salmonella, Campylobacter, Yersinia, welfare, food safety

Summary: In a cross-sectional study, the impact of 'animal-friendly' housing systems on the prevalence of *Salmonella* species, *Campylobacter* species, and *Yersinia enterocolitica* in finishing pigs and pork was investigated. Furthermore, antimicrobial resistance patterns of isolated campylobacter strains were analysed. In faecal samples of two out of 88 fattening pig farms salmonellae were isolated. All 865 samples of pork were found to be negative. Campylobacter was isolated on 98.9 % of the farms but only from 0.2 % of the pork samples. Yersinia were found in samples of 63.3 % of the farms and in 15.4 % of pork samples. For all three bacteria, there was no statistically significant difference in the prevalence between conventional and 'animal-friendly' housing systems. In 'animal-friendly' farms, antimicrobial resistance of campylobacter isolates to fluoroquinolones and streptomycin was significantly less frequent than in conventional farms. Furthermore, fewer isolates had resistance to three or more antimicrobials in 'animal-friendly' farms.

Introduction: 'Animal-friendly' production systems for finishing pigs are promoted by the Swiss Federal Office for Agriculture. Such systems primarily differ from conventional production in the use of straw bedding and outdoor access. In 2000, 28 % of Swiss fattening pigs were kept in farms with 'animal-friendly' production systems (Anonym, 2002). It was shown that these systems improve pig welfare (Cagienard et al., 2002), but they might represent an increased risk for the occurrence of zoonotic pathogens in pigs and pork. Furthermore, there are few data on the effect of these housing systems on antimicrobial resistance of zoonotic pathogens, specifically *Campylobacter* species.

The objective of the study was to investigate the prevalence of *Salmonella* species, *Campylobacter* species and *Yersinia enterocolitica* in finishing pigs and pork in Switzerland. In addition, the effect of 'animal-friendly' housing systems on the load of these pathogens in pigs and pork and on antimicrobial resistance in isolated campylobacter strains was evaluated.

Materials and methods: A cross-sectional study was performed on 88 finishing pig farms with either conventional (41 farms) or 'animal-friendly' (47 farms) housing systems. On each farm, 20 faecal samples were taken. Five samples were combined to make one pooled sample (Steger et al., 2000) and cultured for *Campylobacter* species, *Salmonella* species, and *Yersinia enterocolitica*. At retail, 865 samples of fresh pork, produced either conventionally (48 % of the samples) or 'animal-friendly', were collected in all regions of Switzerland. Culture was performed for all three micro-organisms using standard techniques. For antimicrobial resistance testing, one strain from each campylobacter-positive sample was selected and the disc diffusion method was used (NCCLS, 1997, 1998). Tested antimicrobials included fluoroquinolones, erythromycin, tetracycline, kanamycin, polymyxin, chloramphenicol, gentamicin and streptomycin.

Results: *Salmonella* species were found in samples from two farms (2.3 %). However, all 865 samples of pork at retail were found to be negative. In samples from all but one finishing farms, *Campylobacter* species were isolated. On retail level, only 0.2 % of the pork samples were found positive for *Campylobacter* species. *Yersinia enterocolitica* were isolated in samples from 63 % of the farms, but only in 15 % of pork samples. In pork, 119 out of 133 (89.5 %) yersinia isolates belonged to biotype 1A. Six isolates (4.5 %), belonging to several bio- and serotypes, were considered to be potential human pathogens, and eight

isolates (6 %) could not be further classified. For all three cultured bacteria, there was no statistically significant difference in the prevalence between conventional and 'animal-friendly' housing systems. Statistically significant differences between the two housing systems were observed for resistance to fluoroquinolones and streptomycin. Resistance to fluoroquinolones was present in 31 % of the isolates from traditional farms, but only in 20 % of the isolates from 'animal-friendly' farms. Resistance to streptomycin was common in both housing systems, but more frequent in traditional farms (85 % of the isolates) than in 'animal-friendly' farms (74 % of the isolates). When resistance to multiple antimicrobials was compared, fewer isolates from 'animal-friendly' farms were resistant to three or more of the tested antimicrobials.

Discussion: Our results document that for prevalence of salmonella, campylobacter and yersinia, microbiological quality of Swiss pork was on an equally high level in both conventional and 'animal-friendly' production systems. Thus, the endeavour of Swiss government and Swiss pork industry to combine 'animal-friendly' meat production with food safety was shown to have been successful. As regards antimicrobial resistance, the quality of 'animal-friendly' produced meat was even superior to conventional production. It was shown in another study on the same farms, that pigs in 'animal-friendly' farms had less injuries of the joints and injuries from tail biting than pigs in traditional farms (Cagienard et al., 2002). Fewer injuries might have resulted in a reduced use of antimicrobials. Therefore, reduced antimicrobial resistance in 'animal-friendly' production systems was probably not directly caused by differences in the housing systems, but it could be interpreted as an effect of improved pig health and therefore fewer treatments. This hypothesis will have to be investigated further.

Acknowledgements: We thank the cantonal laboratories for their collaboration. The study was funded by the Swiss Federal Veterinary Office (BVET), the Swiss Federal Office for Agriculture (BLW), the Swiss Federal Office of Public Health (BAG), Suisseporcs, Coop and Migros.

References:

Anonym (2002): Swiss Federal Office for Agriculture. Agrarpolitisches Informationssystem (AGIS). BLW, Bern, Switzerland.

Cagienard, A., Regula, G. and Danuser, J. (2002): The impact of different housing systems on health and welfare of fattening pigs. Proceedings of the Conference of the Society of Veterinary Epidemiology and Preventative Medicine. Cambridge, UK, April 3 to 5, 2002. pp 120-126.

National Committee for Clinical Laboratory Standards (1997): Performance Standards for Antimicrobial Disc Susceptibility Tests. 6th edn. Approved standard M2-A6. Wayne, NCCLS, pp 1-17.

National Committee for Clinical Laboratory Standards (1998): Performance Standards for Antimicrobial Susceptibility Testing. 8th international supplement M100-S8. Wayne, NCCLS, pp 14-15.

Stege, H., Jensen, T.K., Møller, K., Baekbo, P. Joesal, S.E. (2000): Prevalence of intestinal pathogens in Danish finishing pig herds. *Prev. Vet. Med.* **46**, 279-292.

O 44 *Campylobacter* species distribution in outdoor pigs

A. N. Jensen¹ and E. M. Nielsen²

¹ Danish Veterinary Institute, Bülowvej 27, DK-1790 Copenhagen V, Denmark, tel. ++45 35300328, fax ++ 45 35300120, anj@vetinst.dk. ² Statens Serum Institut, DK-2300 Copenhagen S.

Keywords: hippuricase gene, DIG nucleotide probe, colony hybridization,

Summary: A colony blot hybridization method with a digoxigenin-(DIG)labelled nucleotide probe was developed to enable *Campylobacter jejuni* species-specific identification of colonies present