



Space–time clustering of ampicillin resistant *Escherichia coli* isolated from Danish pigs at slaughter between 1997 and 2005

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ABSTRACT

In Denmark, antimicrobial resistance in bacteria in animals, animal products and humans, is routinely monitored. This study aimed at determining whether the observed variations in the prevalence of ampicillin resistant *Escherichia coli* isolated from healthy pigs at slaughter were random or clustered in space and time. Data on *E. coli* isolates between 1997 and 2005 were obtained from the Danish Integrated Antimicrobial Resistance Monitoring and Research Programme (DANMAP) whereas data on the quantity of ampicillin consumed was obtained from the Danish Register of Veterinary Medicines (VetStat). Space–time interaction was assessed using the space–time *K*-function and detection and location of significant space–time clusters was done using the space–time scan statistic. The space–time *K*-function analysis provided evidence of space–time interactions in ampicillin resistant *E. coli* (AREC) isolates in both Funen and Jutland, and Zealand. Significant space–time clusters of resistant *E. coli* isolates were found in the north eastern part of Jutland and Funen and in the southern part of Zealand. Seasonality was found to have a highly significant effect on space–time clustering in Funen and Jutland. The clusters of ampicillin resistant *E. coli* appeared at the same time as the national consumption of ampicillin in pigs increased, however antimicrobial consumption at the herd level did not appear to have any effects on space–time clustering in this study. The results could serve as a platform to highlight areas where more investigations on the occurrence and spread of ampicillin resistant *E. coli* in pig herds should be initiated.

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1. Introduction

Since the introduction of antimicrobial agents into the livestock and poultry industries, animal health has improved significantly and the production capacities of farms have also increased (Angulo et al., 2004). However, the efficacy of antimicrobial agents is being threatened by the emergence of resistance in pathogenic, commensal as well as zoonotic bacteria through mutations or transfer of genetic material (Lathers, 2001). When resistant bacteria

persist, the health status of infected animals may deteriorate and treatment may become more complicated.

The increasing awareness of the public health consequences of antimicrobial resistance in bacteria in animals and humans has led to the establishment of antimicrobial resistance monitoring and surveillance systems. Examples of well-established programmes include the Danish Integrated Antimicrobial Resistance Monitoring and Research Programme (DANMAP) in Denmark, the National Antimicrobial Resistance Monitoring System (NARMS) in the US, The Norwegian Monitoring programme for antimicrobial resistance in feed, food and animals (NORM-VET) in Norway, Swedish Veterinary Antimicrobial Resistance Monitoring (SVARM) in Sweden,

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and Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) in Canada. Overall, surveillance systems aim at detecting occurrence and analysing changes in prevalence of antimicrobial resistance. They provide information that is useful to guide veterinary practice and control activities such as curbing the spread and re-emergence of resistance and assessing the impact of intervention programmes (Bax et al., 2001; McEwen et al., 2006). All the aforementioned programmes use non-pathogenic *E. coli* as an indicator of antimicrobial resistance in the intestinal flora of healthy livestock as well as bacteria in food. This is because they readily respond to the selective pressure of antimicrobial agents and most known mechanisms of resistance can be found in them (Jordan, 2003).

Analyses from surveillance data have indicated significant regional, seasonal and temporal variations in the prevalence of antimicrobial resistant bacteria in animals (Anonymous, 2003, 2005a,b; Guerin et al., 2005; Abatih et al., 2008). However, spatio-temporal patterns have rarely been investigated in detail due to the lack of geographical coordinates of the isolates collected from animals. This has limited the knowledge about the occurrence, distribution and trends in antimicrobial resistant bacteria in animals. The identification of space–time clusters will provide information on the distribution and persistence of antimicrobial resistance in bacteria in animals. In addition, it will enable the identification of areas of excess localised risk for the occurrence of resistance in bacteria and help generating hypothesis about factors that have impact on the prevalence of resistance in *E. coli*.

The main objective of this study was to determine whether the observed variations in the prevalence of

ampicillin resistant *E. coli* isolated from healthy pigs at slaughter in Denmark were simply random or clustered in space and time. The study also aimed at identifying factors influencing space–time patterns such as seasonality and the quantity of ampicillin consumed in each herd until the time of sampling. As an example, this study focussed on ampicillin resistance among *E. coli* isolated from Danish pigs at slaughter between 1997 and 2005.

2. Materials and methods

2.1. Study region and data collection

The study area consisted of the three main regions of Denmark; Funen, Jutland, and Zealand (Fig. 1). Bornholm, a distant small island, was not included in the study due to the very small sample sizes resulting from the stratification by year and by season.

2.1.1. Data on ampicillin resistant *E. coli* (AREC)

Data on *E. coli* isolates were obtained from the DANMAP database. It contains a stratified random sample of *E. coli* and other bacteria isolates from pigs, cattle and poultry obtained each year at slaughter since 1995. Isolates were collected monthly by meat inspection staff and all the four seasons in a year are represented in order to account for any seasonal effects. The number of isolates from each slaughter house was stratified according to the number of pigs slaughtered the previous year (Bager, 2000). Each isolate was tested against a battery of antimicrobial agents. Isolates were classified as resistant against or susceptible to various antimicrobial agents based on the minimum inhibitory concentration (MIC) values, however for this study only the

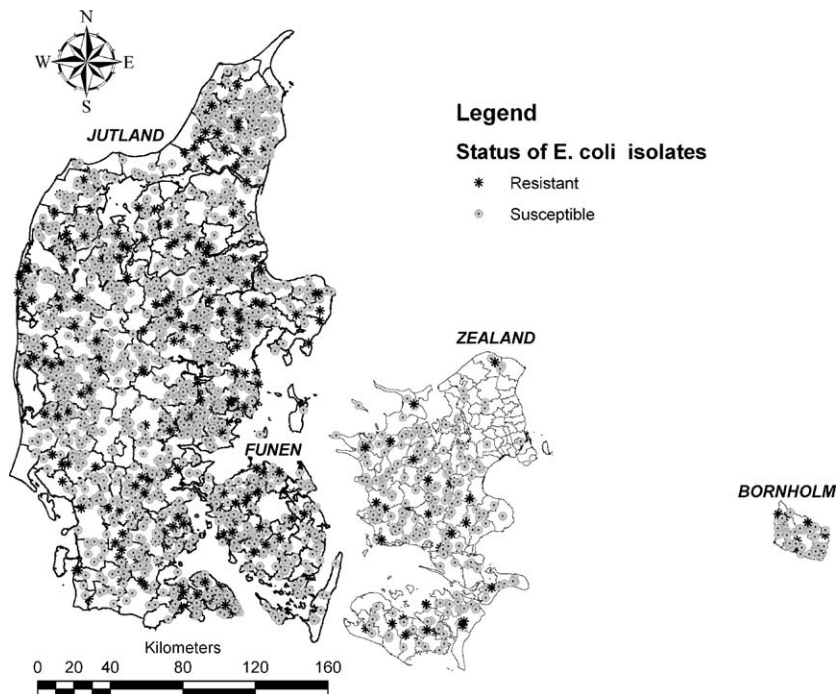


Fig. 1. Study region: Funen, Jutland, Zealand and Bornholm showing the location of herds from which *E. coli* isolates were obtained between 1997 and 2005.

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