P1517
Paper Poster Session
Antibacterial resistance: the animal and food production part of one health

Dynamics of faecal carriage of ESBL-producing Escherichia coli in dairy cattle

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Background: Although the presence of extended spectrum beta-lactamases producing *E. coli* (ESBL) in dairy cattle has been reported, little is known about its dynamics within herds. The purpose of this study was to determine the dynamics of faecal carriage of ESBLs in dairy cattle in different age groups and presence of ESBLs in people working or living on the farm. Such knowledge is important to identify control options.

Material/methods: Initially (T0), 20 Dutch farms with a relatively high antimicrobial usage were selected and approximately 100 samples were taken from individual animals on each farm distributed over 4 age groups, being 0-8 wks, 8 wks-1 yr, 1-2 yrs and >2 yrs. Next, sampling on 10 farms with the highest ESBL prevalence was continued every 2 months for 1 year (T2 to T12). At each sampling, all new animals in the youngest age group, all animals that had moved to another group and all animals tested positive previously were sampled. Human samples were collected at T4 and T12. Individual samples were cultured in Luria-Bertani broth supplemented with 1 mg/L cefotaxime and subsequently streaked onto MacConkey agar supplemented with 1 mg/L cefotaxime (MCC). In parallel, a dilution range was made of all samples, which were subsequently inoculated on MCC for quantitative analysis. ESBL suspected isolates were screened by PCR and sequencing analysis.

Results: At the start 8 farms were positive for ESBL, of which 3 showed a relatively high prevalence (10% to 28%), and 5 farms had a low prevalence (below 2.6%). These 8 positive farms were completed with 2 negative farms for studying the dynamics of ESBL carriage. The 3 farms with a relatively high prevalence in phase 1 continued to be the farms with the highest number of positive animals. At each sampling moment, a single ESBL variant was predominant, suggesting epidemic spread. At consecutive sampling moments these predominant variants changed suggesting low persistence and exposure of the animals to other ESBL types from potentially different sources. ESBL variants clustered mostly in young calves and adult animals, and within the same stable. The use of 1st/2nd generation cephalosporins or extended spectrum penicillins was identified as a risk factor with an OR of 5, however this could only explain 16% of all newly acquired ESBL positive samples. At T4 1

out of 38 human faecal samples was positive, and at T12 1 out of 25 human samples was positive. The ESBLs found in human samples could not be linked to the ESBLs found in cattle.

Conclusions: The presence of ESBLs on Dutch dairy farms is suggested to be caused mainly by (re)introduction from not yet identified sources.