Detection of Campylobacter carriage rate in different poultry production systems in Ethiopia

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Introduction

- Poultry in Ethiopia are predominantly indigenous chicken ecotypes maintained under rural, traditional scavenging or semi-scavenging systems.
- A greater demand for poultry and poultry products has seen growth in urban and peri-urban flocks under semi-intensive management systems. Such flocks often include exotic or exotic/indigenous hybrid birds.
- Studies have identified poultry, cattle, sheep, goats, pigs, cat and dogs as asymptomatic carriers of C.jejuni and C.coli in Ethiopia, with a higher prevalence of bacteria in chickens and poultry meat compared with other farm animal and meat products.
- Shared environment/co-habitation by humans and chickens presents a putative risk factor for zoonotic Campylobacter infection.
- This study investigates whether the intensification of poultry production systems in Ethiopia may impact on the epidemiology and ecology of Campylobacter, and considers the potential implications of this changing dynamic for human health in the country.

Methodology

- A cross-sectional study was conducted between October 2012 to April 2013 in 3 woredas (administrative regions), Horro, Jarso and Debre Zeit (within the Ada’a woreda) in the Oromia region of Ethiopia.
- Sampling was conducted in 4 villages in each of the two rural districts. Twenty households were randomly selected from a list of farmers in each village, provided by local development agents. Households were excluded from the study if they did not own at least two chickens. A further 60 backyard flocks and 20 intensive/semi-intensive farms within the Debre Zeit town area were purposively selected for sampling during the same time period as the cross-sectional study.
- Disposable fabric overshoes (boot socks) were worn and used to collect samples of faeces on the ground (Fig.2) by walking through the household/farm environment.
- Bacterial DNA extraction from collected faecal material was extracted using a commercial DNA extraction kit.
- DNA isolates were analysed using a PCR assay specific for the genus Campylobacter on the basis of 16s rRNA sequences and further confirmed to species level (C.jejuni and C.coli) by multiplex PCR based on differences in the IpxA gene.
- Multivariate regression modelling was used to compare the prevalence of Campylobacter carriage rate of chickens reared in different geographical areas and to compare proportion of positive samples among chickens from the same area reared under different production systems.

Results

- Boot sock samples (n=239) were collected from Horro (n=79), Jarso (n=80) and Debre Zeit (n=80).
- Prevalence of Campylobacter detected across the three sampled regions was 18.41% (44/239). Of these, 16 isolates could be speciated using multiplex PCR, all of which were identified as C.jejuni.
- Results from the multivariate model (Table.1) suggested that peri-urban flocks were more likely to be Campylobacter positive (Odds Ratio 15.6, 95% C.I. 6.0 – 40.2). Flocks which consisted only of Rhode Island Red or RIR hybrids were also at greater risk (Odds Ratio 5.0, 95% C.I. 1.0-24.9) whilst the Cobb 500 birds, which were only kept in intensive or semi-intensive farms tended to be at slightly, although not significantly, greater risk.

Conclusions

- The greatest risk factor identified in our study for Campylobacter infection in chicken flocks was location in the peri-urban area, where many farms are starting to intensify their production systems.
- Whilst more intensively farmed flocks appear at increased risk, it is of particular concern that traditionally managed flocks of indigenous birds in nearby areas also have high rates of carriage. These may potentially contaminate the home environment of smallholder farmers, increasing risks to human health.
- More research needs to be done to evaluate the effect of changing production systems on the epidemiology of Campylobacter and identify ways to minimise risks to health.

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Table 1. Results from multivariate model.