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

CHICKEN HEALTH 4 DEVELOPMENT

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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 and 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.

Campylobacter

- *Campylobacter* bacteria are a major cause of foodborne diarrhoeal illness in humans and represent the main cause of infant enteric disease in developing countries.
- *Campylobacter* is an important zoonosis, with infection occurring mainly through ingestion of contaminated food and water, or direct contact with contaminated food animal species or their carcasses.
- The bacteria are typically spiral, S-shaped or curved rods (Fig.1). Within the 17 species and 6 subspecies of the genus, *C.jejuni* and *C.coli* are the most frequently reported in human disease.

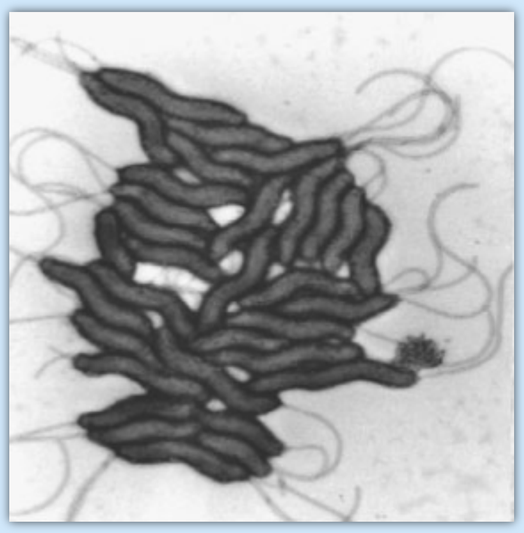


Fig. 1. Electron micrograph of *Campylobacter jejuni*. Source: Roslin Institute

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 lpxA 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.

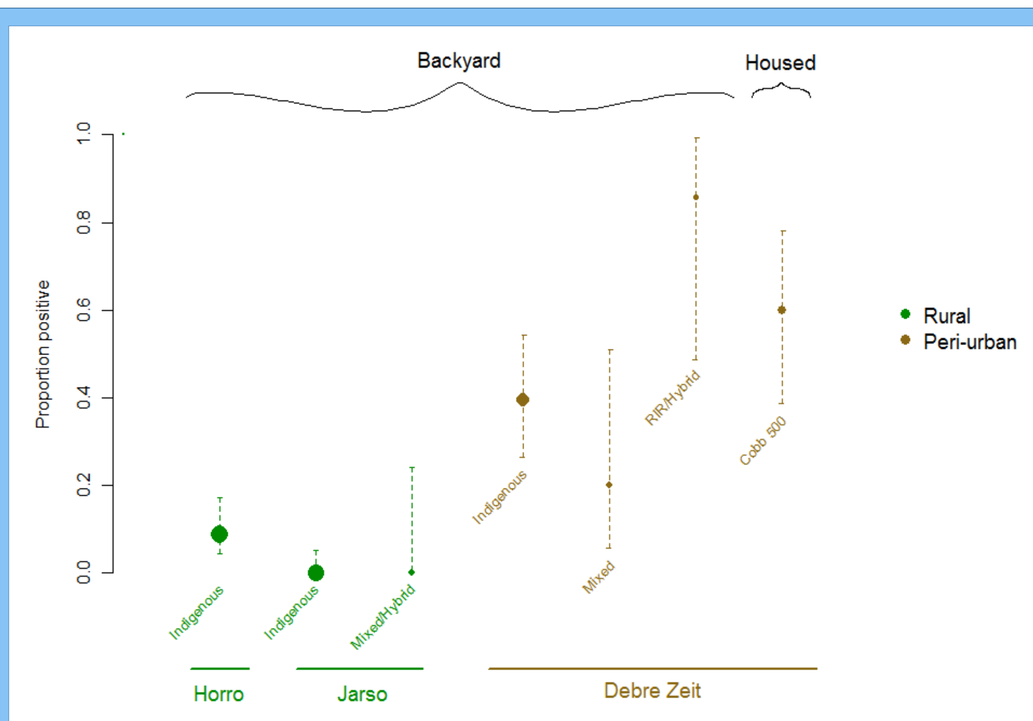
Fig. 2. Boot sock sampling of chicken faeces. Source: Farming UK

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.

Variable	Levels	coefficient	se	OR	95% C.I.	P
Intercept		-3.10	0.39	0.04	0.02 - 0.10	0.000
Area	Rural	reference				
	Peri-urban	**2.74**	**0.48**	**15.56**	**6.03 - 40.15**	**0.000**
Flock type	Backyard - Indigenous	reference				
	Backyard - Mixed	-1.11	0.83	0.33	0.06 - 1.67	0.180
	Backyard – RIR/Hybrid	**1.61**	**0.82**	**5.02**	**1.02 - 24.87**	**0.048**
	Housed - Cobb 500	0.76	0.55	2.15	0.73 - 6.29	0.163

Table. 1. Results from multivariate model.



Proportion of flocks tested positive for Campylobacter, showing location, bird and farm type. Points are scaled relative to the number of flocks of each type tested.

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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