



# Changing risk of environmental campylobacter exposure with emerging poultry production systems in Ethiopia



J. M. Bettridge<sup>1</sup>, M. C. Brena<sup>1</sup>, Y. Mekonnen<sup>2</sup>, N. J. Williams<sup>1</sup>, P. Wigley<sup>1</sup>, T. Sisay Tessema<sup>3</sup>, R. M. Christley<sup>1,4</sup>

<sup>1</sup> Institute of Infection & Global Health, University of Liverpool, UK; <sup>2</sup> College of Veterinary Medicine & Agriculture, Addis Ababa University, Debre Zeit, Ethiopia, <sup>3</sup> Institute of Biotechnology, Addis Ababa University, Addis Ababa, Ethiopia, <sup>4</sup> HPRU Health Protection Research Unit in Emerging & Zoonotic Infections, Liverpool, UK



## The problem

- *Campylobacter*, particular *C. jejuni* and *C. coli*, are major causes of diarrhoea in people, and particularly of infant enteric disease, in developing countries.
- Chickens are likely to be key sources of human infection.
- Indigenous chicken ecotypes maintained under backyard scavenging systems account for >95% of chicken production in Ethiopia.
- There has been rapid growth of intensive & semi-intensive producers, with larger, housed flocks in peri-urban areas. *Campylobacter* is highly prevalent in intensified systems, with birds having high infection levels.

## Our approach

- Between October 2012 and April 2013 we sampled 239 farms in three regions of Ethiopia (Fig 1).
- Environmental samples were collected by wearing disposable fabric overshoes (boot socks) (Fig 2).
- *Campylobacter* was detected using 16S rRNA PCR and confirmed to species level (*C. jejuni* / *C. coli*) by multiplex PCR based on differences in the *lpxA* gene.
- The effect of region, production system and breed was assessed using multilevel multivariable logistic regression.



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

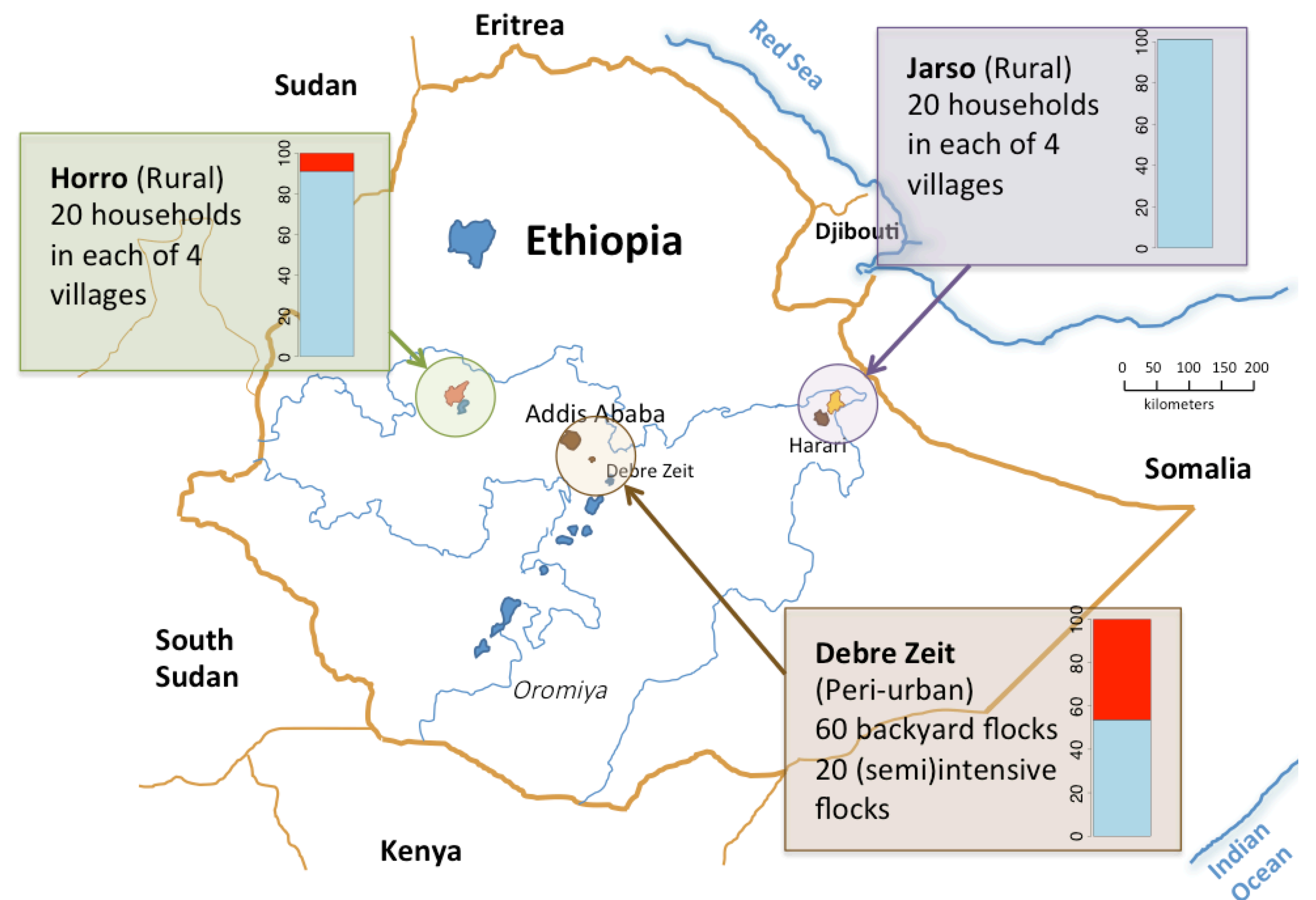


Fig. 1. location of the three sampling areas and the number and type of premises sampled in each area. The bar plots indicate the percentage of premises in each area positive (red) and negative (light blue) for *Campylobacter*.

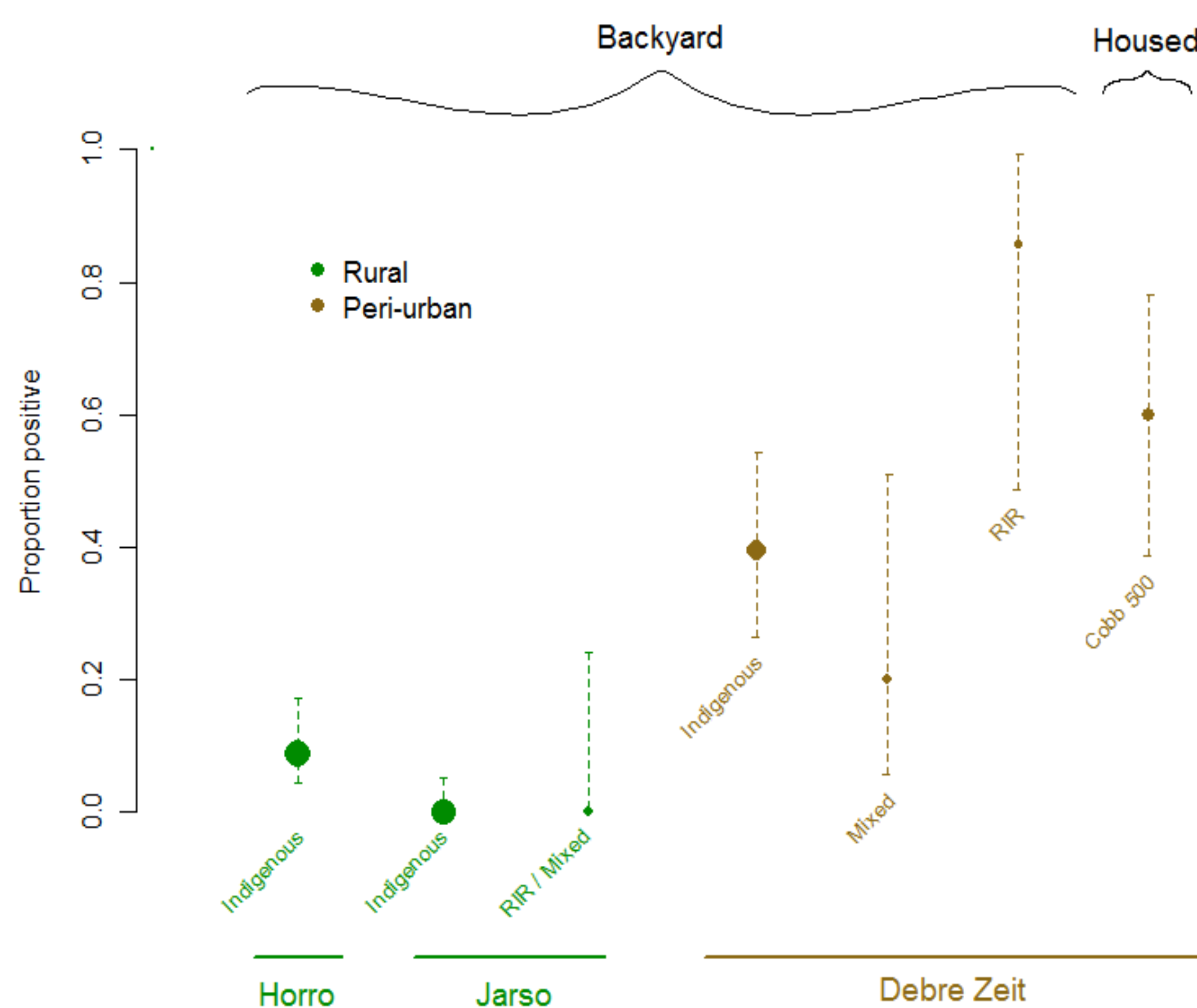


Fig. 3. The proportion (95% CI) of premises positive for *Campylobacter* by region, breed and production type. Size of the point is proportional to the number of premises of each type sampled.

## Our findings

- *Campylobacter* was detected in samples from 18% (44/239) of farms.
- 16 isolates could be speciated using multiplex PCR; all were *C. jejuni*.
- Peri-urban flocks were substantially more likely to be *Campylobacter* positive compared to rural flocks (Table 1, Fig. 3).
- Backyard flocks consisting of only Rhode Island Red or RIR hybrids and housed flocks of Cobb 500 birds were also at greater risk. The effect of breed and management system was highly correlated and could not be clearly distinguished.

Table 1	Levels	OR	95% C.I.	P value
Area	Rural	reference		0.04*
	Peri-urban	15.6	2.0 – 235.0	0.01
Flock type	Backyard - Mixed	reference		0.03*
	Backyard - Indigenous	0.3	0.6 – 15.2	0.2
	Backyard - RIR/Hybrid	5.0	1.8 – 183.9	0.01
	Housed - Cobb 500	2.2	1.1 – 38.7	0.04

## Our conclusions

- The risk of environmental contamination with *Campylobacter* was greatest in the peri-urban area, where many farms are starting to intensify their production systems.
- High levels of detection in traditionally managed flocks of indigenous birds in the peri-urban areas are of particular concern due to the close interaction between people and their birds in these settings.
- We postulate that (semi-)intensification of chicken production may alter the ecology and epidemiology of *Campylobacter* in the environment, chickens and people, and that this may drive emergence of new epidemiological patterns of disease.