# Five endemic pathogens of British cattle

K.A. Woodbine, L.E. Green, S.J. Moore, S.A. Mason, A. Ramirez-Villaescusa, G.F. Medley Ecology & Epidemiology Group, Department of Biological Sciences, University of Warwick, Coventry, CV4 7AL. Email: K.A.Woodbine@warwick.ac.uk

#### Introduction

Five worldwide & economically important cattle pathogens:

- •Bovine Viral Diarrhoea virus (BVDV) a pestivirus closely related to the viruses that cause classical swine fever in pigs & border disease in sheep. BVDV causes a complex of diseases including reproductive problems & can lead to fatal mucosal disease (MD)
- •Bovine Herpes virus type 1 (BHV-1) causes the acute virus disease Infectious Bovine Rhinotracheitis (IBR) that principally affects the upper respiratory tract & can cause fatal pneumonia
- Mycobacterium avium subsp. Paratuberculosis (MAP) causes Johne's disease a contagious wasting condition. Infection affects the small intestine causing weight loss & diarrhoea with normal appetite & is fatal
- •Neospora caninum a protozoan parasite first recognised in the 1980s. It is now considered an important cause of sudden abortions & neonatal morbidity in both dairy & beef cattle worldwide
- •Leptospira hardjo following infection, bacteria localise in the reproductive tract & kidneys causing abortions, stillbirths, infertility & loss of milk production in cattle

## **Project Outline**

- •Longitudinal study on 5 endemic pathogens in cattle herds in SW England
- •Most herds were visited 3 times
- •Herds with a BVDV antigen positive sample were visited up to 5 times
- ullet For each herd visit all animals  $\geqslant 2$  yrs of age were blood sampled, unless a herd had a confirmed BVD virus persistently infected animal then the whole herd was blood sampled
- •Each sample was tested for antibodies against the agents described
- •Samples negative for anti-BVDV antibodies (Ab) were subsequently tested for BVDV antigen (E<sup>rns</sup>)
- •Blood samples were collected from 15,736 cattle from 114 herds between December 2002 & April 2006
- •A total of 29,782 serum samples were collected, of which 26,207 (91%) were from the 3 planned visits & from cattle  $\geq$  2 yrs of age

# **Objectives**

To develop a understanding of the seroepidemiology of 5 different pathogens (e.g. viral, bacterial & protozoan) in a sample of British cattle herds

#### Results

Mean & median herd sizes were approx: 188 & 171 (range 3-847). Herds consisted of 38 (33%) suckler, 46 (40%) dairy, 10 (9%) dairy/beef & 20 (18%) suckler/beef. 70 herds did not vaccinate against any disease: 2 herds = 1 disease, 2 herds = 2 diseases, 7 herds = 3 diseases, 14 herds = 4 diseases & 45 had all 5 diseases.

#### Herd prevalence

Only non-vaccinated herds. Positive herd = herd with ≥1 animals with positive Ab titre

	Positive herds Number (%)
BVDV	97 (100)
BHV-1	89 (83)
MAP	101 (89)
N. caninum	107 (94)
L. hardjo	71 (91)

### Animal prevalence

-Only animals from non-vaccinated positive herds

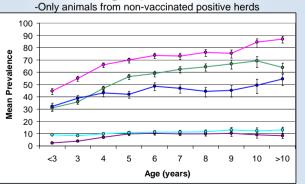
	Always Negative	Ever Positive	Positive & Negative
	Number (%)	Number (%)	Number (%)
BVDV	3541 (30)	8138 (70)	1481 (13)
BHV-1	6993 (49)	7250 (51)	1194 (8)
MAP	14164 (90)	1572 (10)	896 (6)
N. caninum	13697 (87)	2039 (13)	733 (5)
L. hardjo	3932 (55)	3218 (45)	426 (6)

# Within herd prevalence

-Only non-vaccinated positive herds

	Mean prevalence	Median prevalence	Range
BVDV	65.4	71.6	1.3-100.0
BHV-1	43.1	40.0	0.9-99.2
MAP	7.1	5.9	0.4-26.2
N. caninum	11.6	9.7	0.7-56.1
L. hardjo	44.1	42.0	1.1-100.0

## Age profile





# Average herd size profile

- Only non-vaccinated positive herds 100 90 80 Prevalence 70 60 50 40 30 20 10 3-68 200-274 284-847 141-199 Average herd size categorised

#### Conclusions

- •All 5 pathogens were found to be endemic within the sampled population, however the within herd prevalence for all 5 pathogens differed greatly
- •Larger herds had higher BHV-1 seropositivity, this may be explained by the herd type or other management factors influencing infectious contacts
- •Seropositivity of BVDV, BHV-1, L. hardjo increased with age
- •These are unique data that will allow better understanding of the transmission dynamics & control of these infections



# Acknowledgements



