

Proportion of *Mycobacterium avium* subspecies *paratuberculosis* infected animals which are not detected in infected dairy herds

Anne Lehébel^{1,2}, Raphaël Guatteo^{1,2}, Clara Marcé^{1,2}, Christine Fourichon^{1,2}

¹ Oniris, Nantes Atlantic College of Veterinary Medicine, Food Science and Engineering, F-44307 Nantes, France

² INRA, UMR 1300 Bio-Agression, Epidémiologie et Analyse de Risque, F-44307 Nantes, France

Introduction

Paratuberculosis is a chronic disease of ruminants that causes economic losses to dairy farmers worldwide. Control programs have been implemented in many countries. They rely on the detection and cull of infected and infectious animals. Major limitations of these programs are the long incubation period of paratuberculosis and the poor sensitivity of the diagnostic tests. Therefore, a high proportion of infected animals are not detected. However, this proportion is unknown.

OBJECTIVE: To estimate the proportion of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) infected animals which are not detected in infected dairy herds.

Selection of the study population

- Dairy herds enrolled in the MAP voluntary control program with a test and cull scheme conducted by the farmer health service (GDS) of the west of France after the 1st of January 2002
- Herds with a yearly follow up of at least 3 years (i.e. with at least 4 annual results)
- Herds with more than 20 animals tested in the first year

Data and analysis

• MAP individual status is determined for each annual test of selected animal: *clinical shedder / asymptomatic shedder / infected non shedder / non infected animal*

according to the type and test result (serum ELISA on blood sample, faecal culture or PCR, Ziehl Neelsen coloration).

- The different test results for each animal over the control program are combined to correct for under detection at the initial test:
 - attribution of a retrospective infection status
 - consolidation of the non-infected status according to the number of negative results during the follow up.

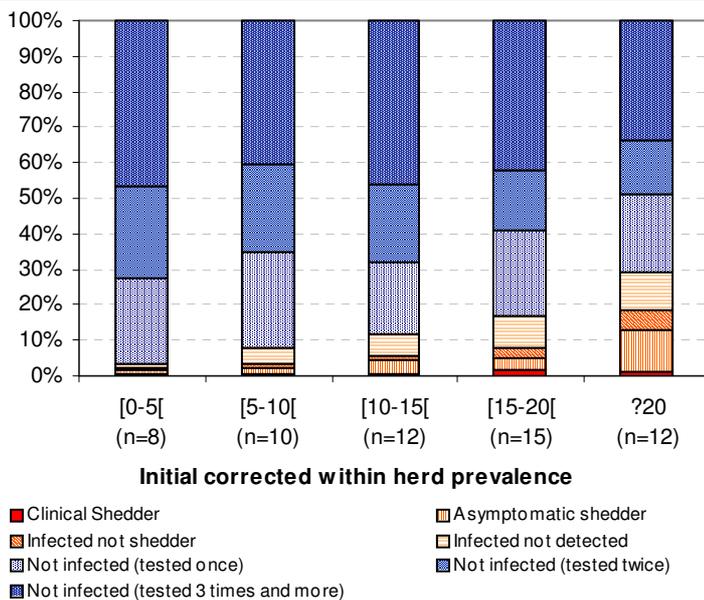
Example of retrospective corrected MAP infection status depending on the longitudinal results

	Year 0	Year 1	Year 2	Year 3
Animal A				
<i>Before correction</i>	NI	NI	I	
<i>After correction</i>	IND	IND	I	
Animal B				
<i>Before correction</i>	NI	NI	NI	ND
<i>After correction</i>	(tested 3 times)	(tested 3 times)	(tested 3 times)	ND

I: Infected, ND: Not Done, IND: Infected Not Detected, NI: Not Infected

Results

Distribution of the different Map infection status within herds



57 herds were included in the study with an average of 68 animals tested annually.

Within-herd prevalence:

- Initial "apparent" prevalence : **8.2%** (std=7.3)
- Initial "corrected" prevalence : **14.8%** (std=9.5)
- Proportion of infected animals which are not detected at the initial sampling among all infected animals: **47.3%** (std=34.6)

Conclusion & Perspectives

- ✓ A unique sampling enables to detect about half of the animals that will be found infected overall.
 - ✓ The proportion in the herd of infected animals which are not detected increases with the prevalence.
 - ✓ The "corrected" prevalence is possibly under-estimated because of several animals with only one negative (or two) test result.
- *Next step:* Description of non-detected animals profile (age, stage in lactation, parity) at the first test in order to identify animals which are potentially infected but non-detected.