RVC OPEN ACCESS REPOSITORY – COPYRIGHT NOTICE

This document is the Accepted Manuscript version of a Published Work that appeared in final form in *Livestock*, copyright © MA Healthcare, after peer review and technical editing by the publisher. To access the final edited and published work see: <u>https://doi.org/10.12968/live.2019.24.4.176</u>.

The full details of the published version of the article are as follows:

TITLE: The specificity of phage testing for MAP — where might it fit into the diagnostic armoury?

AUTHORS: Benjamin MC Swift, Catherine ED Rees

JOURNAL: Livestock

PUBLISHER: MA Healthcare

PUBLICATION DATE: 11 July 2019

DOI: 10.12968/live.2019.24.4.176



1 The specificity of phage testing for MAP – where might it fit into the diagnostic armoury?

2 Abstract

3 The current individual tools available for the diagnosis of Johne's disease are far from suitable to tackle 4 this endemic disease. Culture, PCR and ELISA tests, when used together can be useful in managing the 5 disease in the later stages of infection at a herd level. They are, however, ill-suited to detecting the 6 causative agent M. avium subsp. paratuberculosis (MAP) at the early stages of infection and at an 7 individual level. Phage technology offers another tool in the attempt to better manage and control this disease. Phage-technology has been demonstrated to rapidly and sensitively detect and 8 9 specifically identify viable MAP in the milk and blood of cattle. Although in relatively-early stages of 10 development, phage technology offers a strong addition to the armoury of tests used to detect MAP 11 in blood and milk, and may go on to be part of ongoing control measures to reduce the burden of 12 disease to farmers and veterinarians.

13

14 Introduction - Johne's disease

Mycobacterium avium subspecies paratuberculosis (MAP) is the causative agent of Johne's disease; a chronic infectious granulomatous enteritis of ruminants that is endemic in the UK as well as many countries worldwide.^{9, 16} As well as being a serious disease from an animal health perspective, Johne's disease also places a significant economic burden on farmers.

19 There are generally four stages of infection for Johne's disease, which often span several years: silent, sub-clinical, clinical and advanced.²⁹ Shedding of MAP cells in faeces can occur during the 20 21 subclinical stages of infection, resulting in transmission on farm via the faecal oral route. MAP can also 22 be shed into the milk of infected animals leading to transmission to newly born animals. Whatever 23 the route of transmission, it is believed that initial MAP-infection occurs within the first few days of life, but clinical signs often do not appear until animals reach 3–4 years of age.²⁴ This long incubation 24 25 period before Johne's disease becomes detectable using conventional tests makes effective control schemes difficult to implement. 26

27

28 Tried and tested: current tools for diagnosing Johne's disease

Although classical laboratory culture of MAP is considered the gold standard method of 29 30 detection, in practice it is very difficult to perform because MAP is a slow growing organism that is 31 both difficult and expensive to culture. It can take over 16 weeks to culture the bacterium on 32 laboratory media and there are high failure rates due to the high risk of contamination by faster growing organisms.³⁰ To counter this problem, samples such as milk, faeces or tissue biopsies are 33 34 decontaminated using chemicals, but these can also affect the viability of the MAP cells in the sample, thus reducing the sensitivity of culture further.⁵ Not only does this inability to routinely culture MAP 35 make the gold standard diagnostic test impractical, it also means that fundamental aspects of the 36 37 pathophysiology of Johne's disease are not well understood, which hinders the development of 38 control programmes.

39 There are a range of immunological-based diagnostics that have been developed to diagnose 40 Johne's disease. There are many commercial and in-house enzyme-linked immunosorbent assays 41 (ELISA) to detect anti-MAP antibodies in bovine milk, serum or plasma. However there can be issues with cross-reactions occurring if the animals have been exposed to other pathogenic or environmental 42 mycobacteria which may result in false-positive results.²³ Another issue identified is that depending 43 44 on the age and stage of infection, sensitivity of detection can be as low at 2 % in calves to 55 % in older 45 cattle.^{11, 12} Poor sensitivity of ELISA tests remains a significant problem and is an unavoidable 46 consequence of the chronic nature of the disease. Since commercial ELISA tests are generally only 47 capable of routinely diagnosing Johne's disease in animals at the later stages of infection, or only 48 during the very late stages of the subclinical phase of infection, they are not really sensitive enough 49 to be used on an individual animal basis to reliably confirm infection. Most control programmes test herds annually,²³ however to compensate for the lack of sensitivity, and the fact that antibody levels 50 51 in infected animals are known to fluctuate, quarterly testing of individual animals is often carried out, 52 with the pattern of positive test results being used to classify the infection risk status of an animal.

Despite this limitation, ELISA tests are routinely used as part of disease management programmes as
 the high-throughput format and low cost per sample means herds can be screened very quickly and
 simply. In addition, ELISAs can be prognostic indicators for reduced milk yield or faecal shedding.¹⁵

56 Molecular detection methods have been developed for the detection of MAP based on 57 detection of signature DNA sequences by PCR amplification (or other nucleic acid amplification 58 technologies) that enables the rapid and accurate detection of these bacteria in a variety of matrices. The most commonly used genetic target is the IS900 insertion element found in multiple copies in the 59 60 MAP genome and is considered to be unique to MAP, although the rare occurrence of IS900-like sequences have been reported in the literature.^{6,7}The fact that IS900 is found in multiple copies within 61 the MAP genome makes it an ideal signature sequence as the PCR-based detection will be more 62 63 sensitive than tests that target single copy genetic elements.²¹

64 PCR-based detection is often used when MAP is present in matrices such as faeces or milk to 65 overcome the problems associated with direct culture described previously. However these matrices also contain many PCR inhibitors. Hence, accurate and sensitive detection of mycobacterial DNA by 66 67 PCR relies on both efficient lysis of the bacilli and DNA purification to remove PCR inhibitors and concentrate DNA.¹⁰ Efficient lysis is one of the biggest problems when using direct PCR to detect 68 69 mycobacterial DNA because mycobacteria have a very thick cell wall, which make traditional lysis 70 methods very inefficient, thus reducing the sensitivity of any PCR-based detection event. Where 71 experimentally, nucleic acid amplification technologies can be shown to specifically and sensitively 72 detect MAP, the sample preparation and DNA lysis steps are often inefficient, reducing the power of 73 these technologies. Therefore direct PCR-based detection often require the MAP cells to be present 74 in high concentrations but the reliability of such methods is confounded by the fact that the 75 concentration of MAP cells in a sample also fluctuates and is very much dependant on the stage of infection and bacterial shedding levels.² 76

77

78 A new approach: Phage Technology

79 Bacteriophage are viruses that infect bacteria and they will only successfully replicate within 80 a viable host. Like all viruses they identify their correct host cells by binding to specific structures 81 (receptors) on the outside of the bacterial cells. Once bound, phage inject their own DNA into the 82 bacterial cell and then take over its machinery to make many copies of themselves before finally 83 producing enzymes that break down the cell wall and cause the cell to break open, releasing new 84 phage particles into the environment (Table 1). Phage have been used for many years to rapidly detect different bacterial pathogens, including members of the *Mycobacterium* genus.²⁰ Several different 85 86 phage-based detection assays have been described, such as genetically engineered reporter-phage 87 that produce a fluorescent or bioluminescent signal when they infect their host cells, or phage binding to host cells can be detected using physical methods such as plasmon resonance-based spectrometry 88 (for a full review see Schofield et al., 2012).²⁰ However more recently the detection of mycobacteria 89 90 using bacteriophage amplification technology has been developed where the natural life cycle of the 91 phage is exploited to detect its bacterial host.

92 Bacteriophage amplification technology has been exploited to detect a range of mycobacteria. 93 One of the original uses that was commercialised was to detect *M. tuberculosis* -the causative agent 94 of tuberculosis (TB) - in human sputum samples.¹ The assay was a low cost and simple petri-dish based test that enabled mycobacteria to be detected within 48 h (for review see Rees & Botsaris, 2012).¹⁸ To 95 96 develop this assay a broad spectrum bacteriophage, D29, was used which is capable of detecting a 97 wide range of mycobacteria, including pathogenic and non-pathogenic species. The ability of the assay 98 to detect many strains, led to the phage amplification assay being applied in the agricultural and food 99 sectors. However, the broad host range of phage D29 was both an advantage and disadvantage where 100 in human clinical samples, mycobacteria in the sputum would be treated in the same way regardless 101 of what species was present. However in food and agriculture settings, many other mycobacterial 102 species, both pathogenic and environmental may be present in the samples. This results in the 103 detection of a range of mycobacteria not of interest reducing the specificity of the assay in this plate 104 based format. Thus the assay was further developed to be able to specifically identify MAP by 105 combining the phage assay with the IS900 PCR, where the plaques formed on the plates were picked 106 and screened for these MAP-specific DNA sequences.²² This assay was subsequently used to detect MAP in a range of matrices including, milk, cheese, infant powdered formula and blood.^{3, 4, 25} There is 107 108 great difficulty in assessing the sensitivity and specificity of any new diagnostic test especially in the absence of a gold standard. However Botsaris et al,³ had demonstrated that using the phage-PCR 109 110 assay, one could accurately predict with a sensitivity of 90 % and specificity of 99 % when a bulk tank 111 milk sample was positive for MAP based on the number of plaques. Most recently this assay has been 112 used to detect viable MAP cells in retail milk, where viable MAP cells were detected in 10 % of pasteurised milk in England.⁸ However this technology is still reliant on classic microbiological methods 113 114 and techniques, which are not particularly suitable for high-throughput samples.

This phage technology has now advanced to a single tube format (Actiphage[®], PBD Biotech), 115 which is more sensitive than the original phage amplification assay²⁷ and suitable for use on a large 116 117 number of samples and relies on the four characteristics for phage technology (Table 1). The 118 Actiphage® assay again relies on the use of bacteriophage, however there is no need for plating or 119 incubation with fast growing mycobacteria. This assay essentially uses the phage's ability to lyse 120 mycobacteria resulting in the efficient release of genomic mycobacterial DNA (Fig. 1). The limitations 121 of the original phage assay, where plaques were picked and scrutinised for signature DNA sequences, 122 are negated using this new technique, as a simple PCR or nucleic acid amplification event is carried 123 out directly on the sample to detect signature MAP DNA sequences. The presence of other 124 mycobacteria or other bacteria does not affect the assay, as specificity of the assay is all predicated 125 on the amplification method used (Fig. 2).

The data generated using the phage assay has demonstrated that viable mycobacteria can be present in the blood of cattle before reaching the latter stages of infection,^{25, 26} where viable MAP cells detected in cattle were either inconclusive or negative by milk and serum ELISA in both naturally and experimentally infected cattle. Indeed a recent study in France has demonstrated that MAP can be found in the blood of calves from a Johne's infected at less than one month of age.¹⁷ However it is 131 difficult to validate a new test for a disease such at Johne's, where there is no appropriate gold 132 standard and as such a detection event would be seen as a false positive when compared to the 133 insensitive ELISA or culture, thus raising questions about the specificity of the assay, whereas a 134 detection event can only happen in certain circumstances (Table 1). Here a larger study is needed 135 where further data are required to understand the performance of the phage assay in a wider range 136 of samples. In the absence of a Gold Standard, other statistical approaches would be required such as Bayesian analysis, to begin to predict the performance of phage technology as a diagnostic.²⁸ These 137 138 data however, may also provide a tool to delve into the complexities of Johne's disease to ask novel 139 questions about the pathophysiology of infection, ideally resulting in more information for the control 140 of this disease.

141

142 A new tool in the armoury?

143 Overall, current diagnostic assays for MAP based on serology or faecal testing have poor 144 sensitivities and cannot detect early stages of infection, therefore there is need to find new diagnostic markers for early infection detection and disease stages.¹³ DNA amplification technologies, when 145 146 applied in the right format have the potential to be both specific and sensitive, however processing 147 steps required for efficient DNA amplification are not currently suitable to make the most of the ability 148 of PCR to detect very low levels of DNA. On an individual cow basis, where an ideal approach would 149 be to use serological assays to screen herds for the presence of Johne's disease, then to use a more 150 sensitive and robust tool that has the specificity of PCR, but with an improved sensitivity, allow 151 detection of Johne's disease at a much early stage of infection in individual animals, thus giving 152 veterinarians and farmers another tool to control Johne's disease.

The ability to rapidly detect and specifically identify mycobacteria responsible for infections has been very difficult to achieve due the slow growing, fastidious natures of organisms such a MAP. Phage technology has opened to the door to not only detecting these organisms far quicker than traditional culture, but also allows novel aspects of the pathophysiological nature of infection to be

- 157 studied and understood to fully comprehend diseases just as Johne's disease. Phage technology is an
- 158 attractive new tool which has the potentially to be used in combination with existing technologies and
- 159 management schemes to improve and reduce the burden of Johne's disease on farmers and
- 160 veterinarians.
- 161
- 162 Keywords
- 163 Johne's disease; bacteriophage; phage; paratuberculosis; MAP; detection

164 Key Points

- 165 Novel detection methods are needed to control Johne's disease.
- 166 Current diagnostics for Johne's disease are ill-suited for early detection or on an individual animal
- 167 basis.
- 168 Phage technology can rapidly, sensitively and specifically detect *M. paratuberculosis* is blood and milk
- 169 Phage technology may be used as another tool in the armoury to tackle Johne's disease.

170 Ref	ferences
----------------	----------

171 1. Albert H, Heydenrych A, Brookes R, Mole RJ, Harley B, Subotsky E, Henry R, Azeved	do V. 2002
--	------------

172 Performance of a rapid phage-based test, fastplaquetb(tm),to diagnose pulmonary tuberculosis from

sputurn specimens in south africa. Int J Tuberc Lung D. 6(6):529-537.

174

- 175 2. Bauman CA, Jones-Bitton A, Jansen J, Kelton D, Menzies P. 2016. Evaluation of fecal culture and
- 176 fecal rt-pcr to detect mycobacterium avium ssp paratuberculosis fecal shedding in dairy goats and
- dairy sheep using latent class bayesian modeling. Bmc Vet Res. 12.

178

- 179 3. Botsaris G, Slana I, Liapi M, Dodd C, Economides C, Rees C, Pavlik I. 2010. Rapid detection methods
- 180 for viable mycobacterium avium subspecies paratuberculosis in milk and cheese. Int J Food

181 Microbiol. 141:S87-S90.

182

- 183 4. Botsaris G, Swift BMC, Slana I, Liapi M, Christodoulou M, Hatzitofi M, Christodoulou V, Rees CED.
- 184 2016. Detection of viable mycobacterium avium subspecies paratuberculosis in powdered infant

185 formula by phage-pcr and confirmed by culture. Int J Food Microbiol. 216:91-94.

186

187 5. Bradner L, Robbe-Austerman S, Beitz DC, Stabel JR. 2013. Optimization of hexadecylpyridinium

188 chloride decontamination for culture of mycobacterium avium subsp. Paratuberculosis from milk. J

189 Clin Microbiol. 51(5):1575-1577.

190

191 6. Cousins DV, Whittington R, Marsh I, Masters A, Evans RJ, Kluver P. 1999. Mycobacteria distenct

- 192 from mycobacterium avium subsp. Paratuberculosis isolated from the faeces of ruminants possess
- is900-like sequences detectable is900 polymerase chain reaction: Implications for diagnosis. Mol Cell

194 Probes. 13(6):431-442.

195	7. Englund S, Bolske G, Johansson KE. 2002. An is900-like sequence found in a mycobacterium sp
196	other than mycobacterium avium subsp paratuberculosis. Fems Microbiol Lett. 209(2):267-271.
197	
198	8. Gerrard ZE, Swift BMC, Botsaris G, Davidson RS, Hutchings MR, Huxley JN, Rees CED. 2018.
199	Survival of mycobacterium avium subspecies paratuberculosis in retail pasteurised milk. Food
200	Microbiol. 74:57-63.
201	
202	9. Gilardoni LR, Paolicchi FA, Mundo SL. 2012. Bovine paratuberculosis: A review of the advantages
203	and disadvantages of different diagnostic tests. Rev Argent Microbiol. 44(3):201-215.
204	
205	10. Kolia-Diafouka P, Godreuil S, Bourdin A, Carrere-Kremer S, Kremer L, Van de Perre P, Tuaillon E.
206	2018. Optimized lysis-extraction method combined with is6110-amplification for detection of
207	mycobacterium tuberculosis in paucibacillary sputum specimens. Front Microbiol. 9:2224.
208	
209	11. Laurin EL, Sanchez J, Chaffer M, McKenna SLB, Keefe GP. 2017. Assessment of the relative
210	sensitivity of milk elisa for detection of mycobacterium avium ssp paratuberculosis infectious dairy
211	cows. J Dairy Sci. 100(1):598-607.
212	
213	12. Li LL, Wagner B, Freer H, Schilling M, Bannantine JP, Campo JJ, Katani R, Grohn YT, Radzio-Basu J,
214	Kapur V. 2017. Early detection of mycobacterium avium subsp paratuberculosis infection in cattle
215	with multiplex-bead based immunoassays. Plos One. 12(12).
216	
217	13. Magombedze G, Shiri T, Eda S, Stabel JR. 2017. Inferring biomarkers for mycobacterium avium
218	subsp paratuberculosis infection and disease progression in cattle using experimental data. Sci Rep-
219	Uk. 7.

220	14. Nielsen SS, Toft N. 2008. Ante mortem diagnosis of paratuberculosis: A review of accuracies of
221	elisa, interferon-gamma assay and faecal culture techniques. Vet Microbiol. 129(3-4):217-235.
222	
223	15. Nielsen SS. 2009. Use of diagnostics for risk-based control of paratuberculosis in dairy herds. In
224	Practice. 31(4):150-154.
225	
226	16. Patterson S, Bond K, Green M, van Winden S, Guitian J. 2019. Mycobacterium avium
227	paratuberculosis infection of calves - the impact of dam infection status. Prev Vet Med.
228	10.1016/j.prevetmed.2019.02.009
229	
230	17. Pelletier C, Haas C, Dangien C, Meunier A, Caplain C, Pez F, Potaufeux V, Clarke B, Rees C, Swift B
231	et al. 2018. Detection of active infection of new-born calves by mycobacterium avium subsp.
232	Paratuberculosis (map) in first days of life. Paper presented at: 5TH CONGRESS OF THE EUROPEAN
233	ASSOCIATION OF VETERINARY LABORATORY DIAGNOSTICIANS.
234	
235	18. Rees C, Botsaris G. 2012. The use of phage for detection, antibiotic sensitivity testing and
236	enumeration. Understanding Tuberculosis - Global Experiences and Innovative Approaches to the
237	Diagnosis. 293-306.
238	
239	19. Roach DR, Debarbieux L. 2017. Phage therapy: Awakening a sleeping giant. Emerging Topics in
240	Life Sciences. 1(1):93-103.
241	
242	20. Schofield DA, Sharp NJ, Westwater C. 2012. Phage-based platforms for the clinical detection of
243	human bacterial pathogens. Bacteriophage. 2(2):105-283.
244	

245	21. Sevilla IA, Garrido JM, Molina E, Geijo MV, Elguezabal N, Vazquez P, Juste RA. 2014. Development
246	and evaluation of a novel multicopy-element-targeting triplex pcr for detection of mycobacterium
247	avium subsp. Paratuberculosis in feces. Appl Environ Microbiol. 80(12):3757-3768.
248	
249	22. Stanley EC, Mole RJ, Smith RJ, Glenn SM, Barer MR, McGowan M, Rees CED. 2007. Development
250	of a new, combined rapid method using phage and pcr for detection and identification of viable
251	mycobacterium paratuberculosis bacteria within 48 hours. Appl Environ Microb. 73(6):1851-1857.
252	
253	23. Stevenson K. 2010. Diagnosis of johne's disease: Current limitations and prospects. Cattle Pract.
254	18:104-109.
255	
256	24. Sweeney RW. 1996. Transmission of paratuberculosis. Vet Clin N Am-Food A. 12(2):305.
257	
258	25. Swift BMC, Denton EJ, Mahendran SA, Huxley JN, Rees CED. 2013. Development of a rapid
259	phage-based method for the detection of viable mycobacterium avium subsp paratuberculosis in
260	blood within 48 h. J Microbiol Meth. 94(3):175-179.
261	
262	26. Swift BMC, Huxley JN, Plain KM, Begg DJ, de Silva K, Purdie AC, Whittington RJ, Rees CED. 2016.
263	Evaluation of the limitations and methods to improve rapid phage-based detection of viable
264	mycobacterium avium subsp paratuberculosis in the blood of experimentally infected cattle. Bmc
265	Vet Res. 12.
266	
267	27. Swift BMC, Convery TW, Rees CED. Evidence of Mycobacterium tuberculosis complex
268	bacteraemia in intradermal skin test positive cattle detected using phage-RPA. 2016. Virulence
269	7(7):779-788.
270	

- 271 28. Wang C, Turnbull BW, Nielsen SS, Grohn YT. 2011. Bayesian analysis of longitudinal Johne's
- disease diagnostic data without a gold standard test. J. Dairy Sci. 94(5):2320-2328.

- 274 29. Whitlock RH, Buergelt C. 1996. Preclinical and clinical manifestations of paratuberculosis
- 275 (including pathology). Vet Clin N Am-Food A. 12(2):345.
- 276
- 277 30. Whittington RJ. 2009. Factors affecting isolation and identification of mycobacterium avium
- subsp paratuberculosis from fecal and tissue samples in a liquid culture system. Journal of Clinical
- 279 Microbiology. 47(3):614-622.

280 Fig 1. Bacteriophage lysis



- 282 The efficient lysis of bacteria caused by bacteriophage (white arrows). Figure adapted from Roach &
- 283 Debarbieux, 2017).¹⁹

284 Fig 2. Schematic of Actiphage[®] Assay



Diagram shows the stages of receiving a biological sample, to results. 1. Delivery of sample to the
laboratory, 2. Processing at a central facility, 3. Isolation of peripheral blood mononuclear cells
where mycobacteria are present, 4. Add phage for mycobacteria to sample, 5. Allow phage to infect
any mycobacteria present in the sample, 6. Isolate DNA after cell lysis, 7. Perform DNA amplification
of signature MAP DNA.

293

285

295 Table 1. Steps required by phage to enable a successful detection event

PHAGE REQUIREMENTS	
BINDING	Phage will only bind to specific bacterium. Here phage D29 will ONLY bind to <i>Mycobacterium</i> and no other bacteria
REPLICATION	This will only occur inside a VIABLE host, where phage will hijack their bacterial hosts machinery and replicate
LYSIS	Specific enzymes are made when the phage is ready to break open their host cell
DNA RELEASE	This DNA is efficiently released from inside the cell and a species specific PCR is carried out to confirm the identity of the mycobacteria present