

Dr Ian Marsh (Research Officer)

Microbiology and Parasitology, Elizabeth Macarthur Agricultural Institute

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Qualifications

- Bachelor of Technology Management (Biotechnology) (First Class Honours) University of Western Sydney, Macarthur)
- Doctorate of Philosophy (University of Sydney, Faculty of Veterinary Science)

Current appointment: Professional Officer (Research), NSW DPI, 1996 -present.

Relevant employment and academic history:

- 1991-1993: Undergraduate degree, University of Western Sydney, Macarthur).
- 1994-1995: Honours, University of Western Sydney, Macarthur) with research work undertaken at the Elizabeth Macarthur Agricultural Institute NSW Agriculture, Microbiology Laboratory Menangle.
- 1995-1996: Technical Officer, NSW Agriculture, Microbiology Laboratory Menangle.
- 1996-2001: Professional Officer (Research), NSW Agriculture/NSW DPI, Microbiology Laboratory Menangle.
- 2001-2004: PhD, University of Sydney, Faculty of Veterinary Science with research work undertaken at the Elizabeth Macarthur Agricultural Institute NSW Agriculture, Microbiology Laboratory Menangle.
- 2004 - present: Professional Officer (Research), NSW DPI,

Research interests

1. Molecular diagnosis of genetic disorders in production animals
2. Molecular biology-based research of pathogens that affect terrestrial and aquatic species
3. Development of diagnostic tests of pathogens that affect terrestrial and aquatic species

Experience Molecular microbiology (25 years) with particular emphasis on the development of microbiological techniques including:

1. Polymerase chain reaction (PCR)-based research and diagnostics using:
 - 1.1. *in silico* (internet)-based molecular characterisation of relevant opportunities for PCR-based diagnostic test development
 - 1.2. Conventional PCR
 - 1.3. Real-Time or quantitative (qPCR)
 - 1.4. Efficiency corrected quantitative PCR
2. Molecular strain typing
 - 2.1. PCR restriction endonuclease analysis (PCR-REA)
 - 2.2. Restriction fragment Length Polymorphism (RFLP)
 - 2.3. Microarray analysis
 - 2.4. Surface-enhanced laser desorption/ionization (SELDI)
 - 2.5. Proteomics
 - 2.6. Pulsed Field Gel Electrophoresis (PFGE)
 - 2.7. Sanger sequencing of PCR-based amplified product
 - 2.8. Next Generation sequencing (NGS) of PCR-based amplified product
3. Optimization and validation of diagnostic techniques
4. Expert technical support for the diagnostic techniques
5. Deployable, Point of Care (POC) predictive and diagnostic molecular tests

Project administration and co-ordination including Milestone and Final Reports for:

1. Development of molecular-based microbiological diagnostic capability in the RVL, EMAI (NSW DPI funded project).
2. Possibilities for improving the D-PCR test for *M. a. paratuberculosis* from faeces (MLA funded project).
3. QX disease surveillance and window of infection experiment 2006 (NSW DPI funded surveillance).
4. Genomic and proteomic comparative study of the sheep and cattle strains of *Mycobacterium avium* subsp. *paratuberculosis* (PhD Thesis) (MLA funded project).
5. Bovine Johne's Disease: basic and applied research for improved diagnosis and prevention (MLA funded project).
6. Ovine Johne's Disease: Applications of basic research on enhanced diagnosis and prevention (MLA funded project).

7. "What role does wildlife play in emergency disease? The role of the feral pig" – Genotyping salmonella from feral pigs to model exotic disease outbreak (ARC funded project)
- 8.

Dissertations

Honours

I. Marsh (1994). An immunomagnetic ELISA for the detection of EHNV from large water samples. University of Western Sydney, Faculty of Science.

PhD

I. Marsh (2006). Genomic and proteomic comparative study of the sheep and cattle strains of *Mycobacterium avium* subsp. *paratuberculosis*. University of Sydney, Faculty of Veterinary Science.

Selected Bibliography

1. Ruijter, JM, Barnewall, RJ, Marsh, IB, Szentirmay, AN, Quinn, JC, van Houdt, R, Gunst, QD & van den Hoff, MJB 2021, 'Efficiency correction is required for accurate quantitative PCR analysis and reporting', *Clinical Chemistry* vol. 67, no. 6, pp. 829-842.
2. Spiers ZB, Gabor M, Fell SA, Carnegie RB, Dove M, O'Connor W, Frances J, Go J, **Marsh IB**, Jenkins C. Longitudinal study of winter mortality disease in Sydney rock oysters *Saccostrea glomerata*. *Dis Aquat Organ*. **2014** Jul 24;110(1-2):151-64
3. Plain KM*, **Marsh IB***, Waldron AM, Galea F, Whittington AM, Saunders VF, Begg DJ, de Silva K, Purdie AC, Whittington RJ. High-throughput direct fecal PCR assay for detection of *Mycobacterium avium* subsp. *paratuberculosis* in sheep and cattle. *J Clin Microbiol*. **2014** Mar;52(3):745-57. (*Co-lead author)
4. Ward MP, Cowled BD, Galea F, Garner MG, Laffan SW, **Marsh I**, Negus K, Sarre SD, Woolnough AP. Salmonella infection in a remote, isolated wild pig population. *Vet Microbiol*. **2013** Mar 23;162 (2-4):921-9.
5. Boys CA, Rowland SJ, Gabor M, Gabor L, **Marsh IB**, Hum S, Callinan RB. Emergence of epizootic ulcerative syndrome in native fish of the Murray-Darling River System, Australia: hosts, distribution and possible vectors. *PLoS One*. **2012**;7(4):e35568.
6. Go J, **Marsh I**, Gabor M, Saunders V, Reece RL, Frances J, Boys C, Gabor LJ. Detection of *Aphanomyces invadans* and epizootic ulcerative syndrome in the Murray-Darling drainage. *Aust Vet J*. **2012** Dec;90(12):513-4.
7. Kennan RM, Wong W, Dhungyel OP, Han X, Wong D, Parker D, Rosado CJ, Law RH, McGowan S, Reeve SB, Levina V, Powers GA, Pike RN, Bottomley SP, Smith AI, **Marsh I**, Whittington RJ, Whisstock JC, Porter CJ, Rood JI. The subtilisin-like protease AprV2 is required for virulence and uses a novel disulphide-tethered exosite to bind substrates. *PLoS Pathog*. **2010** Nov 24;6(11):e1001210.
8. **Marsh, I. B.** and R. J. Whittington. **2007**. Genomic diversity in *Mycobacterium avium*: single nucleotide polymorphisms between the S and C strains of *M. avium* subsp. *paratuberculosis* and with *M. a. avium*. *Mol Cell Probes*. *Mol Cell Probes* 21 (1):66-75.
9. **Marsh, I. B.**, J. P. Bannantine, M. L. Paustian, M. L. Tizard, V. Kapur, and R. J. Whittington. **2006**. Genomic comparison of *Mycobacterium avium* subsp. *paratuberculosis* sheep and cattle strains by microarray hybridization. *J Bacteriol* 188:2290-3.
10. **Marsh, I. B.** and R. J. Whittington. **2005**. Deletion of an mmpL gene and multiple associated genes from the genome of the S strain of *Mycobacterium avium* subsp. *paratuberculosis* identified by representational difference analysis and in silico analysis. *Mol Cell Probes* 19 (6):371-84.
11. **Marsh, I. B.**, R. J. Whittington, B. O'Rourke, A. D. Hyatt, and O. Chisholm. **2002**. Rapid differentiation of Australian, European and American ranaviruses based on variation in major capsid protein gene sequence. *Mol Cell Probes* 16:137-51.
12. Whittington, R. J., **I. B. Marsh**, and R. H. Whitlock. **2001**. Typing of IS1311 polymorphisms confirms that bison (*Bison bison*) with paratuberculosis in Montana are infected with a strain of *Mycobacterium avium* subsp. *paratuberculosis* distinct from that occurring in cattle and other domesticated livestock. *Mol Cell Probes* 15:139-45.
13. **Marsh, I.**, R. Whittington, and D. Cousins. 1999. PCR-restriction endonuclease analysis for identification and strain typing of *Mycobacterium avium* subsp. *paratuberculosis* and *Mycobacterium avium* subsp. *avium* based on polymorphisms in IS1311. *Mol Cell Probes* 13:115-26.