

# Curriculum Vitae

Bryan A Wee

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## Academic Qualifications

**Doctor of Philosophy (Microbial Genomics)** 2015

*The University of Queensland, Australia*

**Thesis title: The diversification and evolution of Integrative and Conjugative Elements associated with MPF<sub>G</sub> Type IV Secretion Systems.**

**Master of Molecular Biology** 2010

*University of Queensland, Australia*

- Postgraduate coursework degree with 50% of units by research.
- CGPA of 6.7 out of 7.
- Dean's commendation for high achievement

**Bachelor of Science (Honours)** 2008

*Universiti Kebangsaan Malaysia, Malaysia*

- 3 year undergraduate program majoring in Zoology with a final year project on bioinformatic characterization of immune system proteins of barramundi, *Lates calcarifer*
- CGPA of 3.2 out of 4.0

## Publications (First or Joint First Author)

Quantifying the transmission of antimicrobial resistance at the human and livestock interface with genomics.

**Wee BA**, Muloi DM, van Bunnik BAD

Clinical Microbiology and Infection, 2020 – PMID: 32979568

Emergence and impact of oprD mutations in *Pseudomonas aeruginosa* strains in cystic fibrosis.

Sherrard LJ, **Wee BA**, Duplancic C, Ramsay KA, Dave KA, Ballard E, Wainwright CE, Grimwood K, Sidjabat HE, Whiley DM, Beatson SA, Kidd TJ, Bell SC

Journal of Cystic Fibrosis, 2020 – PMID: 33775602

Whole genome sequencing reveals the emergence of a *Pseudomonas aeruginosa* shared strain sub-lineage among patients treated within a single cystic fibrosis centre.

**Wee BA**, Tai AS, Sherrard LJ, Ben Zakour NL, Hanks KR, Kidd TJ, Ramsay KA, Lamont I, Whiley DM, Bell SC, Beatson SA  
BMC Genomics, 2018 – PMID: 30165811

A retrospective pilot study to determine whether the reproductive tract microbiota differs between women with a history of infertility and fertile women.

**Wee BA**, Thomas M, Sweeney EL, Frentiu, FD, Samios, M, Ravel J, Gajer P, Myers G, Timms P, Allan JA, Huston WM.  
Australian & New Zealand Journal of Obstetrics & Gynaecology, 2018 – PMID: 29280134

A distinct and divergent lineage of genomic island-associated type IV secretion systems in *Legionella*

**Wee BA**, Woolfit M, Beatson SA, Petty NK

PLoS ONE, 2013 – PMID: 24358157

## Publications (Co-author)

Secrets of the hospital underbelly: abundance of antimicrobial resistance genes in hospital wastewater reflects hospital antimicrobial use and inpatient length of stay

Perry M, van Bunnik B, McNally L, **Wee B**, Munk P, Warr A, Moore B, Kalima P, Philip C, de Roda Husman AM, Aarestrup F, Woolhouse M

- Contributed to bioinformatic analysis

Transmission, adaptation and geographical spread of the *Pseudomonas aeruginosa* Liverpool epidemic strain.

Moore MP, Lamont IL, Williams D, Paterson S, Kukavica-Ibrulj I, Tucker NP, Kenna DTD, Turton JF, Jeukens J, Freschi L, **Wee BA**, Loman NJ, Holden S, Manzoor S, Hawkey P, Southern KW, Walshaw MJ, Levesque RC, Fothergill JL, Winstanley C. Microbial Genomics. 2021– PMID: 33720817

- Contributed to bioinformatic analysis

Metagenomic sequencing of clinical samples reveals a single widespread clone of *Lawsonia intracellularis* responsible for porcine proliferative enteropathy.

Bengtsson RJ, **Wee BA**, Yebra G, Bacigalupe R, Watson E, Guedes RM, Jacobson M, Stadejek T, Archibald AL, Fitzgerald JR, Ait-Ali T. Microbial Genomics. 2020 - PMID: 32238228

- Supervised genomic and phylogenetic analyses

The *Aedes aegypti* Domino Ortholog p400 Regulates Antiviral Exogenous Small Interfering RNA Pathway Activity and ago-2 Expression.

McFarlane M, Almire F, Kean J, Donald CL, McDonald A, **Wee B**, Lauréti M, Varjak M, Terry S, Vazeille M, Gestuveo RJ. mSphere. 2020 - PMID: 32269152

- Analysed qPCR data and performed statistical calculations

Bovine *Staphylococcus aureus* superantigens stimulate the entire T cell repertoire of cattle.

Wilson GJ, Tuffs SW, **Wee BA**, Seo KS, Park N, Connelley T, Guinane CM, Morrison WI, Fitzgerald JR. Infection and Immunity 2018 – PMID: 30201699

- Performed all population level analysis of superantigen gene distribution and phylogenetic analysis of superantigen families using whole genome sequencing data.

The *Staphylococcus aureus* superantigen SEIX is a bifunctional toxin that inhibits neutrophil function.

Tuffs SW, James DBA, Bestebroer J, Richards AC, Goncheva MI, O'Shea M, **Wee BA**, Seo KS, Schlievert PM, Lengeling A, van Strijp JA, Torres VJ, Fitzgerald JR. PLoS Pathogens 2017- PMID: 28880920

- Contributed phylogenetic analysis

Within-host whole genome analysis of an antibiotic resistant *Pseudomonas aeruginosa* strain sub-type in cystic fibrosis

Sherrard LJ, Tai AS, **Wee BA**, Ramsay KA, Kidd TJ, Zakour NL, Whaley DM, Beatson SA, Bell SC. PloS one. 2017 Mar 8;12(3):e0172179. - PMID: 28273168

- Planned and performed majority of genomic and phylogenetic analyses

Tandem amplification of SCCmec can drive high level methicillin resistance in MRSA.

Gallagher LA, Coughlan S, Black NS, Lalor P, Waters EM, **Wee B**, Watson M, Downing T, Fitzgerald JR, Fleming GT, O'Gara JP. Antimicrobial Agents and Chemotherapy. 2017 Jul 17:AAC-00869.- PMID: 28717043

- Contributed to analyses of copy number estimation of SCCmec using short read data.

A *Chlamydia trachomatis* strain with a chemically generated P370L mutation in the *cthtrA* gene shows impaired production of infectious progeny

Marsh JM, **Wee BA**, Tyndall JDA, Lott WB, Bastidas RJ, Caldwell HD, Valdivia RH, Kari L, Huston WM BMC Microbiology, 2015 – PMID: 26424482

- Performed all short-read whole genome sequencing analyses and variant detection of mutant *Chlamydia* genomes.

Genomic evolution of the pathogenic *Wolbachia* strain, wMelPop.

Woolfit M, Iturbe-Ormaetxe I, Brownlie JC, Walker T, Riegler M, Seleznev A, Popovici J, Rances E, **Wee BA**, Pavlides J, Sullivan MJ, Beatson SA, Lane A, Sidhu M, McMeniman CJ, McGraw EA, O'Neill SL Genome Biology and Evolution, 2013 - PMID: 24190075

- Contributed to part of the SNP and indel variant analyses using short read whole genome sequencing

Genome sequence of the emerging pathogen *Aeromonas caviae*.

Beatson SA, das Graças de Luna M, Bachmann NL, Alikhan NF, Hanks KR, Sullivan MJ, **Wee BA**, Freitas-Almeida AC, Dos Santos PA, de Melo JT, Squire DJ, Cunningham AF, Fitzgerald JR, Henderson IR

Journal of Bacteriology, 2011 - PMID: 21183677

- Contributed to genome annotation and phylogenetic analyses

*Legionella pneumophila* strain 130b possesses a unique combination of type IV secretion systems and novel Dot/Icm secretion system effector proteins.

Schroeder GN, Petty NK, Mousnier A, Harding CR, Vogrin AJ, **Wee B**, Fry NK, Harrison TG, Newton HJ, Thomson NR, Beatson SA, Dougan G, Hartland EL, Frankel G

Journal of Bacteriology, 2010 - PMID: 20833813

- Contributed to phylogenetic analysis

## Manuscripts in preparation

Population analysis of *Legionella pneumophila* reveals the basis of resistance to complement-mediated killing.

**Wee BA\***, Alves J\*, Lindsay D, Cameron R, Jones B, Corander J, Marttinen P, Smith A, Fitzgerald JR – Under peer review

Population genomics of *Escherichia coli* in livestock-keeping households across a rapidly developing urban landscape.

Muloi DM\*, **Wee BA\***, McClean DM et al. – Under peer review

\*Authors contributed equally

## Relevant Work Experience

### Postdoctoral Research Fellow

Jun 2018 - present

Line Manager: Prof Mark Woolhouse

*The Usher Institute, University of Edinburgh, United Kingdom*

- Comparative and population genomics of *Escherichia coli*.
- Genomic analysis of antimicrobial resistance gene dynamics at the human-livestock interface

### Postdoctoral Research Fellow

Feb 2016 – May 2018

Line Manager: Prof J Ross Fitzgerald

*The Roslin Institute, University of Edinburgh, Midlothian, United Kingdom*

- Comparative and population genomics of *Legionella* spp., *Staphylococcus* spp.
- Metagenomic sequencing of clinical samples on the Oxford Nanopore MinION platform

### Research Assistant / Bioinformatician

Aug 2015 – Jan 2016

Line Manager: Assoc. Prof. Scott Beatson

*School of Chemistry and Molecular Biosciences, The University of Queensland, Brisbane, Queensland, Australia*

- Comparative genomics of emerging epidemic strain of *Pseudomonas aeruginosa* found in Brisbane Cystic Fibrosis clinics

### Research Assistant / Bioinformatician

Sep 2014 – Jan 2016

Line Manager: Dr. Wilhelmina Huston

*Institute of Health and Biomedical Innovation, Queensland University of Technology, Brisbane, Queensland, Australia*

- Led a 16S amplicon-based microbiome project to investigate the role of the microbiome in women who are unsuccessful at IVF treatment and suffer from occult chronic endometritis
- Performed genomic analyses of an Australian clinical collection of persistent *Chlamydia trachomatis* isolates
- Performed genomic analyses of laboratory mutated *C. trachomatis*

**Research Assistant****May – Dec 2008***Malaysia Genome Institute, Universiti Kebangsaan Malaysia, Malaysia***Relevant Technical Research Skills**

- Programming languages: Python, R and Perl.
- Experienced with handling and data management of large genomic datasets.
- Extensive experience with using comparative genomic analysis tools on high-throughput sequencing data (e.g. genome assembly, mapping, annotation, structural variation detection, sequence alignment, ortholog detection, genome-wide association studies).
- Highly experienced with Unix-based environments: Linux, Mac OSX and High-Performance Computing platforms (GridEngine, TORQUE).
- Experienced using phylogenetic inference software including IQ-TREE, RAxML, PhyML, PAML.

**Professional Memberships****Microbiology Society, United Kingdom**  
Member**2016 – present****Australian Society for Microbiology**  
Member**2009 – 2016**