Amir Ariff

Course Convenor of Quality Medical Practice, Office of Medical Education, School of Medicine, University of New South Wales, Australia

Email: amir.ariff@unsw.edu.au

Objective

To secure a postdoctoral position in academic research and teaching. Interests include genomics, genetics, bioinformatics, and molecular (micro)biology.

Education

2012 - 2016

<u>PhD</u> on Genomic Diversity and Bacteriophages of *Moraxella catarrhalis* University of Western Australia, Perth, Australia

Techniques include: bioinformatics, genomic analyses, bacteriology and bacteriophage techniques, whole genome sequencing, epifluorescence microscopy, genomic extraction, PCR, gel electrophoresis, and other molecular techniques.

2009 - 2011

MSc Master of Infectious Disease

University of Western Australia, Perth, Australia

Bioinformatics Molecular and Cell Microbiology
Science Communication Advances in Medical Microbiology
Antimicrobial Agents Epidemiology and Public Health
Mycology and Parasitology Foundations of Infectious Diseases

Independent Research Project: Regulation and stabilisation of the *she* pathogenicity genetic element in *Shigella flexneri*

2004 - 2008

<u>BA</u> Medical & Veterinary Science Tripos (MVST) Corpus Christi College, University of Cambridge, UK

Anatomy Embryology and Developmental Biology

Pharmacology Pathology

Biochemistry Pharmacokinetics and Pharmacodynamics
Physiology Biomedical Statistics and Epidemiology

Independent Research Tripos: Intracellular Calcium Measurement using Calcium-Sensitive Microelectrodes

2002 - 2004

Diploma International Baccalaureate (IB)

Mara College Banting, Malaysia

<u>Higher Level Subjects</u>: <u>Standard Level Subjects</u>: Mathematics <u>Malay Language and Literature</u>

Biology English Language

Chemistry Business and Management

Extended Essays in Business and Management; and Theory of Knowledge

Work and Practical Experience

2022 - current Office of Medical Education, University of New South Wales, Australia

Course coordinator for Quality Medical Practice in Phase 1 (undergraduate) medicine programme. Involved in inter-campus small-group tutorials, lecturing, and managing well-being of students, (including Port Macquarie, Kensington, and Wagga Wagga students). Delivery of all elements of the medical syllabus, including anatomy, physiology, biochemistry, pharmacology, pathology, epidemiology, and medical statistics, amongst others in a scenario-based structure. Involved in course design and re-design of various elements of all phases of medical programme. Active

participation in teaching of medical ethics and professionalism components of clinical medicine. Facilitated student-organised journal club.

2021 – 2022 Port Macquarie Rural Clinical School, University of New South Wales, Australia

Lecturer for Phase 1 (undergraduate) medicine programme. Involved in inter-campus small-group tutorials, lecturing, and managing well-being of students. Tutoring of clinical students in small groups. Delivery of all elements of the medical syllabus, including anatomy, physiology, biochemistry, pharmacology, pathology, epidemiology, and medical statistics, amongst others in a scenario-based structure. Facilitated student-organised journal club.

2019 – 2021 Lowy Cancer Research Centre, University of New South Wales, Australia Post-doctoral research fellow in genomics of ovarian cancer. Whole genome, exome, and targeted sequencing (germline and somatic) of individuals with ovarian cancer. Large dataset analysis using genomics, bioinformatics, and statistics tools of cohorts up to several thousand participants. Involvement in development of custom scripts and pipelines for genomic analysis in collaboration with the University of Cambridge, UWA, UNSW, and the Pawsey data centre. Teaching courses (Personalised Medicine, GENM0295) and supervision of PhD students as listed in teaching portfolio.

2016 – 2018 Centre for Genetic Origins of Health and Disease (GOHaD), Australia University of Western Australia and Curtin University, Australia

Post-doctoral research in human genomics and inheritable complex diseases. Whole genome, exome, and bisulfite sequencing analysis of multiplex families and unrelated individuals with relationship to cardiovascular disease and preeclampsia. Metagenomic analysis on intestinal, liver, and upper-respiratory tract microbiomes in relation to non-alcoholic fatty liver disease (NAFLD), dietary intake, immune response, asthma and allergies, amongst various studied phenotypes. Additionally, involvement in teaching; lecturing on sequencing technologies, whole genome sequencing, exome and bisulfite sequencing, and microbiome analysis for Genetic Epidemiology at UWA, as well as supervising PhD students as listed in teaching portfolio.

2010 – 2018 University of Western Australia, Perth, Australia

Lecturing for Microbiology unit at UWA, Australia. Lecturing and laboratory teaching for Microbiology unit at PSB Academy, Singapore. Tutoring and demonstrating for Master of Infectious Disease course, Podiatric Medicine and undergraduate Medicine for the subjects of Molecular Biochemistry, and Immunology within the School of Pathology and Laboratory Medicine. Tutoring and demonstrating for undergraduate Chemistry and Organic Chemistry courses at the School of Chemistry and Biochemistry. Responsibilities included preparing and presenting lectures, preparing and supervising laboratory sessions, as well as marking and evaluating student progress in the courses.

Research

2019 University of New South Wales (post-doctorate)

Post-doctorate in genomics of ovarian cancer, particularly pertaining to High-Grade Serous Ovarian Cancer (HGSOC), but also including non-HGSOC. Involvement in laboratory experimentation and bioinformatics analysis of deep and shallow whole genome sequencing, exome sequencing, targeted sequencing, and gene expression profiling. Use of custom pipelines and scripts developed in collaboration with the University of Cambridge and the Broad Institute. Extensive use of massively paralleled computational processes on the UNSW Katana system, as well as the National Computing Infrastructure High-Performance Computing system, Raijin. Software used similar to listed below, under Curtin University post-doctorate position, with extensive use of scripting in Perl, Python, and R. Further statistical analysis using SPSS.

Currently involved in production and submission of articles regarding whole genome, exome, and targeted sequencing in ovarian cancer.

2016 Curtin University (post-doctorate)

Post-doctorate in human genomics of complex diseases, particularly pre-eclampsia and cardiovascular disease. Involved in whole genome sequencing, exome sequencing, and bisulfite sequencing procedures and data analysis. Utilisation of publicly available bioinformatics software, including GATK, PLINK, Solar, Annovar, samtools, picard, bismark, BSmooth, CHAMP, and RnBeads.

Additionally, metagenomics analysis of bacterial whole-genome, as well as 16S sequencing using Illumina and 454 reads. Software used includes Qiime, RAST, Micca, and R modules, such as Phyloseq and ggplot. Script-writing for massively paralleled computational jobs on a Cray system (Magnus and Zeus at the PAWSEY centre, Western Australia) using a SLURM allocation method.

2015 University of Western Australia, Perth, Australia (PhD)

PhD on bacteriophages of *Moraxella catarrhalis*; genomic investigation of novel bacteriophages in *M. catarrhalis*, as well genomic and epidemiological analyses of clinical and commensal bacterial strains under supervision of Prof. Barbara Chang and A/Prof. Charlene Kahler.

During this period, learned basic and practical bioinformatics, UNIX programming in bash, scripting with Python, Perl, Bash, C++, R, and the use of publicly available scripts in a variety of languages. Additionally, genomic analyses using various bioinformatics softwares, as well as data analysis and visual representation with bioinformatics and statistics tools. Lab techniques included genomic sequencing (both bacterial and viral, using Illumina methods), DNA extraction and purification, advanced molecular microbiology methods, confocal and epifluorescence microscopy, various bacteriology methods, MALDI-TOF spectrometry, spectrophotometry, genomic annotation, (pro)phage identification and annotation, CRISPR identification.

Presented data at Combined Biological Science Meeting (CBSM) 2013 in Perth, Australia; Australian Society for Microbiology 2014 in Melbourne, Australia; Molecular Genetics of Bacteria and Phages Meeting 2015 in Madison, Wisconsin, U.S.A; and CBSM 2017 in Perth, Australia.

2010 University of Western Australia, Perth, Australia (Masters of Infectious Disease) Research project of Masters of Infectious Diseases; investigation of the mechanisms of regulation of the *she* PAI pathogenicity genetic element in *Shigella flexneri* and its survival in environment by the production of a toxin/antitoxin system; under supervision of Prof. Harry Sakellaris. Performed in conjunction with the School of Biomedical, Biomolecular, & Chemical Sciences, UWA and PathWest Laboratories.

2007 Corpus Christi College, the University of Cambridge, UK (MVST Tripos)

Tripos (research, Honours equivalent) year at the University of Cambridge; measurement of intracellular Calcium levels using Ca²⁺-sensitive microelectrodes in Physiology Department, under supervision of Prof. Roger Thomas.

2002 Mara College Banting, Malaysia

Extended Essay in Biology; measuring antibacterial and antifungal properties of ginger extracts. Worked with fractional distillation and gas chromatography techniques at Malaysian National University (UKM), National University of Malaysia (UM). Also worked in collaboration with Immunology Department at National Heart Institute (IJN), Malaysia.

Awards and Achievements

2014: Recipient of Becton, Dickinson & Co. Student Travel award, in conjunction with the Australian Society for Microbiology.

2004-2016: Awardee of national education scholarship from government of Malaysia (MARA), and International Postgraduate Research Scholarship (IPRS & SIRF) from Australian government.

2004: Smyth scholarship for academic excellence from Corpus Christi College, Cambridge.

2001: Champion of National Science Quiz, gaining opportunity of attending Nobel lectures and award-giving ceremonies in Chemistry, Physics and Physiology in Denmark and Sweden.

1997-2003: Award-holder for various Physics, Chemistry and Biology competitions and prizes at state and national levels (e.g. International Physics Olympiad, and International Chemistry Olympiad). Honorary mention in National and International Mathematics Olympiad (2000 – 2004) representing colleges at state and national level.

Publications

Ariff A, Song Y, Aguilar R, Nhabomba A, Manaca MN, Khoo K, Wiertsma S, Bassat Q, Barbosa A, Quinto L, Laing I, Guinovart C, Alonso PL, Dobano C, LeSouef P, Zhang G (2023). "Genetic variants in *ICAM1* and related immune pathway genes are associated the susceptibility of clinical malaria in young African children." *Malaria Journal* [In submission]

Cadby G, Giles C, Melton PE, Huynh K, Mellett NA, Duong T, Nguyen A, Cinel M, Smith A, Olshansky G, Wang T, Brozynska M, Inouye M, McCarthy NS, **Ariff A**, Hung J, Hui J, Beilby J, Dubé MP, Watts GF, Shah S, Wray NR, Lim WLF, Chatterjee P, Martins I, Laws SM, Porter T, Vacher M, Bush AI, Rowe CC, Villemagne VL, Ames D, Masters CL, Taddei K, Arnold M, Kastenmüller G, Nho K, Saykin AJ, Han X, Kaddurah-Daouk R, Martins RN, Blangero J, Meikle PJ, Moses EK, (2022). "Comprehensive genetic analysis of the human lipidome identifies loci associated with lipid homeostasis with links to coronary artery disease." *Nature Communications* 13(1):3124.

Lee KH, Guo J, Song Y, **Ariff A**, O'Sullivan M, Hales B, Mullins BJ, Zhang G (2021). "Dysfunctional Gut Microbiome Networks in Childhood IgE-Mediated Food Allergy." *International Journal of Molecular Sciences*. 22(4).

Pavanello M, Chan IHY, **Ariff A**, Pharoah PDP, Gayther SA, Ramus SJ (2020). "Rare germline genetic variants and the risks of epithelial ovarian cancer." *Cancers.* 12:3046.

Adams LA, Wang Z, Liddle C, Melton PE, **Ariff A**, Chandraratna H, Tan J, Ching H, Coulter S, de Boer B, Christophersen CT, O'Sullivan TA, Morrison M, Jeffrey GP (2020). "Bile acids associate with specific gut microbiota, low-level alcohol consumption and liver fibrosis in patients with non-alcoholic fatty liver disease." *Liver International*. 40(6):1356-1365.

Ariff A, Melton PE, Brennecke SP, Moses EK (2019). "Analysis of the epigenome in multiplex preeclampsia families identifies *SORD*, *DGKI* and *ICA1* as novel candidate risk genes." *Frontiers in Genetics*. 10(227).

Guo J, Lv Q, **Ariff A,** Zhang X, Peacock CS, Song Y, Wen X, Saiganesh A, Melton PE, Dykes GA, Moses EK, Le Souëf PN, Lu F, Zhang G (2019). "Western oropharyngeal and gut microbial profiles are associated with allergic conditions in Chinese immigrant children." *World Allergy Organization Journal* 12(8):100051.

Melton PE, Johnson M, Gokhale-Agashe D, Rea A, **Ariff A**, Cadby G, Peralta J, McNab T, Allcock R, Abraham L, Blangero J, Brennecke S, Moses E (2019). "Whole-exome sequencing in multiplex preeclampsia families identifies novel candidate susceptibility genes." *Journal of Hypertension*. 37 (5):997–1011.

Roslan SB and **Ariff A** (2019). "Layering of History in Malaysian Modern Architecture through Analytical Diagramming." *IOP Conference Series: Materials Science and* Engineering 636:012011.

Wang Z, Properzi C, Liddle C, Melton PE, **Ariff A**, O'Sullivan T, Sherriff J, Coulter S, Christophersen C, Morrison M (2018). "Bile Acids, Hepatic Steatosis and Gut Microbiome in Patients Undergoing Dietary Intervention for Non-Alcoholic Fatty Liver Disease." *Hepatology*. 68:972A-972A

Blakeway L, Tan A, Lappan R, **Ariff A**, Pickering J, Peacock C, Blyth C, Kahler CM, Chang BJ, Lehmann D, Kirkham L, Murphy T, Jennings M, Bakaletz L, Atack J, Peak I, Sieb K (2018). "*Moraxella catarrhalis* Restriction-Modification Systems are Associated with Phylogenetic Lineage and Disease." *Genome Biology and Evolution*. 10 (11):2932–2946.

Ariff A, Kahler CM, Wise MJ, Tay ACY, Peters F, Perkins, TT, Chang BJ (2015). "Novel *Moraxella catarrhalis* Prophages Display Hyperconserved Non-Structural Genes Despite Their Genomic Diversity." *BMC Genomics* 16:860.

Presentations

Pavanello M, Dicks E, Song H, **Ariff A**, Bolithon A, Intermaggio MP, Pinese M, Moysich K, Odunsi KO, Goode E, Bowtell DD, Fasching P, Doherty JA, Modugno F, Kjær SK, Webb PM, Wu A, deFazio A, Ovarian Cancer Association Consortium, James P, Subramanian D, Campbell I, Gayther SA, Pharoah PDP, Ramus SJ (2019). "Identification of two new candidate susceptibility genes for non-high-grade serous ovarian cancer." 47th Annual Tow Research Awards Day; 2019 Nov 29; Edmund Blacket Functions Room, Prince of Wales Hospital, Sydney, Australia.

Pavanello M, **Ariff A**, Dicks E, Song H, Bolithon A, Intermaggio MP, Pinese M, Moysich K, Odunsi KO, Goode E, Bowtell DD, Fasching P, Doherty JA, Modugno F, Kjær SK, Webb PM, Wu A, DeFazio A, Ovarian Cancer Association Consortium, James P, Subramanian D, Campbell I, Gayther SA, Pharoah PDP, Ramus SJ (2019). "Rare variants associated with susceptibility to non-high-grade serous ovarian cancer." 14th GeneMappers Conference; 2019 Nov 20-22; Sydney, New South Wales, Australia.

Pavanello M, Dicks E, Song H, **Ariff A**, Bolithon A, Intermaggio MP, Pinese M, Moysich K, Odunsi KO, Goode E, Bowtell DD, Fasching P, Doherty JA, Modugno F, Kjær SK, Webb PM, Wu A, deFazio A, Ovarian Cancer Association Consortium, James P, Subramanian D, Campbell I, Gayther SA, Pharoah PDP, Ramus SJ (2019). "Germline mutations in new susceptibility genes for non-high-grade serous ovarian cancer." AACR Advances in Ovarian Cancer Research Special Conference; 2019 Sept 13-16; Atlanta, Georgia, USA: *Clinical Cancer Research. Amer Assoc Cancer Research.* 26: 98-99; 2019. Abstract #B37.

Pavanello M, Dicks E, Song H, **Ariff A**, Bolithon A, Intermaggio MP, Pinese M, Moysich K, Odunsi KO, Goode E, Bowtell DD, Fasching P, Doherty JA, Modugno F, Kjær SK, Webb PM, Wu A, deFazio A, Ovarian Cancer Association Consortium, James P, Subramanian D, Campbell I, Gayther SA, Pharoah PDP, Ramus SJ (2019). "Germline high-throughput sequencing identifies IL31RA and ERCC6 as potential new susceptibility genes for non-high-grade serous ovarian cancer." Familial aspects of cancer: Research and Practice; 2019 Aug 27-30; Kingscliffe, New South Wales, Australia. Abstract #41.

Lee KH, Song Y, O'Sullivan M, Metcalfe J, **Ariff A**, Zhao Y, Loh R, Zhang G (2018). "Messenger-RNA Expression Profiles in Food Allergy." Mark Liveris Research Student Seminar, Perth, Australia.

Guo J, Lv Q, **Ariff A**, Peacock C, Zhang X, Wen X, Saiganesh A, Song Y, Melton PE, Dykes G, Moses E, le Souef P, Lu F, Zhang G (2017). "Distinct Microbiome Profiles in Australian Born Chinese Children in Australia and Chinese Children in China." *CSH Asia* Abstract#10. Beijing, China.

Ariff A, Kahler CM, Wise MJ, Tay ACY, Peters F, Perkins, TT, Chang BJ (2014). "Whole Genome Sequencing and Bacteriophages of *Moraxella catarrhalis.*" *Australian Society for Microbiology,* Melbourne, Australia. Abstract #83 p.108.

Ariff A, Kahler CM, Wise MJ, Tay ACY, Peters F, Perkins, TT, Chang BJ (2013). "Whole Genome Sequencing and Bacteriophages of *Moraxella catarrhalis.*" 23rd Annual Combined Biological Sciences Meeting, Perth, Australia. Abstract #6.

Supervised students

PhD: Claire Lee, Jing Guo, Marina Pavanello, Dnyanada Gokhale-Agashe

Masters: William Flentri, Nitin Sekhar, Jemma Joske, Chloe Thompson, Lydia Prempeh

Honors: Clare Tencabel, Judy Xu

Grants

2018: Whole genome bisulfite sequencing of two multiplex families to evaluate methylation patterns associated with pre-eclampsia. Royal Perth Hospital Medical Research Foundation Springboard Grant. \$20,000. (Withdrawn due to moving to UNSW)

2017: Metagenomic sequencing of a Malaysian cohort to identify the influences of geographical location, diet, and socioeconomic status on gut microbiota, inferring its consequences on health. Royal Perth Hospital Medical Research Foundation Annual Grant. \$20,000. (Unsuccessful)

Reviewed Articles

The effect of alcohol-induced methyl donors consumption on the hypomethylation state of cervical cancer, 2023, International Journal of Molecular Sciences, ijms-2117358

Integrated metabolomics and transcriptomics approaches reveal the metabolic and transcript profile changes of non-alcoholic steatohepatitis (NASH) in high fat diet golden hamsters, 2021, BMC Genomics, GICS-D-21-00441 R1

GFICLEE: ultrafast tree-based phylogenetic profile method inferring gene function at the genomic-wide level, 2021, BMC Genomics, GICS-D-21-00141

Genome-wide mutation landscape of SARS-CoV-2, 2020, BMC Genomics, GICS-D-20-01145

Fluorescent Amplification for Next Generation Sequencing (FA-NGS), 2019, BMC Genomics, GICS-D-19-01767

Weighted burden analysis of exome-sequenced late onset Alzheimer's cases and controls provides further evidence for a role for PSEN1 and suggest involvement of the PI3K/Akt/GSK-3 β and WNT signalling pathways, 2019, Annals of Human Genetics, AHG-MS-19-0093.R1

Whole genome resequencing of the Iranian native dogs and wolves to unravel variome during dog domestication, 2019, BMC Genomics, GICS-D-19-01360R1

Lack of defense systems drives Enterococcus easily evolved into lysogens, 2019, BMC Genomics, GICS-D-19-00600R1

Whole genome analysis of the red-crowned crane provides insight into avian longevity, 2019, BMC Genomics, GICS-D-19-00455R1

Genomic analysis of *Leptospira interrogans* serovar Paidjan and Dadas isolates from carrier dogs and comparative genomic analysis to detect genes under positive selection, 2018, BMC Genomics, GICS-D-18-01678

Genome rearrangements and selection in multi-chromosome bacteria *Burkholderia spp*, 2018, BMC Genomics, GICS-D-18-00663R1 and GICS-D-18-00663R2

A comprehensive analysis of seven putative JHBP in the mud crab *Scylla paramamosain*: putative relationship with methyl farnesoate, 2018, BMC Genomics, GICS-D-18-01308

Genome evolution in Burkholderia spp, 2018, BMC Genomics, GICS-D-18-00663

Use of 23S rRNA gene in phylogenetic analysis and taxonomic identification of *Streptomyces*, 2017, BMC Genomics, GICS-D-17-00513

Genomic analyses of the *Chlamydia trachomatis* core genome show an association between chromosomal genome, plasmid type and disease, 2017, BMC Genomics, GICS-D-17-01404

Plasmid diversity and phylogenetic consistency in the Lyme disease agent *Borrelia burgdorferi*, 2017, BMC Genomics, GICS-D-16-01434

Genome evolution in Burkholderia spp., 2016, BMC Genomics, GICS-D-16-00312

Additional Skills and Interests

Languages: Malay (native, A1 in SPM examinations), English (fluent, IELTS band 9 of 9 in reading, listening, writing, speaking and overall categories), German (conversational), Spanish (basic) Japanese (basic), French (basic), Arabic (basic). Keen interest in literature, involved in various writing and poetry events and contests.

Referees

1) Professor Linda Ferrington

Phase 1 Academic Program Coordinator, Port Macquarie Rural Clinical School **Address**

Port Macquarie Base Hospital Wrights Road,

Port Macquarie New South Wales, 2444

Australia

Email

I.ferrington@unsw.edu.au

2) Professor Susan Ramus

Professor of Molecular Oncology, School of Women's and Children's Health Address

Level 2, Lowy Cancer Research Building Cnr High and Botany St, UNSW, Sydney NSW 2052 Australia

Phone

+61 2 9385 1720

Email

s.ramus@unsw.edu.au

3) Professor Eric K Moses

Centre Director, Centre for Genetic Origins of Health and Disease (GOHaD) Address

Menzies Institute for Medical Research College of Health and Medicine University of Tasmania 17 Liverpool Street | Private Bag 23 Hobart, TAS, 7000

Phone

+61 8 9224 0349

Email

eric.moses@utas.edu.au

4) Dr. Phillip Melton

Senior Research Fellow

Address

Menzies Institute for Medical Research College of Health and Medicine University of Tasmania 17 Liverpool Street | Private Bag 23 Hobart, TAS, 7000 Phone

+61 451 077 155

Email

phillip.melton@utas.edu.au