Dave Ting Pong Tang

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Summary

I am currently a post-doctoral researcher at the Telethon Kids Institute, working on the analysis of human genetic variants with respect to rare diseases. The main goal of my current research is to develop integrative approaches towards identifying disease-causing variants. Prior to this position, I was a Marie Curie Early Stage Researcher in the lab of Piero Carninci in RIKEN Yokohama and was primarily working on the analysis of high-throughput transcriptome sequencing data sets. During my time in RIKEN, I developed methods to identify sequencing artefacts and studied various classes of non-coding RNAs. I am passionate about bioinformatics and maintain a technical blog dedicated to bioinformatics. I am an open science and reproducible research advocate. It is my dream that one day my work will have a direct positive impact on the lives of others.

Personal

DOB	1983 March 31st
Birth place	Hong Kong
Nationality	Australian and British National (Overseas)

Education

2010–2015	PhD Candidate, Vrije University, the Netherlands. PhD thesis: High-throughput sequencing and transcriptomics: methods development and data analysis of large expression data sets.
2001–2005	BSc (Honours) in biochemistry and microbiology, University of Queensland, Australia. Honours thesis: Using a supertree approach to detect laterally transferred genes within *Staphylococcus*.

Past Scientific Positions

2010–2015	Research Associate in the lab of Piero Carninci at RIKEN Yokohama, Japan
2008–2010	Research Assistant in the lab of Sean Grimmond at The University of Queensland, Australia
2006–2008	Research Assistant in the lab of Brian Dalrymple at the Commonwealth Scientific and Industrial Research Organisation, Australia
2005–2006	Research Assistant in the lab of Mark Ragan at the University of Queensland, Australia

Research Interests

- Investigating the potential role of genetic variants in relation to biological function and disease.
- Genomics and transcriptomics; in particular the study of non-coding RNAs and transposable elements.
- The application of bioinformatics, in particular machine learning and data mining methods, to biological problems.

Bioinformatic Skills

- Data analysis of high-throughput sequencing data from DNA-seq, RNA-seq, CAGE-seq, sRNA-seq, and ChIP-seq.
- Knowledge and the ability to use various bioinformatic databases, APIs, repositories, and tools.
- The application of biostatistics for the analysis of high-throughput sequencing data.

Computer Skills

- Operating systems: Linux/Unix (RHEL/CentOS and Ubuntu), OS X, and Windows.
- Programming/scripting languages: Perl, R, C, Bash, JavaScript, SQL, and PHP.
- Open science and reproducible research tools: git, cloud computing (AWS), WordPress, Jekyll, Docker, and R Markdown/Markdown.

Honours and Awards

2010	CSIRO Chairman's Medal
2008	CSIRO Partnership Excellence Award

Grants

2016	Cancer Council WA Collaborative Cancer Grant Scheme CIC AUD 45,669
2015	Telethon - Perth Children's Hospital Research Fund "SeqNextGen: Translating NextGen Sequencing for the Diagnosis of Developmental Anomalies and Rare Diseases" AI4 AUD 192,505

Academic and Administrative Experience

2017	Presenter at the Australian Bioinformatics and Computational Biology Society (ABACBS) WA meeting
2015	MODHEP workshop presenter on analysing CAGE data
2013–2014	Organiser of the Chat with Guest sessions at RIKEN CLST DGT
2013–2014	Organiser of the Student Journal Club at RIKEN CLST DGT
2013	Organising committee for the BrainTrain conference
2013	Organiser of the BrainTrain workshop: Identifying regulatory elements in the genome
2012	Session chair for the Patients and Medicines forum
2012	Presenter at the RIKEN OSC bioinformatics course

Editorial Activities

Referee/Reviewer (number of grant proposals/manuscripts reviewed in parenthesis) for: National Health and Medical Research Council (1), BMC Genomics (1), PeerJ (1), and Scientific Reports (2).

Workshop and Course Attendances

2016	AGHA Workshop: reducing morbidity and mortality from genetic disease through screening
2016	Consumer and Community Involvement in Research workshop
2015	UQ winter school in mathematical and computational biology
2014	RIKEN/KI doctoral course: Employing Genome-wide Technologies for Functional Regulation in Development and Disease
2013	AMATA conference ECR workshop
2013	Coursera data analysis course from Johns Hopkins University
2013	BrainTrain courses and workshops
2013	RIKEN/KI doctoral course: Epigenomics: Methods and Applications to Disease and Development
2012	SISSA summer school on dopaminergic neurons
2012	RIKEN/KI doctoral course: Functional Regulation in Development and Disease
2011	UQ winter school in mathematical and computational biology
2011	RIKEN/EBI bioinformatics roadshow

Hobbies and Interests

Sports (especially basketball), cycling, bioinformatics blogging, reading, and movies.

Academic References

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Publications

[1] F. Roudnicky, L. C. Dieterich, C. Poyet, L. Buser, P. Wild, D. Tang, P. Camenzind, C. Hsien Ho, V. I. Otto, and M. Detmar. High expression of insulin receptor on tumor-associated blood vessels in invasive bladder cancer predicts poor overall and progression-free survival. *J. Pathol.*, Mar 2017. URL: http://www.ncbi.nlm.nih.gov/pubmed/28295307.

[2] C. C. Hon, J. A. Ramilowski, J. Harshbarger, N. Bertin, O. J. Rackham, J. Gough, E. Denisenko, S. Schmeier, T. M. Poulsen, J. Severin, M. Lizio, H. Kawaji, T. Kasukawa, M. Itoh, A. M. Burroughs, S. Noma, S. Djebali, T. Alam, Y. A. Medvedeva, A. C. Testa, L. Lipovich, C. W. Yip, I. Abugessaisa, M. Mendez, A. Hasegawa, D. Tang, et al. An atlas of human long non-coding RNAs with accurate 5' ends. *Nature*, Mar 2017. URL: http://www.ncbi.nlm.nih.gov/pubmed/28241135.

[3] M. B. Abraham, D. Li, D. Tang, S. M. O'Connell, F. McKenzie, E. M. Lim, H. Hakonarson, M. A. Levine, and C. S. Choong. Short stature and hypoparathyroidism in a child with

Kenny-Caffey syndrome type 2 due to a novel mutation in FAM111A gene. *Int J Pediatr Endocrinol*, 2017:1, 2017. URL: http://www.ncbi.nlm.nih.gov/pubmed/28138333.

[4] G. Baynam, N. Pachter, F. McKenzie, S. Townshend, J. Slee, C. Kiraly-Borri, A. Vasudevan, A. Hawkins, S. Broley, L. Schofield, H. Verhoef, C. E. Walker, C. Molster, J. M. Blackwell, S. Jamieson, D. Tang, T. Lassmann, K. Mina, J. Beilby, M. Davis, N. Laing, L. Murphy, T. Weeramanthri, H. Dawkins, and J. Goldblatt. The rare and undiagnosed diseases diagnostic service - application of massively parallel sequencing in a state-wide clinical service. *Orphanet J Rare Dis*, 11(1):77, 2016. URL: http://www.ncbi.nlm.nih.gov/pubmed/27287197.

[5] D. Tang, D. Anderson, R. W. Francis, G. Syn, S. E. Jamieson, T. Lassmann, and J. M. Blackwell. Reference genotype and exome data from an Australian Aboriginal population for health-based research. *Sci Data*, 3:160023, 2016. URL: http://www.ncbi.nlm.nih.gov/pubmed/27070114.

[6] Y. Hasegawa, D. Tang, N. Takahashi, Y. Hayashizaki, A. R. Forrest, et al. CCL2 enhances pluripotency of human induced pluripotent stem cells by activating hypoxia related genes. *Sci Rep*, 4:5228, 2014. URL: http://www.ncbi.nlm.nih.gov/pubmed/24957798.

[7] D. T. Tang, C. Plessy, M. Salimullah, A. M. Suzuki, R. Calligaris, S. Gustincich, and P. Carninci. Suppression of artifacts and barcode bias in high-throughput transcriptome analyses utilizing template switching. *Nucleic Acids Res.*, 41(3):e44, Feb 2013. URL: http://www.ncbi.nlm.nih.gov/pubmed/23180801.

[8] A. Saxena, D. Tang, and P. Carninci. piRNAs warrant investigation in Rett Syndrome: an omics perspective. *Dis. Markers*, 33(5):261–275, 2012. URL: http://www.ncbi.nlm.nih.gov/pubmed/22976001.

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This C.V. was prepared in LaTeX and is available at https://github.com/davetang/cv.