Dave Ting Pong Tang

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Summary

I am currently a post-doctoral researcher at the University of Western Australian working on single cell transcriptomics. Prior to this position, I was working on the analysis of whole exome sequencing in patients with rare genetic disorders at the Telethon Kids Institute. During my PhD I was a Marie Curie Early Stage Researcher in the lab of Piero Carninci in RIKEN Yokohama and was working primarily on the analysis of high-throughput transcriptome sequencing data sets. I have also worked as a bioinformatician at the University of Queensland and the Commonwealth Scientific and Industrial Research Organisation.

Education

2010–2015	PhD, 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

2015–2017	Post-doctoral researcher in the lab of Timo Lassmann at the Telethon Kids Institute, Australia
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

Grants

2017	Dissecting the leukaemia microenvironment - Cancer Council WA Collaborative Cancer Grant Scheme CIC AUD 43,395
2016	Targeting four-stranded DNA conformations to modulate gene expression in breast cancer - Cancer Council WA Collaborative Cancer Grant Scheme CIC AUD 47,669
2015	SeqNextGen: Translating NextGen Sequencing for the Diagnosis of Developmental Anomalies and Rare Diseases Telethon - Perth Children's Hospital Research Fund AI4 AUD 192,505

Honours and Awards

2010	CSIRO Chairman's Medal
2008	CSIRO Partnership Excellence Award

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

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

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).

Bioinformatic Skills

- Data analysis of high-throughput sequencing data including DNA-seq, RNA-seq, CAGE-seq, sRNA-seq, ChIP-seq, and scRNA-seq.
- Knowledge and the ability to use various bioinformatic databases, APIs, repositories, and tools.
- Ability to implement bioinformatic pipelines using pipelining tools such as Bpipe and Snakemake.

Computer Skills

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

Hobbies and Interests

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

Academic References

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Publications

[1] K. M. Rothacker, K. L. Ayers, D. Tang, K. Joshi, J. A. van den Bergen, G. Robevska, N. Samnakay, L. Nagarajan, K. Francis, A. H. Sinclair, and C. S. Choong. A novel, homozygous mutation in desert hedgehog (DHH) in a 46, XY patient with dysgenetic testes presenting with primary amenorrhoea: a case report. *Int J Pediatr Endocrinol*, 2018:2, 2018.

[2] 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.

[3] 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.

[4] 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.

[5] 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.

[6] 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.

[7] 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.

[8] 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.

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[16] D. T. Tang, E. A. Glazov, S. M. McWilliam, W. C. Barris, and B. P. Dalrymple. Analysis of the complement and molecular evolution of tRNA genes in cow. *BMC Genomics*, 10:188, 2009. URL: http://www.ncbi.nlm.nih.gov/pubmed/19393063.

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