

## Summary

I am a statistical geneticist practicing genome informatics. My research career is centred on understanding the relationships between phenotypes and genotypes. In particular, I am interested in uncovering genomic variations underlying diseases, populations, and individuals. On a technical level, I am a data analyst with an interest in developing and implementing statistical and bioinformatics approaches for deciphering genomics data.

## Employment History

### Garvan Institute of Medical Research

**2013 - present**

Position: Senior Research Officer

Laboratory: Human Comparative and Prostate Cancer Genomics

Location: Sydney, Australia

Summary: Working to identify large somatic genomic structural variations, underlying prostate cancer progression. To characterised structural and mitochondrial variations underlying human diversity.

### Monsanto Company

**2009 - 2013**

Position: Statistical Genetics Team Lead

Division: Vegetable Seeds Division

Location: Woodland, California, USA

Summary: Facilitated and developed statistical and computational pipelines for processing and analysing genetics and genomics data related to the advancement of plant breeding. Support analyses and interpretations of genetic linkage studies.

### University of California, Davis

**2008 - 2009**

Position: Postdoctoral Fellow

Mentor: Dr. Daniel Kliebenstein

Department: Plant Sciences

Location: Davis, California, USA

Summary: Genome-wide association mapping of the metabolome using naturally occurring *Arabidopsis thaliana* accessions in the context of plant fitness. Gene network reconstruction using GWAS and gene expression data for candidate gene selection.

### Commonwealth Scientific and Industrial Research Organization

**2006 - 2008**

Position: Postdoctoral Fellow

Mentor: Dr. Antonio (Toni) Reverter

Funding: Underpinning Sciences Committee for the Beef CRC

Department: Livestock Industries

Location: Brisbane, Australia

Summary: Genome-wide association studies of agronomic traits. Studied the genetic/genomic structures of cattle breeds, with the aim to elucidate genetic signature(s) underlying phenotypes such as “fitness” and climatic-adaptation.

## Education

### PhD Computational Genetics and Genomics 2003 - 2006

Award: PhD (conferred 11th September 2007)

Dissertation: The influence of genetic variation in gene expression

Supervisor: Prof. Peter Little

Co-supervisor: Prof. Ian Dawes

Institution: University of New South Wales, Sydney, Australia

Funding: Australian Postgraduate Awards

Summary: Studied the effects of genetic variation on gene expression: determined the extent of *in cis* and *in trans* genetic variations on mRNA levels at a transcriptome-wide level, through the development and implementation of existing and novel computational and mathematical methodologies.

### BSc (Honours) 2002

Award: First Class (in a three class system, First Class ≈ 80%-100%)

Dissertation: Genetic variation in gene expression

Supervisor: Prof. Peter Little, Prof. Ian Dawes

Institution: University of New South Wales, Sydney, Australia

Summary: Demonstrated, *in silico*, that genetic variation is as common in transcription factors as in other protein classes using laboratory inbred mouse strains. *I presented this project at the 68th Cold Spring Harbor Symposia on Quantitative Biology.*

### BSc 1999 - 2001

Award: BSc (Biochemistry) [1999-2000]; BSc [2001]

Institution 1: University of Sydney, NSW, Australia

Institution 2: University of Queensland, NSW, Australia

## Publications

### Peer-Reviewed Articles

2016

Kalsbeek AMF, Chan EKF, Grogan J, Petersen DC, Jaratlerdsiri W, Gupta R, Lyons RJ, Haynes A, Kench JG, Stricker PD, Hayes VM. (2016) Mutational load of the mitochondrial genome predicts pathological features and biochemical recurrence in prostate cancer. **Aging**. AOP 5 Oct 2016. 10.18632/aging.101044.

McCrow J, Petersen DC, Louw M, Chan E, Harmeyer K, Vecchiarelli S, Lyons R, Bornman R, Hayes V. (2016) Spectrum of Mitochondrial Genomic Variation and Associated Clinical Presentation of Prostate Cancer in South African Men. **The Prostate**. 76 (4), 349-358.

## 2015

Chan EKF, Hardie RA, Petersen DC, Beeson K, Bornman MSR, Smith AB, Hayes VM. (2015) Revised timeline and distribution of the earliest diverged human maternal lineages in southern Africa. **PLoS ONE**. 10(3): e0121223.

## 2014

Morris A, Heinze A, Chan EKF, Smith AB, Hayes VM. (2014) First Ancient Mitochondrial Genome from a Pre-Pastoralist Southern African. **Genome Biology and Evolution**. 6(10): 2647-2653.

Porto-Neto LR, Reverter A, Prayaga KC, Chan EKF, Johnston DJ, Hawken RJ, Fordyce G, Garcia JF, Sonstegard TS, Bolormaa S, Goddard ME, Burrow HM, Henshall JM, Lehnert SA, Barendse W. (2014) The genetic architecture of climatic adaptation of tropical cattle. **PLoS ONE**. 9(11): e113284.

## 2012

Sandlin K, Prothro J, Heesacker A, Khalilian N, Okashah R, Xiang W, Bachlava E, Caldwell DG, Taylor CA, Seymour DK, White V, Chan E, Tolla G, White C, Safran D, Graham E, Knapp S, McGregor C. (2012) Comparative mapping in watermelon [*Citrullus lanatus* (Thunb.) Matsum. et Nakai]. **Theoretical and Applied Genetics**. 125 (8): 1603-1618.

Ainu Husna AMSS, Flatscher-Bader T, Lehnert SA, Reverter A, Chan EKF, Phillips NJ, McGowan M and D'Occhio MJ. (2012) Gene expression of GnRH, kisspeptin, neuropeptide Y and receptors for estrogen and leptin in the hypothalamus of suckled and weaned beef cows. **Journal of Tropical Agriculture and Food Science**. 40(2): 245-255.

## 2011

Chan EKF, Rowe HC, Corwin JA, Joseph B, Kliebenstein DJ. (2011) Combining genome wide association mapping and transcriptional networks to identify novel genes controlling glucosinolates in *Arabidopsis thaliana*. **PLoS Biology**. 9(8): e1001125.

## 2010

Chan EKF, Rowe HC, Hansen BG, Kliebenstein DJ. (2010) The Complex Genetic Architecture of the Metabolome. **PLoS Genetics** 6(11): e1001198. [*This publication appeared in Nature Research Highlights (2010) Genetics: Metabolic variation's roots. Nature 468: 349.*]

Chan EKF, Rowe HC, Kliebenstein DJ. (2010) Understanding the evolution of defense metabolites in *Arabidopsis thaliana* using genome-wide association mapping. **Genetics** 185: 991 – 1007.

Rowe HC, Walley JW, Corwin J, Chan EK-F, Dehesh K, Kliebenstein DJ. (2010) Deficiencies in Jasmonate-Mediated Plant Defense Reveal Quantitative Variation in Botrytis cinerea Pathogenesis. **PLoS Pathogens** 6(4): e1000861.

Chan EKF, Nagaraj SH, Reverter A. (2010) The evolution of tropical adaptation: Comparing Taurine and Zebu cattle. **Animal Genetics** 41(5): 467 – 477.

## 2009

Cowley MJ, Cotsapas CJ, Williams RBH, Chan EKF, Pulvers JN, Liu MY, Luo OJ, Nott DJ, Little PFR. (2009) Intra- and inter- individual genetic differences in gene expression. **Mammalian Genome** 20(5): 281–295.

Chan EKF and Reverter A. (2009) The combined effect of SNP-marker and phenotype attributes in genomewide association studies. **Animal Genetics** 40(2): 149-156.

## 2008

Reverter A, Chan EKF. (2008) Combining partial correlation and an information theory approach to the reversed-engineering of gene co-expression networks. **Bioinformatics** 24(21):2491-2497. [*The method presented in this paper was implemented into an R package R/PCIT by Nathan S Watson-Haigh.*]

Meadows, JRS., Chan EKF, and Kijas, JW. (2008) Linkage Disequilibrium Compared Between Five Populations of Domestic Sheep. **BMC Genetics** 9:61.

Reverter A, Chan EKF, Lehnert SA, Barris W, McWilliams SM, Dalrymple BP, Barendse W. (2008) Dissection of beef quality phenotypes using a myogenin network-anchored systems biology approach. **Australian Journal of Experimental Agriculture** 48(8):1053-1061.

## 2007

Chan EKF\*, Williams RBH\*, Cowley MJ, Little PFR. (2007) The influence of genetic variation on gene expression. **Genome Research** 17: 1707-1716. doi: 10.1101/gr.6981507 (\* equal first authors)

Nott DJ, Yu Z, Chan E, Cotsapas C, Cowley C, Pulvers J, Williams R and Little P. (2007) Hierarchical Bayes variable selection and microarray experiments. **Journal of Multivariate Analysis** 98 (4): 852-872.

## 2006

Williams RBH, Cotsapas CJ, Cowley MJ, Chan E, Nott CJ, Little PFR. (2006) Microarray normalisation and detection of linkage signal in genetical-genomics experiments. **Nature Genetics** 38: 855-856.

Cotsapas CJ, Williams RBH, Pulvers JN, Nott DJ, Chan EKF, Cowley MJ, Little PFR. (2006) Genetic dissection of gene regulation in multiple mouse tissues. **Mammalian Genome** 17 (6): 490-495

## 2003

Cotsapas CJ, Chan E, Kirk M, Tanaka M, Little PFR. (2003) Genetic Variation and the Control of Transcription. **Cold Spring Harbor Symposia on Quantitative Biology** 68: 109 - 114.

## Patents

### 2015

Garcia-Andres S, Bachlava E, Chan EKF, Joobeur T, King JJ, Kraakman PJ, Krishnamurthy S, Mills JM, de Vries J. (2015) Melon Plants with Improved Disease Tolerance. United States patent 14/880,050. Filed 9 October 2015.

Black L, Chan EKF, Colcol JF, Jones R, Kramer C, Xiang W. (2015) Disease resistance loci in Onion. **United States patent** 20150150155. Published 28 May 2015.

### 2014

Braun CJ III, Chan EKF, Garvey GS, Jones CM, Just BJ, Kniskern JM, Mein JR, Osborn TC, Van Poppel PMJA. (2014) Selection of Mature Fruit Color in Pepper Plants. **WIPO patent** WO/2014/204815. 24 December 2014.

### 2011

Caldwell D, Chan E, De Vries J, Joobeur T, King J, Reina A, Shetty N. (2011) Methods and Compositions for identifying Downy Mildew resistance in cucumber plants. **WIPO patent** WO/2011/050,296. 28 April 2011. [Also published as **United States patent** 8809622 on 19 August 2014]