

# Claire Prowse-Wilkins

cprowsewilkins@ucdavis.edu

---

## Geneticist

---

Research scientist with extensive laboratory and bioinformatics experience. Skilled in novel and high-throughput sequencing. Proficient in analysis of multi-omics data with a focus on epigenetics.

---

## Education

---

Ph.D. (Veterinary and Agricultural Science) 2017-2022 - University of Melbourne

Master of Science (Genetics) 2012-2013 - University of Melbourne

Bachelor of Science (Genetics) 2008-2011 - University of Melbourne

---

## Relevant Research Experience and Employment

---

### **Postdoctoral Scholar-University of California Davis-March 2022-current**

- Laboratory experience
  - Optimising cutting-edge sequencing technologies in chicken samples (eg Cut&Run and long read RNA-sequencing) to identify regulatory variation.
  - Analysing and integrating multi-omics datasets such as Cut&Run, ChIP-seq, ATAC-seq, WGBS, short and long-read RNA-seq, and FAIREseq.
  - Assisting wet-lab scientists in bioinformatics analysis to prepare their manuscripts.

### **Research Scientist-Agriculture Victoria-September 2019-February 2022**

- Developed methods for extraction and sequencing of long read DNA from rumen fluid.
- Developed pipelines for the analysis of long-read DNA to ensure data was high quality.

### **Ph.D Candidate-University of Melbourne-May 2017-February 2022**

Topic: Functional genomics to discover biologically relevant regulatory variation

- Optimised ChIP-seq in multiple bovine tissues, resulting in improved annotation of the bovine genome.
- Developed high-throughput ChIP-seq to assay 100 bovine mammary gland biopsies for 3 histone modifications in a timely manner.
- Developed pipelines for the analysis of large amounts of functional genomic data, successfully identifying Allele Specific Binding in histone modifications and variants associated with epigenetic variation in dairy cows.

### **Research Scientist-Agriculture Victoria-March 2014-March 2017**

- Extracted and sequenced DNA/RNA from milk, blood, tissue and tail hair from 100's-1000's of samples leading to multiple high impact papers and the improvement of genomic selection in Australian dairy cows.

### **Master of Science (Genetics)-University of Melbourne-January 2012-December 2014**

Topic: Genetic Rescue of Endangered Species

- Developed microsatellite markers which were used to assess inbreeding in a captive Dunnart species.
- Participated in routine trapping and sampling of Mountain Pygmy Possums.

### **Tutor and Head Demonstrator-University of Melbourne 2012-2014 and 2017-2019**

- Presented basic genetics to high school and undergraduate biology students in an interesting and engaging manner.

---

### Peer Reviewed Publications

---

Bolormaa, S., Behrendt, R., Knight, M. I., Mason, B. A., **Prowse-Wilkins, C. P.**, Slocombe, L., Vander Jagt, C. J., Hayes, B. J., & Chamberlain, A. J. (2015). Connecting gene expression and phenotype-preliminary results from RNA sequencing of 150 lambs. *Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics (AAABG)*, Lorne, Victoria, Australia, 28-30 September 2015, 489–492.

Bolormaa, S., Chamberlain, A. J., Khansefid, M., Stothard, P., Swan, A. A., Mason, B., **Prowse-Wilkins, C. P.**, Duijvesteijn, N., Moghaddar, N., & van der Werf, J. H. (2019). Accuracy of imputation to whole-genome sequence in sheep. *Genetics Selection Evolution*, 51(1), 1–17.

Chamberlain, A. J., Beatson, P., Mason, B. A., **Prowse-Wilkins, C.P.**, Reich, C. M., Schrooten, C., Hayes, B. J., Tibbits, J., & Hayden, M. (2015). A comparison of genotypes generated by Infinium beadchips and a targeted genotype by sequencing method in cattle. *Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics (AAABG)*, 21, 65–68.

Dorji, J., MacLeod, I. M., Chamberlain, A. J., Vander Jagt, C. J., Ho, P. N., Khansefid, M., Mason, B. A., **Prowse-Wilkins, C. P.**, Marett, L. C., & Wales, W. J. (2021). Mitochondrial protein gene expression and the oxidative phosphorylation pathway associated with feed efficiency and energy balance in dairy cattle. *Journal of Dairy Science*, 104(1), 575–587.

Dorji, J., Vander Jagt, C. J., Garner, J. B., Marett, L. C., Mason, B. A., Reich, C. M., **Prowse-Wilkins, C. P.**, Xiang, R., Ho, P. N., & Pryce, J. (2020). Mitochondrial genome diversity and association of mitochondrial protein gene expression with energy metabolism in dairy cattle. *Journal of Dairy Science*, 103, 12.

**Prowse-Wilkins, C. P.**, Lopdell, T. J., Xiang, R., Vander Jagt, C. J., Littlejohn, M. D., Chamberlain, A. J., & Goddard, M. E. (2022). Genetic variation in histone modifications and gene expression identifies regulatory variants in the mammary gland of cattle. *BMC Genomics*, 23(1), 1–19.

**Prowse-Wilkins, C. P.**, Wang, J., Garner, J. B., Goddard, M. E., & Chamberlain, A. J. (2023). Allele specific binding of histone modifications and a transcription factor does not predict allele specific expression in correlated ChIP-seq peak-exon pairs. *Scientific Reports*, 13(1), 15596.

**Prowse-Wilkins, C. P.**, Wang, J., Goddard, M. E., Xiang, R., & Garner J.B. and Chamberlain A.J. (2021). Narrowing the search space: putative causal variants are enriched in annotated functional regions from 6 bovine tissues. *Proceedings of the 24<sup>th</sup> Conference of the Association for the Advancement of Animal Breeding and Genetics (AAABG)*, 24, 304–307.

**Prowse-Wilkins, C. P.**, Wang, J., Xiang, R., Garner, J. B., Goddard, M. E., & Chamberlain, A. J. (2021). Putative causal variants are enriched in annotated functional regions from six bovine tissues. *Frontiers in Genetics*, 12.

Pryce, J. E., Douglas, P., Reich, C. M., Chamberlain, A. J., Bowman, P. J., Nguyen, T. T. T., Mason, B. A., **Prowse-Wilkins, C. P.**, Nieuwhof, G. J., & Hancock, T. (2016). Reliabilities of Australian Dairy Genomic Breeding Values increase through the addition of genotyped females with excellent genotypes. *Proceedings of the 22<sup>nd</sup> Conference of the Association for the Advancement of Animal Breeding and Genetics (AAABG)*, 22, 133–136.

Wang, M., Chamberlain, A. J., **Prowse-Wilkins, C. P.**, Vander Jagt, C. J., Hancock, T. P., Pryce, J. E., Cocks, B. G., Goddard, M. E., & Hayes, B. J. (2019). Genome-wide profiling of microRNAs and prediction of mRNA targets in 17 bovine tissues. *bioRxiv*, p.574954

Xiang, R., Breen, E. J., **Prowse-Wilkins, C. P.**, Chamberlain, A. J., & Goddard, M. E. (2021). Bayesian genome-wide analysis of cattle traits using variants with functional and evolutionary significance. *Animal Production Science*.

Xiang, R., Hayes, B. J., Vander Jagt, C. J., MacLeod, I. M., Khansefid, M., Bowman, P. J., Yuan, Z., **Prowse-Wilkins, C. P.**, Reich, C. M., & Mason, B. A. (2018). Genome variants associated with RNA splicing variations in bovine are extensively shared between tissues. *BMC Genomics*, 19(1), 1–18.

Xiang, R., Van Den Berg, I., MacLeod, I. M., Hayes, B. J., **Prowse-Wilkins, C. P.**, Wang, M., Bolormaa, S., Liu, Z., Rochfort, S. J., & Reich, C. M. (2019). Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits. *Proceedings of the National Academy of Sciences*, 116(39), 19398–19408.

Yuan, Z., Sunduimijid, B., Xiang, R., Behrendt, R., Knight, M. I., Mason, B. A., Reich, C. M., **Prowse-Wilkins, C. P.**, Vander Jagt, C. J., & Chamberlain, A. J. (2021). Expression quantitative trait loci in sheep liver and muscle contribute to variations in meat traits. *Genetics Selection Evolution*, 53(1), 1–14.