

Craig Anderson

Craig.Anderson@ed.ac.uk

- 2005-2008 BSc Biological Sciences. First Class Hons
The University of Plymouth, UK
- 2008-2012 PhD Molecular Ecology: Mechanistic bases of metal tolerance
Cardiff University, UK. **Awarded: 9 April 2013**
Supervisors: Dr David Spurgeon, Prof Peter Kille
- 2012-2015 OCE Postdoctoral Fellow. Entomological population genetics.
CSIRO, Black Mountain, Australia
Supervisor: Dr Tom Walsh
- 2015-2018 Postdoctoral Researcher. Radioecology
University of Stirling, UK
Supervisor: Prof David Copplestone
- 2018-Present Postdoctoral Fellow. Computational cancer genomics
MRC Human Genetics Unit, University of Edinburgh, UK
Supervisor: Prof Martin Taylor

- Expert in evolutionary biology, cancer genomics and bioinformatics
- Skilled in variant calling, DNA replication and expression analysis, with experience in development of novel methods for analysis of enormous data
- User of Unix, Python and R (Github User: **CraigJAnderson**)
- Extensive toxicant exposure experience of aquatic and terrestrial models
- Multi-generational culturing of various species of field-derived invertebrate lab lines
- Fundamental molecular biology skills, including custom high-throughput sequencing library preparation, DNA/RNA purification and quantitation, PCR, cloning, etc.
- Field work coordination at disused mine sites (UK) and across Chernobyl (Ukraine)

Significance of Key Research Outputs:

Initially in my career, I sought insight into adaptation to toxins in nonmodel organisms, leading to the acquisition of a prestigious postdoctoral fellowship with the CSIRO in Australia. This climaxed in the discovery of hybridisation between moth pest species in Brazil, which has had broad-reaching impact on agriculture across the Americas and was widely covered by international media. Though successful, the research I desired to conduct was only possible via cancer genomics. I now employ novel computational methods to understand how patterns of mutations change during tumourigenesis.

My major discoveries have come about as part of a long-standing collaboration with the Liver Cancer Evolution consortium, where we discovered that DNA damage is inherited, in a process called lesion segregation. I personally discovered that DNA damage is repeatedly used as the template for replication, leading to a previously unrealised source of genetic variation in cancer. This work was used as a bannerhead discovery in my institutes most recent bid for funding: "...discovery of pervasive lesion segregation in cancer is a paradigm shift in our understanding the evolution of tumour genomes and highlights new drivers of tumourigenesis"

Subsequently, I resolved mutagenic variability associated with how DNA damage is tolerated and repaired in a recently published manuscript. A reviewer commented: "Overall, the work significantly advances the field of mutagenesis on a number of fronts, not least methodologically, and is beautifully performed and analysed". I dispelled an assumption that aspects of DNA replication were responsible for the tolerance of DNA damage and also

discovered “collateral mutagenesis” in cancer. To do this, I created analytical pipelines that are distributed online, maximising the impact of my research. This is also true of a another recent article where my coauthors and I discovered that the majority of DNA damage in genes is tolerated.

Selected Publications:

Anderson CJ and 17 others. Strand-resolved mutagenicity of DNA damage and repair. 2024. *Nature* 630: 744.

Nicholson MD, **Anderson CJ**, Odom DT, Aitken SJ & Taylor MS. DNA lesion bypass and the stochastic dynamics of transcription coupled repair. 2024. *PNAS* 121: 20

Aitken SJ, **Anderson CJ** and 27 others. Pervasive lesion segregation shapes cancer genome evolution. 2020. *Nature*, 582: 7815

Anderson CJ*, Oakeshott JG, Tay WT, Gordon KHJ, Zwick A and Walsh TK. Hybridisation and gene flow in the mega-pest lineage of moth, *Helicoverpa*. 2018. *PNAS*, 115: 19

Anderson CJ*, Cunha L, Sechi P, Kille P and Spurgeon D. Genetic Variation in Populations of the Earthworm, *Lumbricus rubellus*, Across Contaminated Mine Sites. 2017. *BMC Genetics*, 18: 97.

Pearce S and 59 others. Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive *Helicoverpa* pest species. 2017. *BMC Biology*, 15: 63.

Anderson CJ*, Tay WT, McGaughran A, Gordon K and Walsh T. 2016. Global population structure of the pest moth, *Helicoverpa armigera*. *Molecular Ecology*, 25: 5296-5311.

Liebeke M, Garcia-Perez I, **Anderson CJ** and 7 others. Earthworms produce phytochelatin in response to arsenic. *PLOS one*, 8: 11

Anderson CJ, Kille P, Lawlor AJ, Spurgeon DJ. 2013. Life-history effects of arsenic toxicity in clades of the earthworm *Lumbricus rubellus*. *Environmental Pollution* 172: 200-207

***Corresponding author.**

A complete list of my publications is available: <http://bit.ly/3amJwLC>

Grants:

- 2010 A novel eRAD approach for transcriptomic quantification to inform a systems toxicology model of arsenic tolerance in the earthworm *L. rubellus*. NBAF small grants round, rated alpha 5. £7,790. Co-I.
- 2010 Mechanistic bases of metal (copper) and metalloid (arsenic) tolerance: linking phenotype to genotype. NERC small grants round, rated high alpha 4. £6,000. Co-I.

Selected Posters and Presentations:

- 2024 Weatherall Institute of Molecular Medicine, University of Oxford, UK - Invited seminar
- 2024 Wellcome Sanger Institute, UK - Invited seminar
- 2023 Gordon Research Conference: Mammalian DNA Repair. **Craig Anderson**, The Liver Cancer Evolution Consortium and Martin Taylor. Strand-resolved mutagenicity of DNA damage and repair using lesion segregation. Ventura, USA. Poster.
- 2013 International Environmental ‘Omics synthesis conference. **Anderson CJ**, Walsh T. Contemporary GBS for following and controlling the global pest *Helicoverpa armigera*. Cardiff University, UK. Platform presentation.
- 2012 SETAC World Congress – Environmental OMICs: a global answer to environmental questions. **Anderson CJ**, Bundy JG, Spurgeon DJ and Kille P. Metabolism of and adaptation to arsenic in *Lumbricus rubellus*. Berlin, Germany. Platform presentation.

Training Awards & Awards:

- 2024 CRUK Bridge to Academic Leadership programme, UK
- 2024 Shortlisted for SULSA postdoctoral award, UK
- 2024 CRUK/Wellcome Broadening Horizons Mentoring programme, UK
- 2021 Research Leader- New and Aspiring PIs. Edinburgh, UK
- 2010 Wellcome Trust advanced course: Functional Genomics and Systems Biology, Wellcome Trust Sanger Institute, UK.

Teaching and Leadership:

- 2023 – present Developed and delivered “Critical Evaluation Skills” workshops for first year PhD students, University of Edinburgh, UK
- 2024 Creator and lead organiser of international conference: “Mutations in Time and Space”, Edinburgh, UK

Seed funding from the MRC Human Genetics Unit (£5,000) and the Genetics Society (£3,090), generating £70,000 in attendance fees. See www.mutationmeeting.com.

Supervision:

- Formal supervision of Zicheng Yu (PhD): DNA-embedded ribonucleotides in the genome: Locations, quantities and functions.
- UE06 laboratory assistant Susan Campbell
- Development and supervision of postgraduate and undergraduate student projects.

Professional Engagement:

- Executive Committee member of the Genetics Society (2022-2023)
- Grant reviewer for BBSRC
- Journal reviewer for Nature Communications, Molecular Ecology and Genome Medicine