

Tom R. Booker

RESEARCH INTERESTS	Theoretical and empirical population genetics, biodiversity, evolution, genomics, bioinformatics, statistical analysis
EMPLOYMENT	University of British Columbia , Vancouver, Canada <ul style="list-style-type: none">- Postdoctoral Research Fellow (Sept 2018 - <i>present</i>)- Supervised by Professor Michael Whitlock and Assistant Professor Samuel Yeaman (University of Calgary)
EDUCATION	University of Edinburgh , Edinburgh, Scotland <p>PhD., Evolutionary Genetics, October 2014 - October 2018</p> <ul style="list-style-type: none">- Thesis Title: UNDERSTANDING PATTERNS OF GENETIC DIVERSITY IN THE HOUSE MOUSE GENOME- Supervisors: Professor Peter Keightley and Professor Brian Charlesworth <p>MSc., Evolutionary Genetics, 2013 - 2014 (Distinction)</p> <ul style="list-style-type: none">- Thesis Title: SEARCHING FOR BALANCING SELECTION ON A MIMICRY SUPERGENE IN THE BATESIAN MIMIC <i>Papilio polytes</i>- Supervisors: Professor Deborah Charlesworth and Assistant Professor Rob W. Ness <p>University of Stirling, Stirling, Scotland</p> <p>BSc Hons, Ecology, 2009 - 2013 (First Class)</p> <ul style="list-style-type: none">- Dissertation Title: AN INVESTIGATION INTO THE FITNESS AND DISTRIBUTION OF A NEWLY DISCOVERED ALLOPOLYPLOID SPECIES, <i>Mimulus peregrinus</i>- Supervisor: Dr Mario Vallejo-Marin- Study abroad at Simon Fraser University, Vancouver, Canada. 2011-2012.
PAPERS	<ol style="list-style-type: none">7. Booker, T. R. (<i>In revision</i>) "Inferring parameters of the distribution of fitness effects of new mutations when beneficial mutations are strongly advantageous and rare". Preprint available at: https://www.biorxiv.org/content/10.1101/855411v16. Booker, T. R., S. Yeaman & M. C. Whitlock. (<i>In revision - Evolution Letters</i>). "Global adaptation confounds the search for local adaptation". Preprint available at: https://www.biorxiv.org/content/10.1101/742247v15. Booker, T. R., & Keightley, P. D. (2018). "Understanding the factors that shape patterns of nucleotide diversity in the house mouse genome". <i>Molecular Biology and Evolution</i>, 35(12) 2971-29884. Booker, T. R., Jackson, B. C., & Keightley, P. D. (2017). "Detecting positive selection in the genome". <i>BMC Biology</i>, 15:98.3. Booker, T. R., Ness, R. W., & Keightley, P. D. (2017). "The recombination landscape in wild house mice inferred using population genomic data". <i>Genetics</i>, 207(1) 297-3092. Keightley, P. D., Campos, J. L., Booker, T. R., & Charlesworth, B. (2016). "Inferring the frequency spectrum of derived variants to quantify adaptive molecular evolution in protein-coding genes of <i>Drosophila melanogaster</i>". <i>Genetics</i>, 203(2), 975-984.1. Booker, T., Ness, R. W., & Charlesworth, D. (2015). "Molecular evolution: breakthroughs and mysteries in Batesian mimicry". <i>Current Biology</i>, 25(12), R506-R508.

PAPERS IN
PREPARATION

- **Booker, T. R.**, S. Yeaman & M. C. Whitlock. "Heterogeneous landscapes of F_{ST} under neutrality due to variation in recombination rate".
- **Booker, T. R.**, Jackson, B. Craig, R. Charlesworth, B. & Keightley, P. D. "Patterns of genetic diversity around protein-coding exons and conserved non-coding elements are explained by strong selective sweeps in mice".
- Byers K.A., **Booker T.R.**, Combs M., Munshi-South J., Patrick D.M., Whitlock M.C., Himsworth C.G. 2019. "Deciphering patterns of pathogen prevalence among urban rats in relation to rat relatedness and movement".

ACADEMIC
HONOURS AND
AWARDS

- Registration Award - Society of Molecular Biology and Evolution 2019
- *Runner up* Best student talk at Population Genetics Group 51 2018
- *Runner up* Best student poster at Population Genetics Group 50 2017
- Environment Yes! *Won regional heat - runner up at the national final* Sept 2016
- EASTBIO Doctoral Training Partnership Studentship 2014-2018
- Genetics Society, Sir Kenneth Mather Memorial Prize 2013/2014
- University of Edinburgh, Douglas Falconer Award, best MSc dissertation 2013/2014
- Funding for Undergraduate Summer Project:
Botanic Society of Scotland and the Society of Biology Summer 2012
- *Nominated*, Simon Fraser University Student Conservation Prize May 2012

ACADEMIC
SERVICE

- I have reviewed articles for the following journals:
Molecular Biology and Evolution, Genome Biology and Evolution, Ecology and Evolution
- 2019 - Poster Judge BIOL 310 Animal Behaviour - UBC
- 2019 - *Ongoing* Co-organiser of the Vancouver Evolution Group (VEG)
- 2019 I took part in a mentor scheme for undergraduate students attending SMBE 2019 in Manchester, UK
- 2017 I started and organised a journal club on classic population genetic papers at the University of Edinburgh in 2017

TEACHING

Mentoring

C. Atkinson - Undergraduate project co-supervisor- *Undergraduate student at UBC*

K.A. Byers - Bioinformatics/genomics mentor - *PhD student at UBC*

S-A. Xerri - Master's project co-supervisor - *Now PhD student at the Max Planck Institute*

C. Barata - Master's project co-supervisor- *Now PhD student at the University of St. Andrews*

B. Lecher - Honour's project co-supervisor- *Now Pre Doctoral Fellow at the European Bioinformatics Institute*

Course Instruction

Statistics and Data Analysis, MSc course 2014-2017
Demonstrated in computer practical sessions, ran tutorials on probability theory and statistical analysis and marked term papers

Population and Quantitative Genetics, MSc course <i>Ran tutorial sessions on population genetic theory</i>	2015-2017
Ecology and Evolutionary Genetics, BSc course <i>Demonstrated in computer practical sessions on evolutionary biology</i>	2014-2015

SELECTED PRESENTATIONS	January 2020 - American Society of Naturalists 2020, Asilomar, USA (Oral Presentation) <i>Global adaptation confounds the search for local adaptation</i>
	October 2019 - EcoEvo Retreat, Squamish, Canada (Oral Presentation) <i>Leveraging linkage information in studies of local adaptation</i>
	September 2019 - BLISS, UBC, Vancouver, Canada (Oral Presentation) <i>Global adaptation confounds the search for local adaptation</i>
	July 2019 - SMBE, Manchester, UK (Poster) <i>Patterns of genetic diversity around protein-coding exons and conserved non-coding elements are explained by strong selective sweeps in mice</i>
	September 2018 - EcoEvo Retreat, Squamish, Canada (Oral Presentation) <i>Estimating the parameters of selective sweeps from patterns of diversity around functional elements in wild house mice <i>Mus musculus castaneus</i></i>
	January 2018 - Population Genetics Group 51, Bristol, UK (Oral Presentation) <i>Estimating the parameters of selective sweeps from patterns of diversity around functional elements in wild house mice <i>Mus musculus castaneus</i></i>
	August 2017 - ESEB 2017, Groningen, Netherlands (Poster) <i>Selective sweeps and background selection in the genome of wild house mice, <i>Mus musculus castaneus</i></i>
	January 2017 - Population Genetics Group 50, 2017, Cambridge, UK (Poster) <i>Selective sweeps and background selection in the genome of wild house mice, <i>Mus musculus castaneus</i></i>
	July 2016 - SMBE, Gold Coast, Australia (Oral Presentation) <i>Hill-Robertson Interference in wild mice, <i>Mus musculus castaneus</i></i>
	December 2015 - Population Genetics Group 49, Edinburgh, UK (Oral Presentation - Invited) <i>Hill-Robertson Interference in wild mice, <i>Mus musculus castaneus</i></i>
	July 2015 - SMBE, 2015, Vienna, Austria (Poster) <i>Selective sweeps and background selection in the genome of wild house mice, <i>Mus musculus castaneus</i></i>
	May 2015 - Quantitative Genomics, 2015, London, UK (Oral Presentation) <i>Simulating genome evolution in the house mouse: understanding the contribution of Hill-Robertson interference to patterns of genetic diversity</i>

References

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