

# Simon Henry Martin

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May 2023

## Career and Education

<b>2019 –</b>	Royal Society University Research Fellow, University of Edinburgh
<b>2018</b>	Post-doctoral Research Associate, University of Cambridge
<b>2014 – 2018</b>	Research Fellow, St John's College, University of Cambridge
<b>2015</b>	PhD, University of Cambridge
<b>2010</b>	MSc Genetics, University of Pretoria
<b>2007</b>	BSc (Hon.) Genetics, University of Pretoria

## Teaching

### Lectures

<b>2022 -</b>	4 <sup>th</sup> Year Human Evolutionary Genomics (3 flipped lectures)
<b>2022 -</b>	MSc QGGA, Population Genomic Analysis (1 lecture + tutorial)
<b>2020 -</b>	3 <sup>rd</sup> Year Ecological and Evolutionary Genetics (2 flipped lectures + essay tutorial)
<b>2020 - 2022</b>	MSc Bioinformatics, Next Generation Genomics (2 lectures)

## Research Grants and Awards

### Grants

<b>2022</b>	NERC Exploring the Frontiers of Environmental Sciences (PI) £99,965, 2023
<b>2021</b>	Royal Society Research Fellows Enhanced Research Expenses (PI) £185,540, 2022-2023
<b>2018</b>	Royal Society University Research Fellowship (PI) £598,740, 2019-2023
<b>2018</b>	Royal Society Research Fellows Enhancement Award (PI) £217,200, 2019-2021
<b>2017</b>	National Geographic Society Research Grant (Col) \$29,125, 2017-2018

### Awards

<b>2014</b>	Sir Kenneth Mather Memorial Prize, Genetics Society
<b>2014</b>	William Bateson Research Fellowship, St John's College, Cambridge, 2014-2017
<b>2011</b>	Cambridge Commonwealth Fund studentship, 2011-2013

## Publications in peer-reviewed journals

1. Mackintosh A, Vila R, Laetsch DR, Hayward A, **Martin SH\***, Lohse K\*. 2023. Chromosome fissions and fusions act as barriers to gene flow between *Brenthis fritillaria* butterflies. **Molecular Biology and Evolution** In Press
2. Nouhaud P, **Martin SH**, Portinha B, Sousa VC., Kulmuni J. 2022. Rapid and predictable genome evolution across three hybrid ant populations. **PLOS Biology** 20(12) e3001914
3. Montejo-Kovacevich G, Meier JI, Bacquet CN, Warren IA, Chan YF, Kucka M, Salazar C, Rueda-MN, Montgomery SH, McMillan WO, Kozak, KM, Nadeau NJ, **Martin SH**, Jiggins CD. 2022. Repeated genetic adaptation to altitude in two tropical butterflies. **Nature Communications**, 13(1), pp.1-16.
4. Liu W, Smith DA, Raina G, Stanforth R, Ng'Iru I, Ileri P, Martins DJ, Gordon IJ, **Martin SH**. 2022. Global biogeography of warning coloration in the butterfly *Danaus chrysippus*. **Biology Letters**, 18(6), p.20210639.
5. \*Kim KW, De-Kayne R, Gordon IJ, Omufwoko KS, Martins DJ, **Martin SH**. 2022. Stepwise evolution of a butterfly supergene via duplication and inversion. **Philosophical Transactions of the Royal Society B** 377 (1856), 20210207
6. Ndatimana G, Kayitete L, **Martin SH**, Smith DA, Hagenimana T, Nkundimana A, Muhayimana S, Antony J, Sibomana C, Uwizelimana JDD, Omufwoko KS, Nyirakanani C, Gordon IJ. 2022. Morph frequencies, sex ratios and infections in *Danaus chrysippus* populations in Rwanda. **African Journal of Ecology** 60(3) 633-640.
7. Singh KS, De-Kayne R, Omufwoko KS, Martins DJ, Bass C, Ffrench-Constant R, **Martin SH**. 2022. Genome assembly of *Danaus chrysippus* and comparison with the Monarch *Danaus plexippus*. **G3**, 12(3), p.jkab449
8. **Martin SH** and Amos W. 2021. Signatures of introgression across the allele frequency spectrum. **Molecular Biology and Evolution** 38(2): 716-726
9. Cicconardi F, Lewis JJ, **Martin SH**, Reed RD, Danko CG, Montgomery SH. 2021. The effects of chromosome fusions on genetic diversity and evolutionary turnover of functional loci consistently depends on chromosome size **Molecular Biology and Evolution** 38(10): 4449-4462.
10. Lewis JJ, Cicconardi F, **Martin SH**, Reed RD, Danko CG, Montgomery SH. 2021. The *Dryas iulia* genome supports multiple gains of a W chromosome from a B chromosome in butterflies. **Genome Biology and Evolution** 13 (7), evab128.
11. Smith DA, Bennie JJ, Gordon IJ, **Martin SH**, Ileri P, Omufwoko KS, Ffrench-Constant RH. 2021, Hybrid effects in field populations of the African monarch butterfly, *Danaus chrysippus* (L.) (Lepidoptera: Nymphalidae). *Biological Journal of the Linnean Society* 133 (3): 671-684
12. Morris J, Hanly JJ, **Martin SH**, Van Belleghem SM, Salazar C, Jiggins CD, Dasmahapatra KK. 2020. Deep Convergence, Shared Ancestry, and Evolutionary Novelty in the Genetic Architecture of *Heliconius* Mimicry. **Genetics** 216: 765-80
13. Satokangas I, **Martin SH**, Helanterä H, Saramäki J and Kulmuni J. 2020. Multi-locus interactions and the build-up of reproductive isolation. **Philosophical Transactions of the Royal Society B** 375: 20190543
14. \***Martin SH**, Singh KS, Gordon IJ, Omufwoko KS, Collins S, Warren IA, Munby H, Brattström O, Traut W, Martins DJ, Smith DAS, Jiggins CD, Bass C, Ffrench-Constant RH. 2020. Whole-chromosome hitchhiking driven by a male-killing endosymbiont. **PLOS Biology** 18 (2), e3000610
15. Dierickx E, Sin S, van Veelen P, Brooke M de L, Liu Y, Edwards S, **Martin SH**. 2020. Neo-sex chromosomes and demography shape genetic diversity in the Critically Endangered Raso lark. **Proceedings of the Royal Society B** 287 (1922): 20192613

16. Lawal RA, **Martin SH**, Vanmechelen K, Vereijken, A, Silva P, Al-Atiyat RM, Aljumaah RS, Mwacharo JM, Wu DD, Zhang YP, Hocking PM, Smith J, Wragg D, Hanotte O. 2020. The wild species genome ancestry of domestic chickens. **BMC Biology** 18: 13
17. Montejo-Kovacevich G, **Martin SH**, Meier JI, Bacquet CN, Monllor M, Jiggins CD, Nadeau NJ. 2020. Microclimate buffering and thermal tolerance across elevations in a tropical butterfly. **Journal of Experimental Biology** 223: jeb220426.
18. Moest M, Van Belleghem SM, James JE, Salazar C, **Martin SH**, Barker SL, Moreira GRP, Mérot C, Joron M, Nadeau NJ, Steiner FM, Jiggins CD. 2020. Selective sweeps on novel and introgressed variation shape mimicry loci in a butterfly adaptive radiation. **PLOS Biology** 18 (2), e3000597
19. Yan Z, **Martin SH**, Gotzek D, Arsenault SV, Duchen P, Helleu Q, Riba-Grognuz O, Hunt BG, Salamin N, Shoemaker D, Ross KG, Keller L. 2020. Evolution of a supergene that regulates a trans-species social polymorphism. **Nature Ecology & Evolution** 4(2): 240–249
20. Arias M, Davey JW, Martin SH, Jiggins C, Nadeau N, Joron M, Llaurens V. 2020. How do predators generalize warning signals in simple and complex prey communities? Insights from a videogame. **Proceedings of the Royal Society B** 287(1921): 20200014
21. Marburger S, Monnahan P, Seear PJ, **Martin SH**, Koch J, Paajanen P, Bohutínská M, Higgins JD, Schmickl R and Yant L. 2019. Interspecific introgression mediates adaptation to whole genome duplication. **Nature Communications** (10): 5218
22. Smith DAS, Traut W, **Martin SH**, Ileri P, Omufwoko KS, Gordon IJ. 2019. Neo Sex Chromosomes, Colour Polymorphism and Male-Killing in the African Queen Butterfly, *Danaus chrysippus* (L.). **Insects** 10 (9): 291
23. \***Martin SH**, Davey JW, Salazar C, Jiggins CD. 2019. Recombination rate variation shapes barriers to introgression across butterfly genomes. **PloS Biology** 17:e2006288
24. Merrill RM, Rastas P, **Martin SH**, Melo MC, Barker S, Davey J, McMillan WO, Jiggins CD. 2019. Genetic dissection of assortative mating behavior. **PloS Biology** 17:e2005902
25. Pinharanda A, Rousselle M, **Martin SH**, Hanly JJ, Davey JW, Kumar S, Galtier N, Jiggins CD. 2019. Sexually dimorphic gene expression and transcriptome evolution provides mixed evidence for a fast-Z effect in *Heliconius*. **Journal of Evolutionary Biology** 32:194–204
26. Van Belleghem SM, Baquero M, Papa R, Salazar C, McMillan WO, Counterman BA, Jiggins CD, **Martin SH**. 2018. Patterns of Z chromosome divergence among *Heliconius* species highlight the importance of historical demography. **Molecular Ecology** 27(19) 3852-3872
27. **Martin SH**, Jiggins CD. 2017. Interpreting the genomic landscape of introgression. **Current Opinion in Genetics & Development** 47: 69-74
28. Enciso-Romero J, Pardo-Díaz C, **Martin SH**, Arias C, Linares M, McMillan WO, Jiggins CD, Salazar C. 2017. Evolution of novel mimicry rings facilitated by adaptive introgression in tropical butterflies. **Molecular Ecology** 26(19) 5160-5172
29. Jiggins CD, **Martin SH**. 2017. Glittering gold and the quest for Isla de Muerta. **Journal of Evolutionary Biology** 30(8):1509–1511
30. Davey JW, Barker SL, Rastas PM, Pinharanda A, **Martin SH**, Durbin R, Merrill RM, Jiggins CD. 2017. No evidence for maintenance of a sympatric *Heliconius* species barrier by chromosomal inversions. **Evolution Letters** 1(3):138–154
31. \***Martin SH**, Van Belleghem SM. 2017. Exploring evolutionary relationships across the genome using topology weighting. **Genetics** 206(May):429–428
32. Van Belleghem SM, Rastas P, Papanicolaou A, **Martin SH**, Arias CF, Supple MA, Hanly JJ, Mallet J, Lewis JJ, Hines HM, Ruiz M, Salazar C, Linares M, Moreira GRP, Jiggins CD, Counterman BA,

- McMillan WO, Papa R. 2017. Complex modular architecture around a simple toolkit of wing pattern genes. **Nature Ecology and Evolution** 1(3):52
33. Pinharanda A, Martin SH, Barker SL, Davey JW, Jiggins CD. 2017. The comparative landscape of duplications in *Heliconius melpomene* and *Heliconius cydno*. **Heredity** 118(1):78–87
34. **Martin SH**, Moest M, Palmer WJ, Salazar C, McMillan WO, Jiggins FM, Jiggins CD. 2016. Natural selection and genetic diversity in the butterfly *Heliconius melpomene*. **Genetics** 203(May):525–541
35. Lohse K, Chmelik M, **Martin SH**, Barton NH. 2016. Efficient strategies for calculating blockwise likelihoods under the coalescent. **Genetics** 202(2):775–86
36. Wallbank RWR, Baxter SW, Pardo-Diaz C, Hanly JJ, **Martin SH**, Mallet J, Dasmahapatra KK, Salazar C, Joron M, Nadeau N, McMillan WO, Jiggins CD. 2016. Evolutionary novelty in a butterfly wing pattern through enhancer shuffling. **PLOS Biology** 14(1):1–16
37. Merrill RM, Dasmahapatra KK, Davey JW, Dell'Aglio DD, Hanly JJ, Huber B, Jiggins CD, Joron M, Kozak KM, Llaurens V, **Martin SH**, Montgomery SH, Morris J, Nadeau NJ, Pinharanda a L, Rosser N, Thompson MJ, Vanjari S, Wallbank RWR, Yu Q. 2015. The diversification of *Heliconius* butterflies: What have we learned in 150 years? **Journal of Evolutionary Biology** 28(8):1417–38
38. \***Martin SH**, Davey JW, Jiggins CD. 2015. Evaluating the Use of ABBA-BABA Statistics to locate introgressed loci. **Molecular Biology and Evolution** 32(1):244–57
39. De Vos L, Steenkamp ET, **Martin SH**, Santana QC, Fourie G, van der Merwe N a., Wingfield MJ, Wingfield BD. 2014. Genome-wide macrosynteny among *Fusarium* species in the *Gibberella fujikuroi* complex revealed by amplified fragment length polymorphisms. **PLOS One** 9(12):e114682
40. Seehausen O, Butlin RK, Keller I, Wagner CE, Boughman JW, Hohenlohe P a, Peichel CL, Saetre G-P, Bank C, Brännström A, Brelford A, Clarkson CS, Eroukhanoff F, Feder JL, Fischer MC, Foote AD, Franchini P, Jiggins CD, Jones FC, Lindholm AK, Lucek K, Maan ME, Marques D a, **Martin SH**, Matthews B, Meier JI, Möst M, Nachman MW, Nonaka E, Rennison DJ, Schwarzer J, Watson ET, Westram AM, Widmer A. 2014. Genomics and the origin of species. **Nature Reviews Genetics** 15(3):176–92
41. \***Martin SH**, Dasmahapatra KK, Nadeau NJ, Salazar C, Walters JR, Simpson F, Blaxter M, Manica A, Mallet J, Jiggins CD. 2013. Genome-wide evidence for speciation with gene flow in *Heliconius* butterflies. **Genome Research** 23(11):1817–2
42. Briscoe AD, Macias-Muñoz A, Kozak KM, Walters JR, Yuan F, Jamie G a., **Martin SH**, Dasmahapatra KK, Ferguson LC, Mallet J, Jacquin-Joly E, Jiggins CD. 2013. Female behaviour drives expression and evolution of gustatory receptors in butterflies. **PLOS Genetics** 9(7):e1003620
43. Nadeau NJ, **Martin SH**, Kozak KM, Salazar C, Dasmahapatra KK, Davey JW, Baxter SW, Blaxter ML, Mallet J, Jiggins CD. 2013. Genome-wide patterns of divergence and gene flow across a butterfly radiation. **Molecular Ecology** 22(3):814–26
44. **Martin SH**, Steenkamp ET, Wingfield MJ, Wingfield BD. 2013. Mate-recognition and species boundaries in the ascomycetes. **Fungal Diversity** 58(1):1–12
45. Dasmahapatra KK, Walters JR, Briscoe AD, Davey JW, Whibley A, Nadeau NJ, Zimin A V, Hughes DST, Ferguson LC, **Martin SH**, Salazar C, Lewis JJ, Adler S, Ahn S-J, Baker DA, Baxter SW, Chamberlain NL, Chauhan R, Counterman BA, Dalmay T, Gilbert LE, Gordon K, Heckel DG, Hines HM, Hoff KJ, Holland PWH, Jacquin-Joly E, Jiggins FM, Jones RT, Kapan DD, Kersey P, Lamas G, Lawson D, Mapleson D, Maroja LS, Martin A, Moxon S, Palmer WJ, Papa R, Papanicolaou A, Pauchet Y, Ray DA, Rosser N, Salzberg SL, Supple MA, Surridge A, Tenger-Trolander A, Vogel H, Wilkinson PA, Wilson D, Yorke JA, Yuan F, Balmuth AL, Eland C, Gharbi K, Thomson M, Gibbs RA, Han Y, Jayaseelan JC, Kovar C, Mathew T, Muzny DM, Ongerli F, Pu L-L, Qu J, Thornton RL, Worley KC, Wu Y-Q, Linares M, Blaxter ML, Ffrench-Constant RH, Joron M, Kronforst MR, Mullen SP, Reed

- RD, Scherer SE, Richards S, Mallet J, Owen McMillan W, Jiggins CD. 2012. Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. **Nature** 487(7405):94–8
46. Wingfield BD, Steenkamp ET, Santana QC, Coetzee MPA, Bam S, Barnes I, Beukes CW, Chan WY, De Vos L, Fourie G, Friend M, Gordon TR, Herron DA, Holt C, Korf I, Kvas M, Martin SH, Mlonyeni XO, Naidoo K, Phasha MM, Postma A, Reva O, Roos H, Simpson M, Slinski S, Slippers B, Sutherland R, Van der Merwe NA, Van der Nest MA, Venter SN, Wilken PM, Yandell M, Zipfel R, Wingfield MJ. 2012. First fungal genome sequence from Africa: A preliminary analysis. **South African Journal of Science** 108(1/2)
47. Martin SH, Wingfield BD, Wingfield MJ, Steenkamp ET. 2011. Structure and evolution of the *Fusarium* mating type locus: new insights from the *Gibberella fujikuroi* complex. **Fungal Genetics and Biology** 48(7):731–40
48. **Martin SH**, Wingfield BD, Wingfield MJ, Steenkamp ET. 2011. Causes and consequences of variability in peptide mating pheromones of ascomycete fungi. **Molecular Biology and Evolution** 28(7):1987–2003