John Marshall, PhD

Address: Divisions of Epidemiology & Biostatistics, School of Public Health, 2121 Berkeley Way University of California, Berkeley, CA 94720-7360, USA Phone: +1-510-664-4724, Email: john.marshall@berkeley.edu Website: https://www.marshalllab.com/

Short Bio I am a mathematical biologist with expertise in infectious disease modeling and the use of genetics-based strategies to control mosquito disease vectors. I am PI of a Bill & Melinda Gates Foundation grant to provide modeling support for mosquito genetic control strategies for malaria elimination, and of an NIH project to develop landscape genomics methods to better quantify movement patterns of Aedes aegypti mosquitoes. I collaborate with several groups exploring the use of genetics-based systems to control Anopheles gambiae, the main African malaria vector, and Ae. aegypti, the main vector of dengue and Zika virus. At the UC Berkeley School of Public Health, I lead a research group that specializes in modeling of mosquito vectors and the diseases they transmit, and teach a course on mathematical modeling of infectious diseases. Appointments 2022 (August)-: Honorary Professor Department of Statistics, University of Auckland, Aotearoa/New Zealand • Conducting research on mathematical and statistical aspects of genomic methods to infer demographic parameters of mosquitoes 2022 (July)-: Professor in Residence Divisions of Epidemiology & Biostatistics, School of Public Health, University of California, Berkeley, USA Conducting research on mathematical epidemiology, malaria elimination, • mosquito ecology and novel vector control strategies Teaching graduate level courses on infectious disease modeling Mentoring graduate students in epidemiology, biostatistics, computational biology and mathematical modeling 2020 (July)-2022 (June): Associate Professor in Residence 2015 (January)-2020 (June): Assistant Professor in Residence Divisions of Epidemiology & Biostatistics, School of Public Health, University of California, Berkeley, USA 2012 (October)-2014 (December): Medical Research Council Research Fellow Department of Infectious Disease Epidemiology, Imperial College London, UK Worked towards designing confined field trials of gene drive mosquitoes • on islands off the coast of Africa Developed skills in analysis of large data sets - data cleaning, cluster • analysis, model fitting and Markov chain Monte Carlo methods Mentored graduate students in global health and mathematical modeling 2013 (October)-2014 (April): Visiting Scholar Center for Theoretical Evolutionary Genomics, University of California, Berkeley, USA Investigated methods to determine the structure and demographic history of • malaria-transmitting mosquito populations from genomic data 2010 (August)-2012 (September): Research Associate Department of Infectious Disease Epidemiology, Imperial College London, UK

- Conducted surveys of human movement patterns of relevance to malaria transmission in Mali, Burkina Faso, Zambia and Tanzania
- Developed models for mosquito control and malaria epidemiology
- Co-organized a course on mathematical modeling of infectious diseases for public health professionals

2009 (July)-2010 (July): Postdoctoral Scholar

Division of Biology and Biological Engineering, California Institute of Technology, USA

- Designed new gene drive systems and developed mathematical models describing their spread
- Developed skills in genetic engineering and maintaining laboratory mosquito lines
- Trained graduate and postdoctoral students in population genetics

2009 (January-June): Postdoctoral Fellow

Center for Society & Genetics, University of California, Los Angeles, USA

- Analyzed surveys on the perspectives of people in Mali, West Africa to genetically modified mosquitoes for malaria control
- Analyzed international regulations for the environmental release of genetically modified mosquitoes
- Developed/lectured class on "Genetic engineering in developing countries"

2008 (July-December): Postdoctoral Researcher

Department of Ecology & Evolutionary Biology, University of California, Los Angeles, USA

Based at: Malaria Research and Training Center, University of Bamako, Mali

- Led a research team surveying the perspectives of people in Mali, West Africa to gene drive mosquitoes for malaria control
- Participated in ecological studies of mosquito dispersal
- Lectured and helped organize a WHO-sponsored workshop on developing a regulatory framework for releasing GM mosquitoes in Africa

2001 (January-December): Editor

Craccum magazine, Auckland University Students' Association, Aotearoa/New Zealand

- Edited a 48-page weekly magazine for University of Auckland students
- Managed a staff of ~30 writers, photographers, distributors, designers, webmasters and advertising managers
- Developed skills in written and verbal communication and leadership

Education

2003 (August)-2008 (June): **PhD (Biomathematics)** <u>University of California, Los Angeles, USA</u> PhD thesis: <u>The dynamics of transposable elements in genetically modified</u> <u>mosquito vectors</u>

2003 (August)-2005 (December): MS (Biomathematics) University of California, Los Angeles, USA

2000 (February)-2002 (November): BTech (Hons) (Optoelectronics) University of Auckland, Aotearoa/New Zealand

1997 (February)-1999 (November): BSc (Biological sciences) <u>University of Auckland</u>, Aotearoa/New Zealand

Technical Skills and Competences

Mathematics:

- Multivariate calculus, linear algebra, vector calculus
- Ordinary and partial differential equations, reaction-diffusion systems
- Probability theory, Markov chains, branching processes

Statistics:

- Generalized linear models, maximum likelihood estimation
- Bayesian statistics, Markov chain Monte Carlo model fitting methods

Software and programming:

- Mathematics & statistics: R, Matlab, Mathematica, Berkeley Madonna
- Programming languages: C++, Python

Biology:

- Molecular biology: manipulation of DNA, PCR, gel electrophoresis
- Ecology: mosquito husbandry, mark-release-recapture experiments

Social science and ethics:

- Quantitative & qualitative survey design, ethnography
- Research protocols for Institutional Review Boards

Languages:

- English (mother tongue)
- French, Bambara (African language spoken in Mali) (intermediate)
- Mandarin Chinese, Spanish (beginner)

Teaching

2015-2023: Lecturer, <u>PH 252B: Infectious Disease Modeling</u>, University of California, Berkeley (Fall semester, 3 units, ~20 students)
2015-2019: Lecturer, <u>PH 290: Infectious Disease Modeling Seminar</u>, University of California, Berkeley (Fall semester, 2 units, ~16 students)
2015-2016: Lecturer, <u>PH 145: Statistical Analysis of Continuous Outcome Data</u>, University of California, Berkeley (Fall semester, 4 units, ~45 students)
2011-2014: Co-organizer/lecturer/demonstrator, <u>Short Course in Epidemiology</u>,

Imperial College London (Summer, professional course, ~30 students) 2009: Lecturer, Genetic Engineering in Developing Countries, University of California, Los Angeles (Winter quarter, 2 units, ~20 students)

2008-2010: Lecturer, Biosafety training course for Africa related to the potential release of genetically modified disease vectors, University of Bamako, Mali (Summer, professional course, ~20 students)

2005: Lecturer/demonstrator, Hidden Markov Models for Bioacoustic Analysis, University of California, Los Angeles (Spring quarter, 2 units, ~15 students)

Awards:

School of Public Health Committee on Teaching Excellence Award (Spring & Fall 2015, Spring & Fall 2016, Spring 2017, Spring & Fall 2018, Spring & Fall 2019, Spring 2020, Spring 2021, Spring 2022, Fall 2023)

Postdocs supervised (advisor):

Dr. Rodrigo M. Corder (Bill & Melinda Gates Foundation-funded postdoc, 2021-2023)

Dr. Eileen H. Jeffrey Gutiérrez (NIH-funded postdoc, 2021-2023)

Dr. Sanjay Lamba (Tata Institute Fellow, 2019-2021)

Dr. Yogita Sharma (Innovative Genomics Institute-funded postdoc, 2018-2022)

Dr. Gordana Rašić (DARPA-funded postdoc, 2018-2021) Dr. Tomás León (DARPA-funded postdoc, 2018-2020) Dr. Victor Ferman (DARPA-funded postdoc, 2018-2019) Dr. Héctor M. Sánchez C. (UC Irvine Malaria Initiative-funded postdoc, 2017-2020) Dr. Samson S. Kiware (Wellcome Trust Fellow, 2015-2018)

PhD students supervised (dissertation chair):

Victor Mero (Epidemiology, 2023-) Agastya Mondal (Epidemiology, 2020-) Dr. Váleri N. Vásquez (Energy & Resources, 2018-2023) Dr. Jared B. Bennett (Biophysics, 2017-2021) Dr. Sean L. Wu (Epidemiology, 2016-2020)

MA/MPH students supervised (thesis advisor):

Shuyi Yang (Biostatistics, 2023-) Emma Lonstrup (Epidemiology & Biostatistics, 2022-) Natasha Harrison (Epidemiology & Biostatistics, 2021-2022) Thien-An Ha (Epidemiology & Biostatistics, 2019-2020) Dr. Sean L. Wu (Epidemiology & Biostatistics, 2015-2016) Jaclyn Guerrero (Epidemiology & Biostatistics, 2015-2016)

Undergraduate students supervised (thesis advisor):

Darpa Anireddy (Public Health, 2021-2022) Biyonka Liang (Statistics, 2019-2020)

Grants Awarded

Open Philanthropy grant, <u>"Cost-effectiveness analysis of pgSIT technology for</u> <u>malaria control.</u>" (2022) Role: Subaward PI (\$63,011 to Marshall Lab, \$190,000 total).

Bill & Melinda Gates Foundation grant, <u>"Modeling support for genetics-based</u> <u>malaria vector control strategies.</u>" (2021-2024) Role: PI (\$800,000 award to Marshall Lab).

EPA STAR grant, <u>"Development of data-driven model of assessing benefits and risks</u> <u>pgSIT for *Ae. aegypti* eradication in Hawaii." (2021-2024) Role: Co-I (\$43,405 to Marshall Lab, \$750,000 total).</u>

NIH R01 grant, <u>"Understanding mosquito movement and its relevance to control</u> <u>through genetic analysis.</u>" (2020-2024) Role: PI (\$914,356 to Marshall Lab, \$1,735,802 total).

NIH R01 grant, <u>"Public engagement for gene drive technology.</u>" (2020-2024) Role: Co-I (\$125,955 sub-award to Marshall Lab).

DARPA grant, <u>"Safely engineering various classes of gene drives to control a major</u> <u>invasive disease vector, *Ae. aegypti*.</u>" (2017-2021) Role: Co-PI (\$1,809,506 to Marshall Lab, \$14,949,052 total).

UC Irvine sub-contract, <u>"UC Irvine Malaria Initiative.</u>" (2017-2025) Role: Co-PI (\$1,029,311 sub-award to Marshall Lab).

Innovative Genomics Institute grant, <u>"CRISPR-Cas9-based gene drive architecture</u> for control of agricultural pests." (2017-2020) Role: PI (\$246,000 award to Marshall Lab).

CITRIS and the Banatao Institute seed funding grant, <u>"Machine Learning for Vectorborne Disease Surveillance.</u>" (2019-2020) Role: PI (\$12,500 to Marshall Lab, \$25,000 total).

NIAID grant, "Measuring spillover effects of reactive, focal malaria elimination

interventions." (2019-2023) Role: Co-I (\$586,474 total).

NVIDIA GPU grant, <u>"Statistical and machine learning methods to predict mosquito</u> population densities." (2018) Role: PI (\$3,000 award to Marshall Lab).

University of Washington sub-contract, <u>"Strategic planning tools for staging malaria</u> elimination." (2017-2020) Role: Subaward PI (\$117,740 sub-award to Marshall Lab)

UC Berkeley sub-contract, <u>"Effects of agricultural expansion and intensification on infectious diseases.</u>" (2017) Role: Sub-contractor (\$12,194 sub-award to Marshall Lab).

UC Davis SVM Vector-Borne Disease Pilot Grant Program, <u>"Working toward the eradication of *Aedes aegypti*, an invasive arbovirus vector, in California." (2016-2017) Role: Co-I (\$25,000 total).</u>

Bill & Melinda Gates Foundation sub-contract, <u>"Prototype of technology's role to</u> <u>facilitate surveillance needs for malaria elimination."</u> (2015-2017) Role: Subaward PI (\$26,695 sub-award to Marshall Lab).

University of California Institute for Mexico and the United States grant, "Determining optimal strategies for the control of vectors of dengue and other vector borne diseases in Mexico and the United States." (2015-2016) Role: PI (\$12,500 to Marshall Lab, \$25,000 total).

Sean Parker Foundation grant <u>"Malaria Elimination Initiative on a new vector</u> control for malaria elimination." (2015-2016) Role: Subaward PI (\$80,832 sub-award to Marshall Lab).

UC Davis Signature Research in Genomics Program Award, <u>"Advanced genomic tools for estimating dispersal of African malaria vectors."</u> (2015-2016) Role: Co-I (\$45,000 total).

UK Medical Research Council grant, <u>"Optimal trial design for a confined release of malaria-refractory transgenic mosquitoes.</u>" (2012-2015) Role: PI (£285,103 award to Marshall Lab).

Peer-reviewed Publications	1. Wills P, Marshall JM , Smith P (2004) <u>Genetic information and self-organised</u> <u>criticality</u> . Europhysics Letters 68: 901-907.
	2. Marshall JM , Weiss R (2006) <u>A Bayesian heterogeneous analysis of variance</u> <u>approach to inferring recent selective sweeps</u> . Genetics 173: 2357-2370.
	3. Marshall JM , Morikawa K, Manoukis N, Taylor CE (2007) <u>Predicting the effectiveness of population replacement strategy using mathematical modeling</u> . J. Vis. Exp. 5: 227.
	4. Marshall JM (2008) <u>The impact of dissociation on transposon-mediated disease</u> <u>control strategies</u> . Genetics 178: 1673-1682.
	5. Marshall JM (2008) <u>A branching process model for the early spread of a transposable element in a diploid population</u> . J. Math. Biol. 57: 811-840.
	6. Marshall JM (2009) <u>The effect of gene drive on containment of transgenic</u> <u>mosquitoes</u> . J. Theor. Biol. 258: 250-265.
	7. Marshall JM , Taylor CE (2009) <u>Malaria control with transgenic mosquitoes</u> . PLoS Medicine 6: e1000020.
	8. Marshall JM, Touré MB, Traore MM, Taylor CE (2010) Towards a quantitative

assessment of public attitudes to transgenic mosquitoes: Questions based on a qualitative survey in Mali. AsPac. J. Mol. Biol. Biotechnol. 18: 251-273.

9. **Marshall JM**, Toure MB, Traore MM, Famenini S, Taylor CE (2010) <u>Perspectives of people in Mali toward genetically modified mosquitoes for malaria</u> <u>control</u>. Malar. J 9: 128.

10. **Marshall JM** (2010) <u>The Cartagena Protocol and genetically modified</u> <u>mosquitoes.</u> Nat. Biotech. 28: 896-897.

11. **Marshall JM** (2011) <u>The Cartagena Protocol in the context of recent releases of</u> <u>transgenic and *Wolbachia*-infected mosquitoes</u>. AsPac. J. Mol. Biol. Biotechnol. 19: 93-100.

12. **Marshall JM** (2011) <u>The toxin and antidote puzzle: New ways to control insect</u> <u>pest populations through manipulating inheritance</u>. Bioeng. Bugs. 2: 1-6.

13. **Marshall JM**, Hay BA (2011) <u>Inverse *Medea* as a novel gene drive system for</u> local population replacement: A theoretical analysis. J. Hered. 102: 336-341.

14. **Marshall JM**, Pittman GW, Buchman AB, Hay BA (2011) <u>Semele: A killer-</u> male, rescue-female system for suppression and replacement of insect disease vector populations. Genetics 187: 535-551.

15. Akbari OS*, Chen CH*, **Marshall JM***, Huang H, Antoshechkin I, Hay BA (2012) <u>Novel synthetic *Medea* selfish genetic elements drive population</u> replacement in Drosophila; a theoretical exploration of *Medea*-dependent population suppression. ACS Synth. Biol. 3: 915-928. *Equal contribution

16. De Silva P, **Marshall JM** (2012) <u>Factors contributing to urban malaria</u> <u>transmission in sub-Saharan Africa: A systematic review</u>. J. Trop. Med. 2012: 819563.

17. **Marshall JM**, Hay BA (2012) <u>General principles of single-construct</u> <u>chromosomal gene drive</u>. Evolution. 66: 2150-2166.

18. **Marshall JM**, Hay BA (2012) <u>Confinement of gene drive systems to local</u> populations: A comparative analysis. J. Theor. Biol. 294: 153-171.

19. Gatton ML, Chitnis N, Churcher T, Donnelly MJ, Ghani AC, Godfray HCJ, Gould F, Hastings I, **Marshall JM**, Ranson H, Rowland M, Shaman J, Lindsay SW (2013) <u>The importance of mosquito behavioral adaptations to malaria control in</u> <u>Africa</u>. Evolution 67: 1218-1230.

20. Akbari OS*, Matzen KD*, **Marshall JM***, Huang H, Ward CM, Hay BA (2013) <u>A synthetic gene drive system for local, reversible modification and suppression of insect populations</u>. Curr. Biol. 23: 671-677. *Equal contribution

21. **Marshall JM**, White MT, Ghani AC, Schlein Y, Muller GC, Beier JC (2013) Quantifying the mosquito's sweet tooth: Modelling the effectiveness of attractive toxic sugar baits (ATSB) for malaria vector control. Malar. J. 12: 291.

22. White MT, Lwetoijera D, **Marshall JM**, Caron-Lormier G, Bohan DA, Denholm I, Devine GJ (2014) <u>Negative cross resistance mediated by co-treated bed</u> <u>nets: A potential means of restoring pyrethroid-susceptibility to malaria vectors</u>. PLoS ONE 9: e95640.

23. Okorie PN, **Marshall JM**, Akpa MO, George AO (2014) <u>Perceptions and</u> recommendations by scientists for a potential release of genetically modified <u>mosquitoes in Nigeria</u>. Malar. J. 13: 154.

24. **Marshall JM**, Hay BA (2014) <u>*Medusa*: A novel gene drive system for confined</u> <u>suppression of mosquito populations</u>. PLoS ONE **9**: e102694.

25. Zhu L, Qualls WA, **Marshall JM**, Arheart KL, DeAngelis DL, McManus JW, Traore SF, Doumbia S, Schlein Y, Müller GC, Beier JC (2015) <u>A spatial individual-based model predicting a great impact of copious sugar sources and resting sites on survival of *Anopheles gambiae* and malaria parasite transmission. Malar. J. 14: 59.</u>

26. Zhu L, **Marshall JM**, Qualls WA, Schlein Y, McManus JW, Arheart KL, Hlaing WM, Traore SF, Doumbia S, Müller GC, Beier JC (2015) <u>Modelling</u> optimum use of attractive toxic sugar bait stations for effective malaria vector control in Africa. Malar. J. 14: 492.

27. Cheng Q, Jing Q, Spear RC, **Marshall JM**, Yang Z, Gong P (2016) <u>Climate and timing of imported cases as determinants of the dengue outbreak in Guangzhou</u>, <u>2014: Evidence from a mathematical model</u>. PLoS NTDs 10: e0004417.

28. **Marshall JM**, Touré MB, Ouédraogo AL, Ndhlovu M, Kiware SS, Rezai A, Nkhama E, Griffin JT, Hollingsworth TD, Doumbia S, Govella NJ, Ferguson NM, Ghani AC (2016) <u>Key traveller groups of relevance to spatial malaria transmission:</u> <u>A survey of movement patterns in four sub-Saharan African countries</u>. Malar. J. 15: 200.

29. **Marshall JM**, Bennett A, Kiware SS, Sturrock HJW (2016) <u>The hitchhiking</u> parasite: Why human movement matters to malaria transmission and what we can <u>do about it</u>. Trends Parasitol. 32: 752–755.

30. Killeen GF, Kiware SS, Okumu FO, Sinka ME, Moyes CL, Massey NC, Gething PW, **Marshall JM**, Chaccour CJ, Tusting LS (2017) <u>Going beyond</u> personal protection against mosquito bites to eliminate malaria transmission: population suppression of malaria vectors that exploit both human and animal blood. BMJ Global Health 2: e000198.

31. Killeen GF, Tatarsky A, Diabate A, Chaccour CJ, **Marshall JM**, Okumu FO, Brunner S, Newby G, Williams YA, Malone D, Tusting LS, Gosling RD (2017) <u>Developing an expanded vector control toolbox for malaria elimination</u>. BMJ Global Health 2: e000211.

32. Killeen GF, **Marshall JM**, Kiware SS, Andy S, Chaki PP, Govella NJ (2017) <u>Measuring, manipulating and exploiting behaviors of adult mosquitoes to optimize</u> <u>malaria vector control impact</u>. BMJ Global Health 2: e000212.

33. **Marshall JM**, Buchman B, Sanchez HM, Akbari OS (2017) <u>Overcoming</u> <u>evolved resistance to population-suppressing homing-based gene drives</u>. Nature Scientific Reports 7: 3776.

34. Cheng Q, Jing Q, Spear RC, **Marshall JM**, Yang Z, Gong P (2017) <u>The</u> interplay of climate, intervention and imported cases in determining the potential and final epidemic size of dengue outbreak in Guangzhou. PLoS NTDs 11: e0005701.

35. Zhu L, Muller GC, **Marshall JM**, Arheart KL, Qualls WA, Hlaing WM, Schlein Y, Traore SF, Doumbia S, Beier JC (2017) <u>Is outdoor vector control needed for</u> <u>malaria elimination? An individual-based modelling study</u>. Malaria Journal 16: 266.

36. Adelman Z, Akbari O, Bauer J, Bier E, Bloss C, Carter SR, Callender C, Costero-Saint Denis A, Cowhey P, Dass B, Delborne J, Devereaux M, Ellsworth P, Friedman RM, Gantz V, Hay BA, Hoddle M, James AA, James S, Jorgenson L, Kalichman M, **Marshall JM**, McGinnis W, Newman J, Pearson A, Quemada H, Rudenko L, Shelton A, Vinetz JM, Weisman J, Wong B, Wozniak C (2017) <u>Rules</u> of the road for insect gene drive research and testing. Nat. Biotech. 35: 716-718.

37. Kiware SS, Chitnis N, Tatarsky A, Wu SL, Sanchez HM, Gosling R, Smith DL, **Marshall JM** (2017) <u>Attacking the mosquito on multiple fronts: Insights from the</u> <u>Vector Control Optimization Model (VCOM) for malaria elimination</u>. PLoS ONE 12: e0187680.

38. Benedict MQ, Bier E, Burt A, Capurro ML, De Barro P, Handler AM, Hayes KR, **Marshall JM**, Tabachnick WJ, Adelman ZN (2018) <u>Recommendations for laboratory containment and management of gene drive systems in arthropods</u>. Vector Borne Zoonotic Dis 18: 2-13.

39. **Marshall JM**, Akbari OS (2018) <u>Can CRISPR-based gene drive be confined in</u> <u>the wild? A question for molecular and population biology</u>. ACS Chemical Biology 13: 424-430.

40. Buchman A, Ivy T, **Marshall JM**, Akbari OS, Hay BA (2018) <u>Engineered</u> reciprocal chromosome translocations drive high threshold, reversible population replacement in Drosophila. ACS Synthetic Biology 7: 1359-1370.

41. Buchman A, **Marshall JM**, Ostrovski D, Yang T, Akbari OS (2018) Synthetically engineered *Medea* gene drive system in the worldwide crop pest *D*. *suzukii*. Proc Natl Acad Sci USA 115: 4725-4730.

42. Jing QL, Cheng Q, **Marshall JM**, Hu WB, Yang ZC, Lu JH (2018) <u>Imported</u> <u>cases and minimum temperature drive dengue transmission in Guangzhou, China:</u> <u>Evidence from an ARIMAX model</u>. Epidemiology & Infection 146: 1226-1235.

43. **Marshall JM**, Wu SL, Sánchez HM, Kiware SS, Ndhlovu M, Ouédraogo AL, Touré MB, Sturrock HJ, Ghani AC, Ferguson NM (2018) <u>Mathematical models of</u> <u>human mobility of relevance to malaria transmission in Africa</u>. Nature Scientific Reports 8: 7713.

44. Carami EM, Eckermann KN, Ahmed HMM, Sánchez HM, Dippel S, **Marshall JM**, Wimmer EA (2018) <u>Consequences of resistance evolution in a Cas9-based sex-</u> <u>conversion suppression gene drive for insect pest management</u>. Proceedings of the National Academy of Sciences USA 115: 6189-6194.

45. Arakala A, Hoover CM, **Marshall JM**, Sokolow SH, De Leo GA, Rohr JR, Remais JV, Gambhir M (2018) <u>Estimating the elimination feasibility in the "end</u> game" of control efforts for parasites subjected to regular mass drug administration: <u>Methods and their application to schistosomiasis</u>. PLoS Neglected Tropical Diseases 12: e0006794.

46. Kandul NP, Liu J, Sánchez HM, Wu SL, **Marshall JM**, Akbari OS (2019) <u>Transforming insect population control with precision guided sterile males</u>. Nature Communications 10: 84.

47. Lee Y, Schmidt H, Collier TC, Conner WR, Hanemaaijer MJ, Slatkin M, Marshall JM, Chiu JC, Smartt CT, Lanzaro GC, Mulligan FS, Cornel AJ (2019) <u>Genome-wide divergence among invasive populations of *Aedes aegypti* in <u>California</u>. BMC Genomics 20: 204.</u>

48. Kandul NP, Liu J, Sánchez HM, Wu SL, **Marshall JM**, Akbari OS (2019) <u>Reply to 'Concerns about the feasibility of using "precision guided sterile males" to</u> <u>control insects'</u>. Nature Communications 10: 3955.

49. Sánchez HM, Wu SL, Bennett JB, **Marshall JM** (2019) <u>MGDrivE: A modular</u> simulation framework for the spread of gene drives through spatially-explicit <u>mosquito populations</u>. Methods in Ecology and Evolution 11: 229-239.

50. **Marshall JM**, Raban R, Kandul NP, Edula JR, León T, Akbari OS (2019) <u>Winning the tug-of-war between effector gene design and pathogen evolution in</u> <u>vector population replacement strategies</u>. Frontiers in Genetics 10: 1072.

51. Zhang Z, Jing Q, Chen Z, Li T, Jiang L, Li Y, Luo L, **Marshall JM**, Yang Z (2019) <u>The increasing menace of dengue in Guangzhou, 2001–2016: The most important epicenter in mainland China</u>. BMC Infectious Diseases 19: 1002.

52. Pham TB, Phong CH, Bennett JB, Hwang K, Jasinskiene N, Parker K, Stillinger D, **Marshall JM**, Carballar-Lejarazú R, James AA (2019) <u>Experimental population</u> <u>modification of the malaria vector mosquito, *Anopheles stephensi*. PLoS Genetics 15: e1008440.</u>

53. López VD, Bishop AL, Sánchez HM, Bennett JB, Feng X, **Marshall JM**, Bier E, Gantz VM (2020) <u>A transcomplementing gene drive provides a flexible platform</u> for laboratory investigation and potential field deployment. Nature Communications 11: 352.

54. Li M, Yang T, Kandul NP, Bui M, Gamez S, Raban R, Bennett JB, Sánchez HM, Lanzaro GC, Schmidt H, Lee Y, **Marshall JM**, Akbari OS (2020) Development of a confinable gene-drive system in the human disease vector, *Aedes* <u>aegypti</u>. eLife 9: e51701.

55. Friedman RM, **Marshall JM**, Akbari OS (2020) <u>Gene drives: New and improved</u>. Issues in Science and Technology 36: 72-78.

56. Raban RR, **Marshall JM**, Akbari OS (2020) <u>Progress toward engineering gene</u> <u>drives for population control</u>. Journal of Experimental Biology 223: jeb208181.

57. James SL, **Marshall JM**, Christophides GK, Okumu FO, Nolan T (2020) <u>Toward the definition of efficacy and safety criteria for advancing gene drive-</u> <u>modified mosquitoes to field testing</u>. Vector-Borne and Zoonotic Diseases 20: 237-251.

58. Wu SL, Sánchez HM, Henry JM, Citron DT, Zhang Q, Compton KE, Liang B, Verma A, Cummings DAT, Le Menach A, Scott TW, Wilson AL, Lindsay SW, Moyes CL, Hancock PA, Russell TL, Burkot TR, **Marshall JM**, Kiware S, Reiner RC, Smith DL (2020) <u>Vector bionomics and vectorial capacity as emergent</u> <u>properties of mosquito behaviors and ecology</u>. PLoS Computational Biology 16: e1007446.

59. Sánchez HM, Bennett JB, Wu SL, Rašić G, Akbari OS, **Marshall JM** (2020) <u>Confinement and reversibility of threshold-dependent gene drive systems in</u> <u>spatially-explicit Aedes aegypti</u> populations. BMC Biology 18: 50.

60. Cheung C, Gamez S, Carballar-Lejarazú R, Ferman V, Vásquez VN, Terradas G, Ishikawa J, Schairer CE, Bier E, **Marshall JM**, James AA, Akbari OS, Bloss CS (2020) <u>Translating gene drive science to promote linguistic diversity in community</u> and stakeholder engagement. Global Public Health 15: 1551-1565.

61. Xu XS, Bulger EA, Gantz VM, Klanseck C, Heimler SR, Auradkar A, Bennett JB, Miller LA, Leahy S, Juste SS, Buchman A, Akbari OS, **Marshall JM**, Bier E (2020) <u>Active genetic neutralizing elements for halting or deleting gene drives</u>. Molecular Cell 80: 246-262.

62. Adolfi A, Gantz VM, Jasinskiene N, Lee HF, Hwang K, Bulger EA, Ramaiah A, Bennett JB, Terradas G, Emerson JJ, **Marshall JM**, Bier E, James AA (2020) Efficient population modification gene-drive rescue system in the malaria mosquito <u>Anopheles stephensi</u>. Nature Communications 11: 5553.

63. Long KC, Alphey L, Annas GJ, Bloss CS, Campbell KJ, Champer J, Chen CH,

Choudhary A, Church GM, Collins JP, Cooper KL, Delborne JA, Edwards OR, Emerson CI, Esvelt K, Evans SW, Friedman RM, Gantz VM, Gould F, Hartley S, Heitman E, Hemingway J, Kanuka H, Kuzma J, Lavery JV, Lee Y, Lorenzen M, Lunshof JE, **Marshall JM**, Messer PW, Montell C, Oye KA, Palmer MJ, Papathanos PA, Paradkar PN, Piaggio AJ, Rasgon JL, Rašić G, Rudenko L, Saah JR, Scott MJ, Sutton JT, Vorsino AE, Akbari OS (2020) <u>Core commitments for field</u> <u>trials of gene drive organisms</u>. Science 370: 1417-1419.

64. Kormos A, Lanzaro GC, Bier E, Dimopoulos G, **Marshall JM**, Pinto J, dos Santos AA, Bacar A, Sacramento Rompão HSP, James AA (2020) <u>Application of the relationship-based model to engagement for field trials of genetically engineered malaria vectors</u>. American Journal of Tropical Medicine and Hygiene 104: 805-811.

65. Ma M, Wu SL, He Z, Yuan L, Bai Z, Jiang L, **Marshall JM**, Lu J, Yang Z, Jing QL (2021) <u>New genotype invasion of dengue virus serotype 1 drove massive</u> <u>outbreak in Guangzhou, China</u>. Parasites & Vectors 14: 126.

66. Kandul NP, Liu J, Bennett JB, **Marshall JM**, Akbari OS (2021) <u>A confinable</u> <u>home-and-rescue gene drive for population modification</u>. eLife 10: e65939.

67. Terradas G, Buchman AB, Bennett JB, Shriner I, **Marshall JM**, Akbari OS, Bier E (2021) <u>Inherently confinable split-drive systems in *Drosophila*. Nature Communications 12: 1480.</u>

68. Rerolle F, Dantzer E, Lover AA, **Marshall JM**, Hongvanthong B, Sturrock HJW, Bennett A (2021) <u>Spatio-temporal associations between deforestation and malaria incidence in Lao PDR</u>. eLife 10: e56974.

69. Fraser KJ, Mwandigha L, Traore S, Traore M, Doumbia S, Junnila A, Revay E, Beier J, **Marshall JM**, Ghani AC, Muller G (2021) <u>Estimating the potential of Attractive Targeted Sugar Baits (ATSBs) as a new vector control tool for *Plasmodium falciparum* malaria. Malaria Journal 20: 151.</u>

70. Wu SL, Bennett JB, Sánchez HM, Dolgert AJ, León TM, **Marshall JM** (2021) MGDrivE 2: A simulation framework for gene drive systems incorporating seasonality and epidemiological dynamics. PLoS Computational Biology 17: e1009030.

71. Buchman A, Shriner I, Yang T, Liu J, Antoshechkin I, **Marshall JM**, Perry MW, AkbariOS (2021) <u>Engineered reproductively isolated species drive reversible</u> <u>population replacement</u>. Nature Communications 12: 3281.

72. Lanzaro GC, Sánchez HM, Collier TC, **Marshall JM**, James AA (2021) Population modification strategies for malaria vector control are uniquely resilient to observed levels of gene drive resistance alleles. BioEssays 43: e2000282.

73. Rerolle F, Jacobson JO, Wesson P, Dantzer E, Lover AA, Hongvanthong B, Smith J, **Marshall JM**, Sturrock HJW, Bennett A (2021) <u>Population size estimation</u> <u>of seasonal forest-going populations in Southern Lao PDR</u>. Nature Scientific Reports 11: 14816.

74. Wang GH, Gamez S, Raban RR, **Marshall JM**, Alphey L, Li M, Rasgon JL, Akbari OS (2021) <u>Combating mosquito-borne diseases using genetic control</u> <u>technologies</u>. Nature Communications 12: 4388.

75. Legros M, **Marshall JM**, Macfadyen S, Hayes KR, Sheppard A, Barrett LG (2021) <u>Gene drive strategies of pest control in agricultural systems: Challenges and opportunities</u>. Evolutionary Applications 14: 2162-2178.

76. Ha T, León TM, Lalangui K, Ponce P, **Marshall JM**, Cevallos V (2021) Household-level risk factors for *Aedes aegypti* pupal density in Guayaquil, Ecuador. Parasites & Vectors 14: 458.

77. Li M, Yang T, Bui M, Gamez S, Wise T, Kandul NP, Liu J, Alcantara L, Lee H, Edula JR, Raban R, Zhan Y, Wang Y, DeBeaubien N, Chan J, Sánchez C. HM, Bennett JB, Antoshechkin I, Montell C, **Marshall JM**, Akbari OS (2021) <u>Eliminating mosquitoes with precision guided sterile males</u>. Nature Communications 12: 5374.

78. Gamez S, Chaverra-Rodriguez D, Buchman A, Kandul NP, Mendez-Sanchez SC, Bennett JB, Sánchez C. HM, Yang T, Antoshechkin I, Duque JE, Papathanos PA, **Marshall JM**, Akbari OS (2021) <u>Exploiting a Y chromosome-linked Cas9 for sex selection and gene drive</u>. Nature Communications 12: 7202.

79. Rašić G, Lobo NF, Jeffrey Gutiérrez EH, Sánchez C. HM, **Marshall JM** (2022) Monitoring needs for gene drive mosquito projects: Lessons from vector control field trials and invasive species. Frontiers in Genetics 12: 780327.

80. Kaduskar B, Kushwah RBS, Auradkar A, Guichard A, Li M, Bennett JB, Ferreira Julio AH, **Marshall JM**, Montell C, Bier E (2022) <u>Reversing insecticide</u> <u>resistance with allelic-drive in *Drosophila melanogaster*</u>. Nature Communications 13: 291.

81. Mondal A, Vásquez VN, **Marshall JM** (2022) <u>Target product profiles for</u> <u>mosquito gene drives: Incorporating insights from mathematical models</u>. Frontiers in Tropical Diseases 3: 828876.

82. Hossain MP, Zhou W, Ren C, **Marshall JM**, Yuan HY (2022) <u>Determining the effects of preseasonal climate factors toward dengue early warning system in Bangladesh</u>. PLoS Global Public Health 2: e0000047.

83. Connolly JB, Mumford JD, Glandorf DCM, Hartley S, Lewis OT, Evans SW, Turner G, Beech C, Sykes N, Coulibaly MB, Romeis J, Teem JL, Tonui W, Lovett B, Mankad A, Mnzava A, Fuchs S, Hackett TD, Landis WG, **Marshall JM**, Aboagye-Antwi F (2022) <u>Recommendations for environmental risk assessment of</u> <u>gene drive applications for malaria vector control</u>. Malaria Journal 21: 152.

84. Vásquez VN, Reddy M, **Marshall JM** (2022) <u>Environmentally appropriate</u> <u>vector control is facilitated by standard metrics for simulation-based evaluation</u>. Frontiers in Tropical Diseases 3: 953212.

85. Kandul NP, Liu J, Buchman A, Shriner IC, Corder RM, Warsinger-Pepe N, Yang T, Yadav AK, Scott MJ, **Marshall JM**, Akbari OS (2022) <u>Precision guided</u> <u>sterile males suppress populations of an invasive crop pest</u>. GEN Biotechnology 1: 372-385.

86. Taitingfong RI, Triplett C, Vásquez VN, Rajagopalan RM, Raban R, Roberts A, Terradas G, Baumgartner B, Emerson C, Gould F, Okumu F, Schairer CE, Bossin HC, Buchman L, Campbell KJ, Clark A, Delborne J, Esvelt K, Fisher J, Friedman RM, Gronvall G, Gurfield N, Heitman E, Kofler N, Kuiken T, Kuzma J, Manrique-Saide P, **Marshall JM**, Montague M, Morrison AC, Opesen CC, Phelan R, Piaggio A, Quemada H, Rudenko L, Sawadogo N, Smith R, Tuten H, Ullah A, Vorsino A, Windbichler N, Akbari OS, Long K, Lavery JV, Evans SW, Tountas K, Bloss CS (2022) <u>Exploring the value of a global gene drive project registry</u>. Nature Biotechnology 41: 9-13.

87. Sharma Y, Bennett JB, Rašić G, **Marshall JM** (2022) <u>Close-kin mark-recapture</u> <u>methods to estimate demographic parameters of mosquitoes</u>. PLoS Computational Biology 18: e1010755.

88. Terradas G, Bennett JB, Li Z, **Marshall JM**, Bier E (2023) <u>Genetic conversion</u> of a split-drive into a full-drive element. Nature Communications 14: 191.

89. Rerolle F, Dantzer E, Phimmakong T, Lover AA, Hongvanthong B, Phetsouvanh R, **Marshall JM**, Sturrock HJW, Bennett A (2023) <u>Characterizing</u> <u>mobility patterns of forest goers in southern Lao PDR using GPS loggers</u>. Malaria Journal 22: 38.

90. Smidler AL, Pai JJ, Apte RA, Sánchez C. HM, Corder RM, Gutiérrez EJ, Thakre N, Antoshechkin I, **Marshall JM**, Akbari OS (2023) <u>A confinable femalelethal population suppression system in the malaria vector, *Anopheles gambiae*. Science Advances 9: eade890.</u>

91. Carballar-Lejarazú R, Dong Y, Pham TB, Tushar T, Corder RM, Mondal A, Sánchez C. HM, Lee HF, **Marshall JM**, Dimopoulos G, James AA (2023) <u>Dual effector population modification gene-drive strains of the African malaria mosquitoes, *Anopheles gambiae* and *Anopheles coluzzii*. Proceedings of the National Academy of Sciences USA 120: e2221118120.</u>

92. Li HH, Su MP, Wu SC, Tsou HH, Chang MC, Cheng YC, Tsai KN, Wang HW, Chen GH, Tang CK, Chung PJ, Tsai WT, Huang LR, Yueh YA, Chen HW, Pan CY, Akbari OS, Chang HH, Yu GY, **Marshall JM**, Chen CH (2023) <u>Mechanical</u> transmission of dengue virus by *Aedes aegypti* may influence disease transmission dynamics during outbreaks. eBioMedicine 94: 104723.

93. Vásquez VN, Kueppers LM, Rašić G, **Marshall JM** (2023) <u>*wMel* replacement</u> of dengue-competent mosquitoes is robust to near-term climate change. Nature Climate Change 13: 848–855.

94. Raban R, **Marshall JM**, Hay BA, Akbari OS (2023) <u>Manipulating the destiny of</u> wild populations using <u>CRISPR</u>. Annual Review of Genetics 57: 1.

95. Vásquez VN, **Marshall JM** (2023) <u>Applications of mathematical programming</u> to genetic biocontrol. SIAM J Appl Math S392-S411.

96. Kormos A, Dimopoulos G, Bier E, Lanzaro GC, **Marshall JM**, James AA (2023) <u>Conceptual risk assessment of mosquito population modification gene-</u> <u>drive systems to control malaria transmission: Preliminary hazards list</u> <u>workshops</u>. Frontiers in Bioengineering & Biotechnology 11: 1261123.

97. Li M, Kandul N, Sun R, Yang T, Benetta ED, Brogan D, Antoshechkin I, **Sánchez C. HM**, Zhan YP, DeBeaubien N, Loh Y, Su M, Montell C, **Marshall JM**, Akbari OS (2024) <u>Targeting sex determination to suppress mosquito</u> <u>populations</u>. eLife 12: RP90199.

Book Chapters

1. **Marshall JM**, Akbari OS (2015) <u>Gene drive systems in mosquitoes</u>. In: Adelman ZN (editor) <u>Genetic Control of Dengue and Malaria</u>. Elselvier/Academic Press, New York.

2. **Marshall JM** (2015) <u>Measuring public attitudes to releases of transgenic</u> <u>mosquitoes for disease control</u>. In: Tyagi BK (editor) <u>WHO/TDR Training Manual:</u> <u>Biosafety for Human Health and the Environment in the Context of the Potential</u> <u>Use of Genetically Modified Mosquitoes</u>. WHO Press, Geneva.

3. **Marshall JM** (2015) <u>The Cartagena Protocol and releases of transgenic</u> <u>mosquitoes</u>. In: Tyagi BK (editor) <u>WHO/TDR Training Manual: Biosafety for</u> <u>Human Health and the Environment in the Context of the Potential Use of</u> <u>Genetically Modified Mosquitoes</u>. WHO Press, Geneva.

4. Suarez-Ramirez CD, Duran-Vega MA, Sanchez C. HM, Gonzalez-Mendoza M, Chang L, **Marshall JM** (2021) <u>Deep learning architectures applied to mosquito</u> <u>count regressions in US datasets</u>. In: Batyrshin I, Gelbukh A, Sidorov G (editors),

Advances in Computational Intelligence: MICAI 2021. Springer, Cham.

5. **Marshall JM**, Vásquez VN (2022) <u>Field trials of gene drive mosquitoes: Lessons</u> from releases of genetically sterile males and *Wolbachia*-infected mosquitoes. In: Tyagi BK (editor), <u>Genetically Modified and other Innovative Vector Control</u> <u>Technologies</u>. Springer, Singapore.

6. **Marshall JM**, North AR (2023) <u>Modeling priorities as gene drive mosquito</u> <u>projects transition from lab to field</u>. In: Carballar-Lejarazú R (editor), <u>Mosquito</u> <u>Gene Drives and the Malaria Eradication Agenda</u>. Jenny Stanford Publishing, Singapore.

Pre-prints

1. Wu SL, Dolgert AJ, Lewnard JA, **Marshall JM**, Smith DL (2020) Principled simulation of agent-based models in epidemiology. bioRxiv doi: <u>https://doi.org/10.1101/2020.12.21.423765</u>.

2. Rašić G, Filipović I, Wu SL, León TM, Bennett JB, Sánchez C. HM, **Marshall JM**, Trewin BJ (2021) Eliminating *Aedes aegypti* from its southern margin in Australia: Insights from genomic data and simulation modeling. bioRxiv doi: <u>https://doi.org/10.1101/2021.08.21.457232</u>.

3. Sánchez C. HM, Smith DL, **Marshall JM** (2023) MGSurvE: A framework to optimize trap placement for genetic surveillance of mosquito populations. bioRxiv doi: <u>https://doi.org/10.1101/2023.06.26.546301</u>.

4. Smidler AL, Apte RA, Pai JJ, Chow ML, Chen S, Mondal A, Sánchez C. HM, Antoshechkin I, **Marshall JM**, Akbari OS (2023) Eliminating malaria vectors with precision guided sterile males. bioRxiv doi: https://doi.org/10.1101/2023.07.20.549947.

5. Gendron W, Raban R, Mondal A, Sánchez C. HM, Smidler A, Zilberman D, Ilboudo PG, D'Allesandro U, **Marshall JM**, Akbari OS (2023) Cost-effectiveness of precision guided SIT for control of *Anopheles gambiae* in the Upper River region, The Gambia. bioRxiv doi: <u>https://doi.org/10.1101/2023.07.20.549762</u>.

6. Mondal A, Sánchez C. HM, **Marshall JM** (2023) MGDrivE 3: A decoupled vector-human framework for epidemiological simulation of mosquito genetic control tools and their surveillance. bioRxiv doi: https://doi.org/10.1101/2023.09.09.556958.

7. Filipović I, **Marshall JM**, Rašić G (2024) Finding divergent sequences of homomorphic sex chromosomes via diploidized nanopore-based assembly from a single male. bioRxiv doi: <u>https://doi.org/10.1101/2024.02.29.582759</u>.

Scientific Meetings and Invited Presentations	Marshall JM (2005) <u>The dynamics of transposable elements in genetically</u> <u>modified mosquito vectors</u> . Contributed talk at the Institute for Pure and Applied Mathematics Biophysical Modeling Workshop, Los Angeles, California.
	Marshall JM , Weiss R (2005) <u>A Bayesian approach to inferring recent selective</u> <u>sweeps in <i>Anopholes gambiae</i> populations</u> . Contributed talk at the 2nd International Meeting on Molecular and Population Biology of Mosquitoes and Other Disease Vectors, Kolymbari, Greece.
	Marshall JM (2006) <u>Successful conditions for the early spread of a transposable</u> <u>element in a disease vector population</u> . Contributed talk at the 55 th Annual Meeting of the American Society for Tropical Medicine and Hygiene, Atlanta, Georgia.
	Marshall JM (2007) The impact of dissociation on transposon-mediated disease

control strategies. Contributed talk at:

- the 3rd International Meeting on Molecular and Population Biology of Mosquitoes and Other Disease Vectors, Kolymbari, Greece,
- the 56th Annual Meeting of the American Society for Tropical Medicine and Hygiene, Philadelphia, Pennsylvania,
- the Workshop for Young Researchers in Mathematical Biology, Columbus, Ohio, and
- the 76th Annual Conference of the Mosquito and Vector Control Association of California, Palm Springs, California.

Marshall JM (2008) <u>Modelling the potential outcomes of releasing GM mosquito</u> <u>vectors</u>. Contributed talk at:

- the Malaria Research and Training Center, Bamako, Mali,
- the Department of Mathematics, University of Bamako, Bamako, Mali, and
- the 57th Annual Meeting of the American Society for Tropical Medicine and Hygiene, New Orleans, Louisiana.

Marshall JM (2009) <u>Can mosquitoes engineered with gene drive systems be</u> <u>contained?</u> Contributed talk at the 58th Annual Meeting of the American Society for Tropical Medicine and Hygiene, Washington, DC.

Marshall JM, Touré MB, Traore MM, Taylor CE (2009) <u>Perspectives of people in</u> <u>Mali, West Africa toward genetically modified mosquitoes for malaria control</u>. Contributed talk at:

- the Center for Society and Genetics, UCLA, Los Angeles, California
- the Malaria Research and Training Center, Bamako, Mali,
- the 4th International Meeting on Molecular and Population Biology of Mosquitoes and Other Disease Vectors, Kolymbari, Greece, and
- the 58th Annual Meeting of the American Society for Tropical Medicine and Hygiene, Washington, DC.

Marshall JM (2009) <u>Releasing GM mosquitoes: Insights from mathematics and</u> <u>Malians</u>. Invited talk at:

- the Department of Infectious Disease Epidemiology, Imperial College, London, England, and
- the Division of Biology, California Institute of Technology, Pasadena, California.

Marshall JM, Hay BA (2010) <u>General principles and novel possibilities for single-construct gene drive</u>. Contributed talk at the 59th Annual Meeting of the American Society for Tropical Medicine and Hygiene, Atlanta, Georgia.

Marshall JM (2010) <u>The Cartagena Protocol and genetically modified mosquitoes</u>. Contributed poster at the 59th Annual Meeting of the American Society for Tropical Medicine and Hygiene, Atlanta, Georgia.

Marshall JM (2011) <u>The Cartagena Protocol in the context of transgenic and</u> <u>*Wolbachia*-infected mosquitoes</u>. Contributed talk at the 60th Annual Meeting of the American Society for Tropical Medicine and Hygiene, Philadelphia, Pennsylvania.

Marshall JM (2011) <u>Malaria and human movement: Beyond Newton's theory of</u> <u>gravity</u>. Invited talk at the Department of Infectious Disease Epidemiology, London School of Hygiene and Tropical Medicine, London, England.

Marshall JM (2011) <u>The toxin and antidote puzzle: New ways to control insect pest</u> populations through manipulating inheritance. Contributed talk at:

- the Department of Biological Sciences, Imperial College London, London, England, and
- the 5th International Meeting on Molecular and Population Biology of Mosquitoes and Other Disease Vectors, Kolymbari, Greece.

Marshall JM (2011) <u>Genetic engineering of local populations</u>. Invited talk at the Department of Biological Sciences, Stanford University, Stanford, California.

Marshall JM, White MT, Ghani AC, Schlein Y, Muller GC, Beier JC (2012) Quantifying the mosquito's sweet tooth: Modelling the effectiveness of attractive toxic sugar baits for vector control. Contributed talk at:

- the Malaria Centre, Imperial College London, London, England,
- the 61st Annual Meeting of the American Society for Tropical Medicine and Hygiene, Atlanta, Georgia, and
- the 6th International Meeting on Molecular and Population Biology of Mosquitoes and Other Disease Vectors, Kolymbari, Greece.

Marshall JM, Hay BA (2012) *Medusa*: A novel gene drive system for confined suppression of mosquito populations. Contributed talk at:

- the Malaria Centre, Imperial College London, London, England, and
- the 61st Annual Meeting of the American Society for Tropical Medicine and Hygiene, Atlanta, Georgia.

Marshall JM (2012) <u>If Mother Teresa was a Genetic Engineer</u>. Invited talk at <u>TEDx LA Miracle Mile</u>, Los Angeles, California.

Marshall JM (2013) <u>What role should mathematical models and transgenic</u> <u>mosquitoes play in dengue control programs in India?</u> Invited talk at Brain Storming Conference on Dengue Scenario in India: Disease Burden, Surveillance and Control, Madurai, India.

Marshall JM (2013) <u>If Mother Teresa was a genetic engineer: From golden rice to</u> <u>GM mosquitoes for malaria control</u>. Invited talk at University College London, London, England.

Marshall JM, Touré MB, Ouédraogo AL, Ndhlovu M, Kiware SS, Rezai S, Nkhama E, Griffin JT, Hollingsworth TD, Doumbia S, Govella NJ, Ferguson NM, Ghani AC (2014) <u>Contributions of women with children and youth workers to</u> <u>spatial malaria transmission in sub-Saharan Africa</u>. Contributed talk/poster at:

- the MRC Centre for Outbreak Analysis and Modeling, Imperial College London, London, England, and
- the 63rd Annual Meeting of the American Society for Tropical Medicine and Hygiene, New Orleans, Louisiana.

Marshall JM (2014) <u>Predicting the utility of novel strategies for vector-borne</u> disease control using mathematical models. Invited talk at:

- the Division of Biostatistics, University of California, Berkeley, California, and
- the Department of Medicine, University of California, San Francisco, California.

Marshall JM, Bennett A, Midekisa A, Gosling R, Sturrock HJW (2015) From risk maps to decision maps for malaria elimination. Contributed poster at the 64th Annual Meeting of the American Society for Tropical Medicine and Hygiene, Philadelphia, Pennsylvania.

Marshall JM (2015) <u>Mathematical modeling in a new era of malaria elimination</u>. Invited talk at:

- the Department of Entomology, University of Maryland, College Park, Maryland, and
- the <u>Bay Area World Malaria Day Symposium</u>, University of California, Berkeley, California.

Marshall JM (2015) <u>The current global policy situation regarding GM insects for</u> <u>disease control</u>. Invited talk at the House of Lords, London, England.

Marshall JM (2016) <u>Overcoming evolved resistance to population-suppressing</u> <u>homing-based gene drives</u>. Contributed poster at the 65th Annual Meeting of the American Society for Tropical Medicine and Hygiene, Atlanta, Georgia.

Marshall JM (2016) <u>Designing disease control strategies using models and data</u> <u>from multiple sources</u>. Invited talk at the ENAR 2016 Spring Meeting, Austin, Texas.

Marshall JM (2016) <u>Zika virus: Insights from mathematical models</u>. Invited talk at the Preparedness for Zika Virus Symposium, University of California, San Francisco, California.

Marshall JM (2017) <u>Parameter estimation in infectious disease epidemiology: Do</u> <u>you have any better ideas?</u> Invited talk at the Workshop in Biostatistics, Department of Biomedical Data Science, Stanford University, Stanford, California.

Marshall JM (2017) <u>Gene drive: What is possible at the population level with</u> <u>currently-available molecular components?</u> Invited talk at:

- the Lorentz Center workshop on "Challenges for the Regulation of Gene Drive Technology", Leiden, the Netherlands,
- the 25th International Congress of Entomology, Orlando, Florida,
- the Statistics and Genomics Seminar, Division of Biostatistics, University of California, Berkeley, California,
- the Department of Medicine, University of California, San Francisco, California,
- the Joint Genome Institute, Walnut Creek, California, and
- Henry Stewart Talks on "Gene Drives and Active Genetics", <u>https://hstalks.com/t/3764/gene-drive-what-is-possible-at-the-population-leve/</u>.

Marshall JM (2017) <u>Gene drive: Modeling replacement, suppression and</u> <u>remediation in quantified ecosystems</u>. Invited talk at the LAVIPAC workshop on "Innovative Vector Control Strategies in the Pacific", Moorea, French Polynesia.

Marshall JM (2017) <u>Why has dengue resurged, why does malaria persist, and can these diseases be controlled by CRISPR-based gene drive and other novel tools?</u> Invited talk at:

- the Guangzhou Center for Disease Control and Prevention, Guangdong, China, and
- the National Health Research Institutes, Zhunan, Taiwan.

Marshall JM (2018) <u>Can malaria, dengue and Zika be controlled by CRISPR-based</u> gene drive and other novel tools? Invited talk at:

- the Harvard Medical School, Harvard University, Boston, Massachusettes,
- the Department of Biological Sciences, University of Notre Dame, Notre Dame, Indiana,
- the Jet Propulsion Laboratory, California Institute of Technology, Pasadena, California, and
- the QIMR Berghofer Medical Research Institute, Brisbane, Australia.

Marshall JM (2018) <u>Designing safe strategies to eliminate malaria using gene editing</u>. Invited talk at:

- the Bay Area World Malaria Day Symposium, Zuckerberg San Francisco General Hospital, San Francisco, California, and
- the <u>School of Public Health 75th Anniversary Research Showcase</u>, University of California, Berkeley, California.

Marshall JM (2018) <u>CRISPR-Cas9-based gene drive architecture for control of agricultural pests</u>. Invited talk at the Plant Genome Engineering Symposium, University of California, Berkeley, California.

Sánchez HM, Wu SL, Bennett JB, **Marshall JM** (2018) <u>MGDrivE: A simulation</u> framework for gene drive in spatially-explicit mosquito populations and its application to threshold-dependent systems. Invited talk/poster at:

- the Annual Meeting of the Society for Mathematical Biology, Sydney, Australia,
- the 67th Annual Meeting of the American Society for Tropical Medicine and Hygiene, New Orleans, Louisiana, and
- the Annual Meeting of the Entomological Society of America, Vancouver, Canada.

Marshall JM (2018) <u>Fighting mosquito-borne diseases with genomics, machine learning and likelihood functions</u>. Invited talk at:

- the School of Public Health, University of California, Berkeley, California,
- the Chan Zuckerberg Biohub, San Francisco, California, and
- Verily Life Sciences, South San Francisco, California.

Marshall JM (2019) <u>Can malaria, dengue and Zika be controlled by a CRISPR-based gene drive? Insights from mathematical models</u>. Invited talk at:

- the Innovative Genomics Institute, Berkeley, California,
- the School of Public Health, University of California, Berkeley, California,
- the David Geffen School of Medicine, University of California, Los Angeles, California,
- Cal Day 2019, University of California, Berkeley, California,
- the Arthropod-borne Diseases in the Age of Quantitative Biology Symposium, Gladstone Institutes, San Francisco, California, and
- INSPI (Instituto Nacional de Investigación en Salud Pública), Quito, Ecuador.

Vasquez VN, **Marshall JM** (2019) <u>Informing risk assessment with the Mosquito</u> <u>Gene Drive Explorer (MGDrivE)</u>. Invited talk at the Gene Drive Modeling Conference, ILSI Research Foundation, Washington, DC.

Marshall JM (2019) <u>Data sharing in gene drive research: Experiences of a</u> <u>mathematical modeler</u>. Invited talk at the Gene Drive Research Forum, African Union, Addis Ababa, Ethiopia.

Marshall JM, Sánchez HM, Bennett JB, Wu, SL, León TM, Rašić G, Akbari OS (2020) <u>Modeling novel genetic control strategies for *Aedes aegypti* disease vectors</u>. Invited talk at:

- the 69th Annual Meeting of the American Society for Tropical Medicine and Hygiene (virtual), and
- the 90th Annual Conference of the Mosquito and Vector Control Association of California, Sacramento, CA.

Marshall JM (2021) <u>Current status of genetic strategies for mosquito-borne disease</u> <u>control</u>. Invited talk at the School of Public Health, University of California, Berkeley, California (virtual).

Marshall JM (2021) <u>Modeling priorities as gene drive mosquito projects transition</u> <u>from lab to field</u>. Invited talk at:

- the Annual Meeting of the Society for Mathematical Biology (virtual),
- the Interdisciplinary Workshop on Synthetic Gene Drives (virtual), and
- the Johns Hopkins Malaria Research Institute (virtual).

	Marshall JM (2022) <u>A roadmap for monitoring gene drive field release scenarios</u>
	over time and the role of models. Invited talk at a pre-meeting to the 8th Annual Conference of the Pan-African Mosquito Control Association in Kigali, Rwanda.
	Corder RM, Marshall JM (2023) Modeling and analytics to support the transition of gene drive mosquito projects from lab to field. Invited talk at the 72 nd Annual Meeting of the American Society for Tropical Medicine and Hygiene, Chicago, Illinois.
	Marshall JM (2023) <u>Close-kin mark-recapture methods to estimate demographic</u> parameters of mosquitoes. Invited talk at:
	 the 72nd Annual Meeting of the American Society for Tropical Medicine and Hygiene, Chicago, Illinois, and the Department of Statistics, University of Auckland, Aotearoa/New Zealand.
	Marshall JM (2024) <u>Modeling needs for gene drive mosquito projects</u> . Invited talk at a pre-meeting to the Gene Drive Research Forum, Marina del Rey, California.
Memberships	2016-current: American Society for Tropical Medicine and Hygiene (ASTMH)
Professional	
Service	Reviewer for: Science; Nature Biotechnology; Nature Communications; Proceedings of the National Academy of Sciences USA; Lancet Infectious Diseases; eLife; PLoS Computational Biology; PLoS Genetics; PLoS ONE; Journal of Theoretical Biology; Journal of the Royal Society Interface; Proceedings of the Royal Society B; Malaria Journal; American Journal of Tropical Medicine and Hygiene; BMC Biology; Mathematical Biosceinces; Acta Tropica; BioSystems; Journal of Computational Science; Transactions of the Royal Society of Tropical Medicine and Hygiene; Infection, Genetics and Evolution; Electronic Journal of Biotechnology; Asia-Pacific Journal of Molecular Biology and Biotechnology; British Journal of Medicine and Medical Research; Evolutionary Applications
	Grant reviewer for: European Research Council, UK Medical Research Council, NordForsk, France Berkeley Fund
	Expert advisor for: US National Academy of Sciences, The Cartagena Protocol on Biosafety to the Convention on Biological Diversity, Ad Hoc Technical Expert Group on Synthetic Biology to the Convention on Biological Diversity, Médecins Sans Frontières
Referees	Professor Bruce A. Hay Division of Biology and Biological Engineering California Institute of Technology Email: <u>haybruce@caltech.edu</u> Phone: +1-626-395-3399
	Professor Azra C. Ghani Department of Infectious Disease Epidemiology Imperial College London Email: <u>a.ghani@imperial.ac.uk</u> Phone: +44-20-7594-5764
	Professor Anthony A. James Department of Molecular Biology and Biochemistry

University of California, Irvine Email: <u>aajames@uci.edu</u> Phone: +1-949-824-5930