

Curriculum Vitae

Joana S. C. Carneiro da Silva, Ph.D.
Professor, Department of Microbiology & Immunology
Institute for Genome Sciences
University of Maryland School of Medicine

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Contact Information

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Languages: Portuguese (native), English (fluent), French and Spanish (working knowledge)

Education

1992 B.Sc., Biology, Universidade Clássica de Lisboa, Faculdade de Ciências, Lisbon, Portugal. Thesis project: "The ichthyoplanktonic community of Long Island Sound, USA". Collaborative project with the Milford Laboratory, Natl. Marine Fisheries Service, Natl. Oceanic and Atmospheric Administration (NOAA), CT, USA.
2000 Ph.D., Genetics, Interdisciplinary Program in Genetics, The University of Arizona, Tucson, AZ, USA. Major Advisor: Margaret G. Kidwell. Thesis: "Population genetics of *P* transposable elements and their host species, with emphasis in *Drosophila willistoni* and *D. sturtevantii*".

Post-Graduate Education

2000-2002 Fogarty International Post-doctoral Fellow, Computational Biology Branch, National Center for Biotechnology Information (NCBI), National Institutes of Health (NIH), Bethesda, MD, USA. Mentor: Alexey A. Kondrashov. Topic: Mammalian Evolutionary Genomics.

Other Education

1991 "Applied multivariate methods using popular statistical computing packages", June 12-14, Institute for Professional Education, Washington, DC.
1994 "Workshop on Molecular Evolution", August 6-19, Marine Biological Lab, Woods Hole, MA.
2003 "Perl Programming". Feb. 3-7. Sun Microsystems, Rosslyn, VA.
2020 Faculty Mentoring Workshops, including modules on "Effective Communication", "Aligning Expectations and Assessing Understanding", "Addressing Equity and Inclusion" and "Supporting Independence and Promoting Professional Development", by the SOM Career and Professional Development Office.
2022 "Raising a Resilient Scientist" Series, Winter 2022, Office of Intramural Training & Education (OITE), National Institutes of Health, by Sharon L. Milgram, Director, NIH OITE

Employment

2002-2004	Staff Scientist I, The Institute for Genomic Research, Rockville, MD.
2005	Staff Scientist II, The Institute for Genomic Research, Rockville, MD.
2006-2007	Assistant Investigator, The Institute for Genomic Research, Rockville, MD.
2007-present	Researcher, Institute for Genome Sciences, University of Maryland School of Medicine
2007-2015	Assistant Professor, Department of Microbiology and Immunology, University of Maryland School of Medicine
2015-2020	Associate Professor, Department of Microbiology and Immunology, University of Maryland School of Medicine
2020-present	Professor, Department of Microbiology and Immunology, University of Maryland School of Medicine

Program Affiliations

2011-present	Associate Member, Center for Vaccine Development and Global Health, University of Maryland School of Medicine
2014-2017	Affiliate Faculty, School of Systems Biology, George Mason University
2018-2019	Sabbatical Leave, Visiting Scholar, Global Health and Tropical Medicine, Instituto de Higiene e Medicina Tropical, Universidade NOVA de Lisboa, Lisbon, Portugal (GHTM / IHMT / NOVA)
2023-present	Honorary Member, Vector-Borne Diseases Group, GHTM / IHMT / NOVA, Lisbon, Portugal

Professional Society Memberships

1988-1994	Portuguese Biologists' Association (APB)
1993-1998	Society for the Study of Evolution
1995-2000	The Genetics Society of America
1996-present	Society for Molecular Biology and Evolution
2005-2012	American Association for the Advancement of Science
2013-present	American Society of Tropical Medicine and Hygiene

Honors and Awards

1992-1996	Doctoral Research Fellowship, Junta Nacional de Investigação Científica e Tecnológica (JNICT), Portugal
1997-1999	Doctoral Dissertation Improvement Award, National Science Foundation
1997-1998	NSF Research Training Group in the Analysis of Biological Diversification Research Fellowship, The University of Arizona
1998-1999	Robert S. Flinn Foundation Research Fellowship, The University of Arizona
2000-2002	Fogarty International Post-doctoral Fellowship, National Institutes of Health
2013	2013 Maryland's Top 100 Women Award, The Daily Record. <i>Maryland's Top 100 Women recognizes high-achieving Maryland women who are making an impact through their leadership, community service and mentoring.</i>
2016	Baltimore City Community College (BCCC), Partnership Award. <i>This award is granted to BCCC community partners who contribute to the success of BCCC programs and the academic development of its students.</i>
2016	Dr. Patricia Sokolove Outstanding Mentor Award. <i>The award was established by the UMB Graduate Student Association (GSA) to honor those who put forth great effort in aiding and mentoring graduate students. The GSA presents the award at the Graduate School's Doctoral Hooding Ceremony in May.</i>

Administrative Service**Institutional Service**

2003-2005	Coordinator, EvoGeno Discussion Group, The Institute for Genomic Research (TIGR)
2005-2007	Staff Scientist Review Committee, TIGR
2006	Faculty Search Committee, TIGR
2007-2010	Co-organizer, "Molecular Evolution and Phylogenetics" discussion group Institute for Genome Sciences (IGS), University of Maryland School of Medicine (UMSOM)
2008	Faculty Search Committee, IGS
2009-2010	Genomics Resource Center Advisory Committee, IGS
2009-2012	Appointments, Promotion and Tenure (APT) Committee, IGS
2009-present	Outreach Committee, IGS
2010	Presenter, IGS-UMBC Collaboration Meeting, UMBC Campus
2010	Organizer, IGS-UMBC Collaboration Meeting, IGS
2012-present	Member, Qualifying Exam Committee, Molecular Medicine, Genomics track, UMB One or two exams per year.
2012-2013	UMB President's Outreach Council, Science Olympiad Work Group
2013-2014	UMB President's Outreach Council, Science Work Group
2013-present	Organizer, "Methods in Evolutionary Genetics (MEG)" journal club, IGS, UMSOM ** Meets every other week and is regularly attended by >12 faculty, postdocs and graduate students
2014	Member, Junior Faculty Site Visit Team, NIH Medical Scientist Training Program (MSTP), University of Maryland School of Medicine, October 27, 2014 ** MSTP was renewed and expanded (from four to eight slots)
2015-2016	Search Committee member, Faculty search, IGS, UMB. **This faculty search resulted in two new faculty hires
2017-2022	Member, Advisory and Admissions Committee, Medical Scientist Training Program (MSTP), UMSOM, UMB
2020-	Member, IGS Operations Committee
2021	Search Committee, IGS Human Resources Manager, IGS, UMB
2021, 22, 23	Member, Qualifying Exam Committee, Molecular Microbiology and Immunology, UMB
2021, 22	Admissions Committee, Molecular Microbiology and Immunology Doctoral Program.

National/International Service

1996	Organizing Committee, 4 th Annual International Meeting of the Society for Molecular Biology and Evolution
2005	<i>Ad hoc</i> proposal reviewer, NSF Division of Molecular and Cellular Biosciences – Genes and Genome Systems Cluster
2006	Program Committee, 9 th Annual Conference on Computational Genomics
2007	Judge, Student Poster Contest, 15 th Annual International Meeting of the Society for Molecular Biology and Evolution
2009	Reviewer, Cottrell College Science Awards, Single Investigator Awards
2010	Panelist, "NIH Career Symposium", Office of Intramural Training and Education, NIH
2010	NSF Review Panel, Evolutionary Processes Cluster of the Division of Environmental Biology, Evolutionary Genetics Panel
2011	NSF Review Panel, Evolutionary Processes Cluster of the Division of Environmental Biology, Evolutionary Genetics Panel
2011-2012	IGS Representative, NIAID-GSCID Eukaryotic Working Group
2012	NIEHS, NIH / NSF Study Section, joint National Institute of Environmental Health Science, NIH, and NSF Study Section.

2015	NSF Review Panel, Evolutionary Processes Cluster of the Division of Environmental Biology, Evolutionary Genetics Panel
2015	NIGMS, NIH, Special Emphasis Panel/Scientific Review Group ZGM1 RCB-0 (SC)
2017	NIAID, NIH, Special Emphasis Panel/Scientific Review Group ZAI1 EC-M (S2)1, System Biology: The Next Generation for Infectious Diseases (U19)
2018	NIH, Genetic Variation and Evolution (GVE) Study Section
2019	NIH, Understanding Vaccine Elicited Protective Immunity to Malaria in Endemic Regions. Special workshop organized by NIAID.
2019	NIH, Special Emphasis Panel/Scientific Review Panel 2020/01 ZRG1 F18-Z (20) L
2020	NIH, Special Emphasis Panel/Scientific Review Panel 2020/05 ZRG1 F18-Z (20) L
2021	NIH, Clinical Research and Field Studies (CRFS) of Infectious Diseases Study Section
2021	<i>Ad hoc</i> proposal reviewer, German Research Foundation (Deutsche Forschungsgemeinschaft, DFG)
2021-present	Member, ASTMH International Membership Committee
2021	NIH, Infectious Diseases and Immunology B, Special Emphasis Review Panel 2022/01 ZRG1 F07B-U (20) L
2022	NIH, Population-based Research in Infectious Diseases (PRID) Study Section

Journal review

2003-present	<i>Ad hoc</i> manuscript reviewer (~6 reviews/year). Have reviewed for the following journals: <i>ACS Infectious Diseases</i> <i>Anais da Academia Brasileira de Ciências</i> <i>BMC Evolutionary Biology, BMC Genomics, BMC Veterinary Research</i> <i>Comparative and Functional Genomics</i> <i>Database</i> <i>Evolution</i> <i>Frontiers In Immunology</i> <i>Gene</i> <i>Genetica</i> <i>Genetics</i> <i>Genome Research</i> <i>Genomics</i> <i>Journal of Biological Chemistry</i> <i>Malaria Journal</i> <i>Microbial Genomics</i> <i>Mini Reviews in Medicinal Chemistry</i> <i>Molecular Biology and Evolution</i> <i>Molecular Ecology</i> <i>Molecular Genetics and Genomics</i> <i>Molecular Phylogenetics and Evolution</i> <i>Nature</i> <i>Nucleic Acids Research</i> <i>PLoS Computational Biology, PLoS Neglected Tropical Diseases, PLoS One</i> <i>Scientific Reports</i> <i>Vaccine</i>
2009-2016	Member, Editorial Board, <i>Database, The journal of biological databases and curation</i>
2016-present	Associate Editor, <i>Journal of Molecular Evolution</i>
2017-present	Academic Editor, <i>PeerJ</i>
2019, 2020	Selection Committee, <i>Journal of Molecular Evolution's</i> annual Zuckerkandl Prize, Dec 2019, Dec 2020
2022-present	Associate Editor, <i>Frontiers in Immunology, Vaccines and Molecular Therapeutics</i>
2022-present	Review Editor, <i>Frontiers in Parasitology, Parasite -Omics</i>
2022-present	Review Editor, <i>Frontiers in Parasitology, Molecular and Cellular Parasitology</i>

Local Service

- 1997 Co-organizer, "Biodiversity Day" at Naylor Middle School, Tucson, AZ.
- 1997, 1998 Presenter, "Biodiversity Day" at Naylor Middle School, Tucson, AZ. "*Drosophila* diversity" and "Species identification".
- 2011 Co-organizer, visit to IGS for students from the Institute of Notre Dame (IND), a female-only high school in East Baltimore. These students, juniors and seniors, attend the IND's Biomedical Sciences Program, with a novel curriculum "Lead the Way Biomedical Sciences".
- 2012, 2013 Presenter, science lectures and hands-on activities, Evergreen Montessori School
- 2012 Co-organizer, IGS participation in BioPark's "BioBlast".
- 2012 Co-organizer, "Young Women in Bio" event at IGS.
- 2012-2013 Member, UM BioPark K-12 Education Task Force
- 2013 Co-organizer and Presenter, IGS participation in the BioPark's "BioBlast".
- 2013 Co-organizer and Presenter, IGS visit by middle school students from the UMB K-12 partner institutions participating in the Science Olympiad.
- 2013 Faculty Interviewer, Mock interview training session for Baltimore City Community College's Life Sciences Institute (BCCC-LSI) students.
- 2013 Presenter, Baltimore City Community College's Life Sciences Institute (BCCC-LSI) round table "Getting to Know U".
- 2013 Panelist, Lunch for Hungry Minds. Topic: "BCCC's Biotechnology Program"
- 2013 Presenter, Center for Talented Youth's Science and Technology Series, a Johns Hopkins University program. Topic: "Genetic Variation and Personalized Genomics".
- 2015 Presenter, "Cells and their organelles", Introductory lecture and hands-on activity, UMSOM MiniMed School Summer Camp session, 40 West Baltimore children ages 6-12.
- 2015 Presenter, Center for Talented Youth's Science and Technology Series, a Johns Hopkins University program. Topic: "Genetic Variation and Personalized Genomics".
- 2017 Presenter, Career Day, Pine Crest Elementary School
- 2017 Faculty participant, Breakfast and Luncheon Mentoring Roundtables, PROMISE Summer Success Institute, a Maryland Pipeline Professional Development Conference to serve graduate students from underserved groups attending any of 15 member institutions of higher education in the State of Maryland.
- 2017 Presenter, Center for Talented Youth's Science and Technology Series, a Johns Hopkins University program. Topic: "Genetic Variation and Personalized Genomics".

Teaching Service**Undergraduate Student Teaching/Mentoring**

- 1996 Teaching Assistant, Genetics 320, University of Arizona
30 3rd yr undergraduate students
6 direct contact hrs/week, for 4 months.
- 1997 Teaching Assistant, Introductory Biology 181, University of Arizona
60 1st yr undergraduate students
6 direct contact hrs/week, for 4 months.
- 1998 Research mentor, Molecular Biology, University of Arizona
2 UofA undergraduate students, LaVonne Honyouti and DeeDee.
10hrs/week, 12 months.
- 2012-2013 Research Mentor, Ingenuity Research Program, Bioinformatics
Raphael Kargon, Baltimore Polytechnic Institute
High school junior and senior years, 15 months Internship.
Was accepted to Brown University.
- 2012 Research Mentor, Individual Research Project,
Hanzel Timmy Gotia, Baltimore City Community College.

- 2013 Entered US Army; currently with US Army Medical Department Regiment.
Research Mentor, Summer Internship, Bioinformatics
Shaikh Bilal Iqbal, Senior, University of Maryland Baltimore County
Graduated. Was hired as Research Assistant.
- 2015 Research Mentor, Individual Research Project,
Jamal El Badaoui, Baltimore City Community College
Transitioned to 4-yr program at University of Maryland.
- 2016-2017 Research Mentor, Semester Internship, Bioinformatics
Saqlain Amin, Senior, University of Maryland Baltimore County
Graduated. Was hired by Digi-Infotek.

Post-Graduate Student Teaching

- 2004 Lecturer, Workshop, "A brief introduction to phylogenetics and tree reconstruction methods"
20-30 staff members, The Institute for Genomic Research (TIGR)
2 contact hours
- 2009-present **Lecturer, GPLS716** Genomics and Bioinformatics, UMSOM
Topic: Eukaryotic Comparative Genomics
12-14 students/yr
3 contact hours/yr
- 2009 **Section Leader, GPLS601** Mechanisms in Biomedical Sciences (Core Course),
Genetics Section, UMSOM
~60 students/yr
40 contact hours
- 2009-2010 **Lecturer, PREV780** Molecular Epidemiology, UMSOM
Topic: Phylogenetics and Molecular Evolution of Infectious Diseases
8-10 students/yr
3 contact hours/yr
- 2010-present **Lecturer, GPLS710** Principles of Microbial Pathogenesis, UMSOM
Topic: Bioinformatics Approaches to Parasitology
12-14 students/yr
1.5 contact hours/yr
- 2012-present **Co-Course Director, GPLS716** Genomics and Bioinformatics, UMSOM
12-14 students/yr
40 contact hours/yr
*Interrupted during academic year of 2018-2019, while I was away on sabbatical
- 2012 **Lecturer, PREV780** Molecular Epidemiology, UMSOM
Topic: Phylogenetics and Molecular Evolution of Infectious Diseases
~8 students
1.5 contact hours
- 2013-2015, **Lecturer, GPLS692** Current Topics in Genome Biology, UMSOM
2019-present Topic: Parasite genomics, drug and vaccine resistance
12-14 students/yr
1.5 contact hours/yr
- 2013-present **Discussion Leader**, small group session, **CIPP907** Responsible Conduct of
Research, UMSOM
2013 topic: Scientific Misconduct
2014 topic: Publications, grants, and the peer review system
2015-2018 topic: Mentor/Mentee responsibilities, duties, and relationships
2022 topic: Authorship, quotation, paraphrasing, citation and plagiarism
~8 students
1.5 contact hours/yr
- 2014-2016 **Lecturer, GPLS716** Genomics and Bioinformatics, UMSOM
Topic: Transcriptomics
12-14 students/yr

- 3 contact hours/yr
- 2019 **Lecturer, Masters in Biomedical Sciences**, Instituto de Higiene e Medicina Tropical, Universidade NOVA de Lisboa, Lisbon, Portugal
Topic: Vaccine Resistance: the case of Malaria
15-20 student
1.5 contact hours
- 2022 **Lecturer, GPLS717 Genomic Applications**, UMSOM
Topics: 3 lectures; Short read sequencing, Sequence enrichment, Non-Model Organism genome assembly/Long read sequencing
8 students
4.5 contact hours/yr

Post-graduate Mentoring activities

Internships

- 2003-2005 Shelby Bidwell, Research Assistant
Research Mentor, The Institute for Genomic Research (TIGR), 2 contact hrs/week
Current position: Bioinformatics Staff, NCBI, NIH, Bethesda, MD
- 2007 Karthik Kota, Master's student in Bioinformatics, University of Georgia.
Research Mentor, Summer Internship, TIGR
Next position: Developer in Technology Pipeline Solutions, Monsanto.
- 2012 Sonal (Patel) Henson, International Livestock Research Institute (ILRI), Nairobi, Kenya
Research Mentor, 1 month, Institute for Genome Sciences, UMSOM
Next position: Bioinformatics Engineer, ILRI, Nairobi, Kenya
- 2013 Martin Norling, PhD candidate in Bioinformatics, Swedish University of Agricultural Sciences (SLU), Uppsala, Sweden
Research Mentor, 3 months, Institute for Genome Sciences, UMSOM
Next position: Postdoctoral fellow, Sweden.
- 2021 Thomas Stabler, PhD student, Swiss Tropical and Public Health Institute (Swiss TPH), Basel, Switzerland
Research Mentor, 6 months, Institute for Genome Sciences, UMSOM

Lab Rotation Research Mentor

- 2010 Christopher Jacob, PhD student, Molecular Medicine, UMSOM
- 2012 Kelly Robinson, PhD student, Molecular Medicine, UMSOM
- 2012 Eugene Gardner, PhD student, Molecular Medicine, UMSOM
- 2013 Kyle Tretina, PhD student, Molecular Microbiology and Immunology, UMSOM
- 2013 Olukemi (Abolude) Ifeonu, PhD student, Bioinformatics and Computational Biology, George Mason University
- 2013 Kara Moser, PhD student, Epidemiology and Human Genetics, UMSOM
- 2014 Timothy Hosteley, PhD student, Molecular Medicine, UMSOM
- 2014 Sonia Agrawal, PhD student, Epidemiology and Human Genetics, UMSOM
- 2015 Daniel Harris, PhD student, Molecular Medicine, UMSOM
- 2015 Alexa Machikas, PhD student, Molecular Medicine, UMSOM
- 2015 Miriam Ismail, PhD student, Epidemiology and Human Genetics, UMSOM
- 2016 Nicholas Palmateer, PhD student, Molecular Medicine, UMSOM
- 2016 Emily Stucke, PhD student, Epidemiology and Human Genetics, UMSOM
- 2017 Gurmanna Kalra, PhD student, Molecular Medicine, UMSOM
- 2017 Gillian Mbambo, PhD student, Molecular Microbiology and Immunology, UMSOM
- 2021 Diego Veliz-Otani, PhD student, Epidemiology and Human Genetics, UMSOM
- 2021 Kaylee Watson, PhD student, Molecular Medicine, UMSOM
- 2021 Ryan Scalsky, MD-PhD student, Epidemiology and Human Genetics, UMSOM
- 2021 Emily Amanian, PhD student, Molecular Microbiology and Immunology, UMSOM
- 2022 Yiwey Wang, PhD student, Molecular Medicine, UMSOM

Thesis Committee Member

- 2008-2010 Jennifer Rathe, MD/PhD student, Medical Scientist Training Program (MSTP), and Program in Molecular Medicine, UMSOM.
Thesis Reader
Current position: Pediatric Medical Resident, Columbia Presbyterian / CHONY
- 2011-2015 Christopher Jacob, PhD student, Program in Molecular Medicine, UMSOM
Thesis Reader
Current position: Research Fellow, Sanger Institute, UK.
- 2012-2014 Elena Artimovich, Program in Epidemiology and Human Genetics, UMSOM
Current position: Post-doctoral fellow, UMB.
- 2014-2019 Sonia Agrawal, Program in Epidemiology and Human Genetics, UMSOM
Current position: Staff Scientist.
- 2015-2019 Daniel Harris, PhD student, Program in Molecular Medicine, UMSOM
Current position: Postdoctoral Fellow.
- 2017-2020 Zalak Shah, PhD student, Program in Molecular Medicine, UMSOM
Current position: PhD candidate, UMSOM.
- 2017-2019 Michael Kessler, PhD student, Program in Molecular Medicine, UMSOM
Current position: Post-doctoral fellow, Johns Hopkins University.
- 2018-2022 Emily Stucke, Program in Epidemiology and Human Genetics, UMSOM
Current position: PhD candidate, UMSOM.
- 2018-2019 Matthew Chung, PhD student, Program in Molecular Medicine, UMSOM
Current position: Postdoctoral Fellow.
- 2018-2020 Albert Zhou, MD/PhD student, Program in Epidemiology and Human Genetics, and Medical Scientist Training Program (MSTP), UMSOM
Thesis Reader
- 2019-2022 John Mattick, PhD student, Program in Molecular Medicine, UMSOM
- 2020-present Matthew Adams, PhD student, Program in Epidemiology and Human Genetics, UMSOM
- 2021-present Alexandra Vlk, MD/PhD student, Program in Molecular Medicine, and Medical Scientist Training Program (MSTP), UMSOM

Doctoral Thesis Mentor or Co-Mentor

- 2012-2016 Kyle Tretina, Program in Molecular Microbiology and Immunology, UMSOM.
Thesis: *Theileria parva* genomics, transcriptomics, and host-pathogen interactions.
Current position: Alliance Manager, AI Platforms, Insilico Medicine.
- 2012-2017 Antoine Dara, Program in Molecular Microbiology and Immunology, UMSOM
Co-Mentor and Thesis Reader
Current position: Assistant Professor, University of Bamako, Mali.
- 2013-2017 Olukemi (Abolude) Ifeonu, Bioinformatics and Computational Biology Program, George Mason University (GMU).
Thesis: Genomic Resources for *Cryptosporidium* Species, human pathogens of public health significance in developing countries
Current position: Bioinformatics Analyst III, IGS.
- 2013-2018 Kara Moser, Program in Epidemiology and Human Genetics, UMSOM.
Thesis: Genomic epidemiology of the malaria parasite *Plasmodium falciparum*: Implications for whole-organism malaria vaccine development
Current position: Research Scientist, Centers for Disease Control and Prevention.
- 2016-2021 Nicholas Palmateer, PhD student, Program in Molecular Medicine, UMSOM.
Thesis: *Theileria* infections in African cattle and buffalo: understanding genetic variation and speciation
Current position: Postdoctoral fellow at the New Jersey Public Health and Environmental Laboratory.
- 2017-present Gillian Mbambo, Program in Molecular Microbiology and Immunology, UMSOM

- 2019-present Current position: PhD candidate, UMSOM.
Wilson Tavares, Program in Biomedical Sciences, Institute for Hygiene and Tropical Medicine, NOVA University, Lisbon, Portugal
- 2021-present Current position: PhD candidate.
Thomas Stabler, PhD student, Swiss Tropical and Public Health Institute (Swiss TPH), Basel, Switzerland
Co-mentor
- 2021-present Ryan Scalsky, MD/PhD student, Program in Epidemiology and Human Genetics, and Medical Scientist Training Program (MSTP), UMSOM
- 2022-present Yiwei Yang, PhD student, Program in Molecular Medicine, UMSOM.

Post-Doctoral or Junior Faculty Mentor

- 2006-2007 Xiang Guo, Postdoctoral Fellow/Bioinformatics Engineer
The Institute for Genome Sciences
Current position: Senior Scientist, MedImmune
- 2009-2012 Shannon Takala-Harrison, PhD, K12 Scholar
K12 Multidisciplinary Clinical Research Career Development Program, UMSOM
Current position: Associate Professor, Center for Vaccine Development, UMSOM
- 2009 Joyce Sakamoto, Institute for Genome Sciences, UMSOM
Current position: Research Associate, Pennsylvania State University
- 2010 - 2013 James Munro, Institute for Genome Sciences, UMSOM
Current position: Insect Identifier, USDA APHIS, Miami Office.
- 2017-2022 Ankit Dwivedi, Institute for Genome Sciences, UMSOM
- 2017-2018 Antoine Dara, Institute for Genome Sciences and Institute for Global Health, UMSOM
Current position: Assistant Professor, University of Bamako, Mali.
- 2019-present Amed Ouattara, PhD, K01 Scholar
Mentored Research Scientist Development Award (K01)

Awards to Mentees Under my Mentorship

- 2015 Ph.D. Scholar Award Nominee, Program in Molecular Microbiology and Immunology. GPILS 2016 Awards, UMB (Kyle Tretina)
- 2015 Poster Session Winner: Graduate Student Research Conference, UMB (Kara Moser)
- 2015-2016 Fellowship, Immunity and Infection T32 Training Grant, UMB (Kyle Tretina)
- 2016 UMB Global Learning Opportunity (GLO) Travel Award. UMB (Kara Moser)
- 2016 Otani Memorial Award Nominee, Program in Molecular Microbiology and Immunology, GPILS 2016 Awards, UMB (Kyle Tretina)
- 2016 STEM Chateaubriand Fellowship Awardee, offered by the Embassy of France in the United States. Declined in order to pursue other research opportunities (Kyle Tretina)
- 2016 Ph.D. Scholar Award Nominee, Program in Epidemiology and Human Genetics. GPILS 2016 Awards. UMB (Kara Moser)
- 2016 1st Place Young Investigator Award: The 65th American Society for Tropical Medicine and Hygiene Meeting (ASTMH). Atlanta, Georgia (Kara Moser)
- 2017 Otani Award Nominee for the Graduate Program in Epidemiology and Human Genetics. GPILS, 2017 Awards, UMB (Kara Moser)
- 2018 Poster Session Winner: Graduate Student Research Conference, UMB (Nicholas Palmateer)
- 2018 Ph.D. Thesis Award Nominee for the Graduate Program in Epidemiology and Human Genetics. GPILS 2018 Awards, UMB (Kara Moser)
- 2020 Travel Award, Species Delimitation Workshop, U Michigan Ann Arbor, (Nicholas Palmateer)

Grant Support

Active Grants

07/01/17 – 06/30/24	Co-Investigator (5%; Yrs 3-5) The Intransigence of Malaria in Malawi: Understanding Hidden Reservoirs, Successful Vectors and Prevention Failures. NIH 2 U19 AI089683-08 Annual Direct Costs (Carneiro da Silva): \$52,776	PI: Taylor, U Michigan
01/01/19 – 12/31/23	PI: Carneiro da Silva (30%) Genome-wide sieve analysis and immunological validation to identify targets of protective efficacy in field trials of a whole-organism malaria vaccine NIH 1 R01AI141900 Annual Direct Costs: \$499,390	
04/01/19 – 03/31/24	Project Leader, Project 4 (20%) NIH 2U19 AI110820-06 Genomic Centers for Infectious Diseases (GCID): A Genomics Based Investigation of the Determinants of Polymicrobial Infectious Disease Outcomes – Project 4: Genomic studies of the impact of external factors on parasite development and disease outcome Annual Direct Costs (Project 4): \$656,081 Total Direct Costs (Project 4): \$3,348,876	PIs: Rasko, Fraser, White, UMSOM
07/01/19 – 06/06/24	Co-Investigator (5%) Malaria variant surface antigen expression and vulnerability to disease in Malian children with Hemoglobin C trait. R01HL146377	PI: Travassos, UMSOM
12/01/19 – 11/30/24	Co-Mentor (No effort supported) Rational design of a multi-antigen multi-variant malaria vaccine NIH, K01	PI: Ouattara, UMSOM
04/01/20 – 03/31/25	Collaborator (5%) Genomic and geospatial analyses of malaria parasite migration to inform elimination NIH, R01A 145852 \$764,847	PI: Takala-Harrison/O'Connor, SOM
7/1/20 – 6/30/2021	PI: Carneiro da Silva (No Effort) Consortium for Malaria Research in Angola (<u>C-MalAng</u>) President's Global Impact Fund (Intramural) Annual Direct Costs (Carneiro da Silva): \$50,000	
7/1/21 – 6/30/2024	Subcontract PI:Carneiro da Silva (3%) Expanding the breadth, magnitude, and durability of PfSPZ vaccines by creating multi-strain, designer hybrid and genetically altered parasites and use of a unique adjuvant NIH, U01 A 155356 Annual Direct Costs (Carneiro da Silva): \$21,000	PI: Sim, Sanaria Inc.

Completed Grants

1993-1994	Principal Investigator (0%) Intramural Small Grants Program, University of Arizona NSF Research Training Group in the Analysis of Biological Diversification Total Direct Costs: \$990	
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1994-1995	Principal Investigator (0%) Intramural Small Grants Program, University of Arizona NSF Research Training Group in the Analysis of Biological Diversification Total Direct Costs: \$960
1997-1998	Principal Investigator (0%) Intramural Small Grants Program, University of Arizona NSF Research Training Group in the Analysis of Biological Diversification Total Direct Costs: \$960
03/01/97-02/28/99	Principal Investigator (0%) "Population genetics of <i>P</i> transposable elements and their host species, with emphasis in <i>Drosophila willistoni</i> and <i>D. sturtevantii</i> ." NSF, Doctoral Dissertation Improvement Grant Total Direct Costs: \$9,980
06/01/06 - 11/30/07	Project Leader (20%) PI: C.M. Fraser "Cryptosporidium muris Genome Sequencing Project" NIH, Network for Large-scale Sequencing of Microbial Genomes Total Direct Costs: \$463,255
06/01/06 – 05/31/09	Site-PI (10%) PI: J.M. Carlton, NYU "Comparative evolutionary genomics and infectious disease" NIH/NIGMS R01 GM070793-01A2 Total Direct Costs: \$577,563
01/01/09 – 12/31/12	Collaborator (5%) PI: C.V. Plowe "Worldwide Antimalarial Resistance Network (WWARN)" University of Oxford/Bill and Melinda Gates Foundation Total Direct Costs: \$767,929
<i>Role: Provides bioinformatics supervision and support.</i>	
04/01/12 – 09/30/13	Project Leader (15%) PI: C.M. Fraser "Genetic variability in <i>Babesia microti</i> , the causative agent of human babesiosis, an emerging infectious disease in the United States" NIH, NIAID Genome Sequencing Centers for Infectious Diseases Contract Total Direct Costs: \$429,250
08/20/12 – 02/19/14	Project Leader (20%) PI: C.M. Fraser "Comparative Genomics of Cryptosporidium Species" NIH, NIAID Genome Sequencing Centers for Infectious Diseases Contract Total Direct Costs: \$436,323
09/15/12 – 03/14/14	Project Leader (20%) PI: C.M. Fraser "Analysis of the role of variant antigen switching in the development of symptomatic malaria using Illumina sequencing" NIH, NIAID Genome Sequencing Centers for Infectious Diseases Contract Total Direct Costs: \$431,320
08/01/15-03/31/16	Co-Investigator (5%) NIH 1U19 AI 110820-02 Genomic Centers for Infectious Diseases – Admin. Supplement Host, Pathogen and the Microbiome: Determinants of Infectious Disease Outcome Annual Direct Costs: \$260,581

- 09/19/14-09/18/16 Co-Investigator (5%) PI: C.V. Plowe, C.M. Fraser, UMSOM
 “A genomic vaccinology approach to malaria vaccine development”
 Dean’s Challenge Award (Intramural)
 Annual Direct Costs: \$50,000
 Total Direct Costs: \$100,000
Role: Leads genomics team to characterize the genomic epidemiology of vaccine efficacy.
- 03/01/16 – 02/28/17 Co-Investigator, Project 5 (1.5%) PI: M. Levine, UMSOM
 NIH 1U19 AI 109776-02 Centers of Excellence in Translational Research -
 Admin. Supplement
 “Sequencing of anthroponotic *Cryptosporidium parvum*”
 Annual Direct Costs: \$35,832
Role: Oversee generation of genome sequence of anthroponotic C. parvum and comparison with genome of bovine-infecting C. parvum strains.
- 11/01/10 - 09/30/17 (2 NCEs) Principal Investigator (20%)
 “DIMENSIONS: Collaborative Research – Uncovering the novel diversity of the copepod microbiome and its effect on habitat invasions by the copepod host”
 NSF, Dimensions of Biodiversity, OCE-1046371
 Total Direct Costs: \$1,093,571
- 07/15/14 – 06/30/18 Site-PI (10%) PI: V. Nene, International Livestock Research Institute, Kenya
 “Application of Evolutionary and Comparative Pathogen Genomics to ECF Vaccinology”
 Bill and Melinda Gates Foundation
 Annual Direct Costs (Carneiro da Silva): \$88,613
 Total Direct Costs (Carneiro da Silva): \$499,645
- 03/01/14 – 02/28/19 Co-Investigator, Project 5 (5%) PI: M. Levine, UMSOM
 “Project 5. Development of strategies to achieve immunoprotection against *C. hominis* and *C. parvum*” (Project Leader: S. Tzipori, Tufts University)
 NIH 1U19 AI 109776-02 Centers of Excellence in Translational Research
 “Immunoprophylactic Strategy to Control Emerging Enteric Infections”
 Annual Direct Costs (Carneiro da Silva): \$6,487
 Annual Direct Costs: \$3,680,802
 Total Direct Costs: \$18,741,747
Role: Leads bioinformatics team in identification of candidate antigens in Cryptosporidium species.
- 04/01/14 – 03/31/19 Project Leader, Project 4 (25%) Overall PI: C.M. Fraser
 “Project 4. Integrated genomics research in parasitic tropical diseases”
 NIH 1 U19 AI110820 Genomic Centers for Infectious Diseases
 “Host, Pathogen and the Microbiome determinants of Infectious Disease Outcome”
 Annual Direct Costs (Project 4): \$631,613
 Total Direct Costs (Project 4): \$2,658,010
 Annual Direct Costs: \$2,111,367
 Total Direct Costs: \$10,390,837
- 02/03/17 – 01/31/22 Co-Investigator (5%; Yr 2) PI: Takala, UMSOM
 Identification and validation of molecular markers of piperazine resistance
 NIH R01AI125579
 Annual Direct: \$291,707

- 04/01/17 – 03/31/24 Co-Investigator (5%) PI: Plowe and Nyunt (PIs)
Myanmar Regional Center of Excellence for Malaria Research.
NIH U19 AI129386
Total Direct Costs (Carneiro da Silva): \$280,000
Role: Core Leader: Leads Molecular and Genomics Core. Grant moved to a different institution after year 1.
- 09/30/15-09/29/19 Co-investigator (5%) PIs: C.V. Plowe and S.A. Fisher
“Variant surface antigens in cerebral malaria pathogenesis”
NIH R01 RFA-HL-15-023 Vascular Dysfunction in the Pathogenesis of Severe Malaria
Total direct costs: \$1,278,325
Role: Oversee genome sequencing and annotation of Plasmodium falciparum infections, and algorithm development for reconstruction of antigen sequences.
- 07/26/17 – 12/31/19 Co-Investigator (5%) PI: Laurens, UMSOM
Supplement: Safety and Efficacy of PfSPZ Malaria Vaccine in Malaria-Exposed Adults
NIH/NIAID 5U01 AI112367
Total Direct: \$671,417
Total Direct (Carneiro da Silva): \$104,654
- 9/16/16 – 11/30/19 (NCE to 06-30-2020) Co-Investigator (10%) PI: K. Kotloff, UMSOM
Safety, Tolerability, Immunogenicity and Protective Efficacy against Naturally-Transmitted Malaria of Infectious, Cryopreserved Plasmodium falciparum Sporozoites (PfSPZ Challenge) administered by Direct Venous Inoculation under Chloroquine Chemoprophylaxis (PfSPZ-CVac), in Malian Adults: A Randomized, Double Blind, Placebo-Controlled Trial, DMID 15-0052; Task Areas B-D, Protocol Implementation and Laboratory Assays.
NIH RTOP, VTEU, HHSN2722013000221 contract
Total direct costs: \$2,655,951
Total Direct Costs (Carneiro da Silva): \$268,605
Role: Lead Options 6 (genomics of parasite vaccine evasion) and 7 (human transcriptomics)

Publications

Peer-reviewed journal articles

1. Carareto, C.M.A., W. Kim, M.F. Wojciechowski, P.M. O'Grady, A.V. Prokchorova, **J.C. Silva** and M.G. Kidwell. 1997. Testing transposable elements as genetic drive mechanisms using *Drosophila P* element constructs as a model system. *Genetica* 101:13-33. DOI: 10.1023/a:1018339603370. PMID: 9465407.
2. **Silva, J.C.**, and M.G. Kidwell. 2000. Horizontal transfer and selection in *P* elements. *Mol. Biol. Evol.* 17: 1542-1557. DOI: 10.1093/oxfordjournals.molbev.a026253. PMID: 11018160.
3. Loreto, E.L.S., L.B. da Silva, A. Zaha, **J.C. Silva**, V.L.S. Valente and M.G. Kidwell. 2001. *Drosophila mediopunctata P* elements: a new example of horizontal transfer. *Journal of Heredity*, 92: 3381. PMID:11773243.
4. Yang H.-P., A.Y. Tanikawa, W.A. Van Voorhies, **J.C. Silva**, A.S. Kondrashov. 2001. Whole-genome effects of ethyl methanesulfonate-induced mutation on nine quantitative traits in outbred *Drosophila melanogaster*. *Genetics* 157:1257-65.
5. Carlton JM, Angiuoli SV, Suh BB, Kooij TW, Perteu M, **Silva JC**, Ermolaeva MD, Allen JE, Selengut JD, Koo HL, Peterson JD, Pop M, Kosack DS, Shumway MF, Bidwell SL, Shallom SJ,

- van Aken SE, Riedmuller SB, Feldblyum TV, Cho JK, Quackenbush J, Sedegah M, Shoaibi A, Cummings LM, Florens L, Yates JR, Raine JD, Sinden RE, Harris MA, Cunningham DA, Preiser PR, Bergman LW, Vaidya AB, van Lin LH, Janse CJ, Waters AP, Smith HO, White OR, Salzberg SL, Venter JC, Fraser CM, Hoffman SL, Gardner MJ, Carucci DJ. Genome sequence and comparative analysis of the model rodent malaria parasite *Plasmodium yoelii yoelii*. *Nature*. 2002 Oct 3;419(6906):512-9. DOI: 10.1038/nature01099. PMID: 12368865.
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 7. **Silva, J.C.**, S.A. Shabalina, D.G. Harris, J. Spouge and A.S. Kondrashov. 2003. Conserved transposable elements in intergenic regions: recruitment of MIR- and L2-derived sequences in the mouse and human genomes. *Genet. Res.* 82:1-18. DOI: 10.1017/s0016672303006268.
 8. **Silva, J.C.** and M.G. Kidwell. 2004. Evolution of *P* elements in natural populations of *Drosophila willistoni* and *D. sturtevantii*. *Genetics* 168: 1323-1335. DOI: 10.1534/genetics.103.025775. PMID: 15579688.
 9. **Silva, J.C.**, E.L. Loreto and J.B. Clark. 2004. Factors that affect horizontal transfer of transposable elements. *Curr. Issues Mol. Biol.* 6:57-72. PMID:14632259.
 10. Carvalho, M.O., **J.C. Silva**, and ELS Loreto. 2004. Analyses of *P*-like transposable element sequences from the genome of *Anopheles gambiae*. *Insect Mol. Biol.* 13:55-63. PMID:14728667.
 11. El-Sayed N.M., P.J. Myler, G. Blandin, M. Berriman, J. Crabtree, G. Aggarwal, E. Caler, H. Renault, E.A. Worthey C. Hertz-Fowler, E. Ghedin, C. Peacock, D.C. Bartholomeu, B. J. Haas, A.N. Tran, J.R. Wortman, U.C. Alsmark, S. Angiuoli, A. Anupama, J. Badger, F. Bringaud, E. Cadag, J.M. Carlton, G.C. Cerqueira, T. Creasy, A.L. Delcher, A. Djikeng, T.M. Embley, C. Hauser, A.C. Ivens, S.K. Kummerfeld, J.B. Pereira-Leal, D. Nilsson, J. Peterson, S.L. Salzberg, J. Shallom, **J.C. Silva**, J. Sundaram, S. Westenberger, O. White, S.E. Meilville, J.E. Donelson, B. Andersson, K.D. Stuart, N. Hall. 2005. Comparative genomics of the trypanosomatid parasitic protozoa. *Science* 309: 404-409.
 12. Gardner MJ, Bishop R, Shah T, de Villiers EP, Carlton JM, Hall N, Ren Q, Paulsen IT, Pain A, Berriman M, Wilson RJ, Sato S, Ralph SA, Mann DJ, Xiong Z, Shallom SJ, Weidman J, Jiang L, Lynn J, Weaver B, Shoaibi A, Domingo AR, Wasawo D, Crabtree J, Wortman JR, Haas B, Angiuoli SV, Creasy TH, Lu C, Suh B, **Silva JC**, Utterback TR, Feldblyum TV, Perteau M, Allen J, Nierman WC, Taracha EL, Salzberg SL, White OR, Fitzhugh HA, Morzaria S, Venter JC, Fraser CM, Nene V. Genome sequence of *Theileria parva*, a bovine pathogen that transforms lymphocytes. *Science*. 2005 Jul 1;309(5731):134-7. PMID: 15994558.
 13. **Silva, J.C.**, F. Bastida, S.L. Bidwell, P.J. Johnson and J.M. Carlton. 2005. A potentially functional *mariner* transposable element in the protist *Trichomonas vaginalis*. *Mol. Biol. Evol.* 22: 126-134. PMID:15371525.
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 16. Lin, H., W. Zhu, **J.C. Silva**, X. Gu and R. Buell. 2006. Intron gain and loss in segmentally duplicated genes in rice. *Genome Biology*: 7: R4. DOI: 10.1186/gb-2006-7-5-r41. PMID: 16719932.
 17. Carlton, J.M., R.P. Hirt, **J.C. Silva**, A.L. Delcher, M. Schatz, Q. Zhao, J.R. Wortman, S.L. Bidwell, U.C.M. Alsmark, S. Besteiro, T. Sicheritz-Ponten, C.J. Noel, J.B. Dacks, P.G. Foster, C. Simillion, Y. Van de Peer, D. Miranda-Saavedra, G.J. Barton, G.D. Westrop, S. Müller, D. Dessi, P.L. Fiori, Q. Ren, I. Paulsen, H. Zhang, F.D. Bastida-Corcuera, A. Simoes-Barbosa, M.T. Brown, R.D. Hayes, M. Mukherjee, C.Y. Okumura, R. Schneider, A.J. Smith, S. Vanacova, M.

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 22. Egan A, A Mahurkar, J Crabtree, JH Badger, JM Carlton, **JC Silva**. 2008. IDEA: Interactive Display for Evolutionary Analyses. *BMC Bioinformatics* 9:524. PMID: 19061522.
 23. Lopes F.R., **J.C. Silva**, M. Benchimol, G.G.L. Costa, G.A.G. Pereira and C.M.A. Carareto. 2009. The protist *Trichomonas vaginalis* harbors multiple lineages of transcriptionally active Mutator-like elements. *BMC Genomics* 10:330. PMID: 19622157.
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75. Thomas C. Stabler, Ankit Dwivedi, Biraj Shrestha, Sudhaunshu Joshi, Tobias Schindler, Amed Ouattara, Guillermo A. García, Claudia Daubenberger, **Joana C. Silva**. Gene Coverage Count and Classification (GC3): a locus sequence coverage assessment tool, and its application to identify and classify histidine-rich protein 2 and 3 deletions in *Plasmodium falciparum* using short-read whole genome sequencing data. *Malaria J.* 2022 Nov 29;21(1):357. doi: 10.1186/s12936-022-04376-3.PMID: 36447234
 76. Alvaro Molina-Cruz, Gaspar E. Canepa, Ankit Dwivedi, Weimin Liu, Nadia Raytselis, Antonio Christophe-Nkondjio, Beatrice H. Hahn, Joana C Silva, Carolina Barillas-Mury. Role of *Pfs47* in the dispersal of ancestral *Plasmodium falciparum* malaria through adaptation to different anopheline vector. *PNAS* (Accepted)
 77. Diana Moita, Teresa G. Maia, Miguel Duarte, Carolina M. Andrade, Inês S. Albuquerque, Ankit Dwivedi, Joana C. Silva, Lilia González-Céron, Chris J. Janse, António M. Mendes, Miguel Prudêncio. A genetically modified *Plasmodium berghei* parasite as a surrogate for whole-sporozoite vaccination against *P. vivax* malaria. *NPJ Vaccines* NPJ Vaccines. 2022 Dec 16;7(1):163. doi: 10.1038/s41541-022-00585-8.PMID: 36526627
 78. Wilson Tavares, Joana Morais, José F. Martins, Ryan J. Scalsky, Thomas C. Stabler, Márcia M. Medeiros, Filomeno J. Fortes, Ana Paula Arez, Joana C. Silva. Malaria in Angola: recent progress, challenges and future opportunities using parasite demography studies *Malaria J* 2022 Dec 28;21(1):396. doi: 10.1186/s12936-022-04424-y.
 79. Palmateer NC, JB Munro, J Crabtree, **JC Silva**. The *Tpr* multigene family in *Theileria* parasites includes both species-specific members and copies with defined orthologs between species. *J Molecular Evolution* (Accepted)

Submitted or In Prep

1. A. Dwivedi, K. A. Moser, A. Molina-Cruz, D. Coulibaly, M. A. Thera, C. Lon, D. Lek, S. D. Tyner, D. L. Saunders, M. M. Nyunt, C. V. Plowe, M. K. Laufer, M. A. Travassos, S. Takala-Harrison, C. Barillas-Mury, and J. C. Silva, Adaptation to mosquito vector species impacts evolution of *Plasmodium falciparum* (in prep).
2. A. Dwivedi*, T. K. Hodges*, J. Matsumura*, A. Dara, K. A. Moser, A. A. Berry, S. Takala-Harrison, J. Crabtree, and J. C. Silva, In silico read capture and assembly enables allele reconstruction of highly variable antigen-encoding loci (in prep).

Book chapters

1. Clark, JB, **JC Silva** and MG Kidwell. Evidence for horizontal transfer of *P* transposable elements. *In* Horizontal Gene Transfer, 2nd edition. Syvanen, M. and Kado (Eds), pp 161-171. Academic Press, San Diego, CA 2002.
2. Carlton, JM, **JC Silva** and N Hall. The genome of model malaria parasites, and comparative genomics. *In* Genomes and the Molecular Cell Biology of Malaria Parasites A Waters and C Janse (Eds), Horizon Scientific Press, 2004.
3. Harb OS, U Boehme, K Crouch, OO Ifeonu, DS Roos, **JC Silva**, F Silva-Franco, S Svard, K Tretina and G Weedall. Protozoan Parasite Genomics. *In* Molecular Parasitology. J Walochnik and M Duchêne (Eds). Springer-Verlag, Vienna, 2016.

Proceedings

1. Widmer G., E. London, L. Zhang, G. Ge, L. Cowen, S. Tzipori, J.M. Carlton and **J.C. Silva** 2007. Preliminary analysis of the *Cryptosporidium muris* genome. Proceeding of the Second International *Giardia* and *Cryptosporidium* Conference, May 13-18, Morelia, Mexico.

Our Group on the Media

1. *CiênciaHoje*, April 26, 2007. Profile: “Luso-American Foundation (FLAD) and the Portuguese Scientists in America. Joana C. Silva”. (<http://www.cienciahoje.pt/index.php?oid=21424>)
2. *Maryland* magazine, 2010, “Unlocking the Promise of Genomics and Translational Medicine: Institute of Genome Sciences”, by James Swyer. (http://issuu.com/dpeterson/docs/2010_maryland_magazine/37)
3. *Bio-IT World*, August 7, 2014. “The genomics of infectious diseases”, by Aaron Krol. (<http://www.bio-itworld.com/2014/8/7/genomics-infectious-diseases.html>)
4. Media coverage of our work on dating the age of malaria parasites

GenomeWeb, Jan 26, 2015. “U of Maryland-led Statistical Study Points to Co-evolution of Plasmodium Parasite, Mammalian Hosts”, by Uduak Grace Thomas. (<https://www.genomeweb.com/informatics/u-maryland-led-statistical-study-points-co-evolution-plasmodium-parasite-mammalian-hosts>)

Press release from the University of Maryland School of Medicine (<http://www.umaryland.edu/news/archived-news/february-2015/newspressreleaseshottopics/carneiro-da-silva.php>)

Press release from the University of Maryland College Park (<https://cmns.umd.edu/news-events/features/2777>)

ScienceDaily, Feb 11, 2015. “Eliminating dangerous mosquitoes? Malaria parasites unlikely to jump from animals to humans” (<http://www.sciencedaily.com/releases/2015/02/150211132115.htm>)

Malaria World, Feb 17, 2015. “Little risk of malaria making a species jump”, by Tim Sandle. (<http://www.digitaljournal.com/life/health/little-risk-of-malaria-making-a-species-jump/article/426307>)

5. *Medicine Bulletin*, University of Maryland, Winter 2015-2016. “Translational genomics improving world health”, by Rita M. Rooney. (http://www.medicalalumni.org/wp-content/uploads/2016/01/Bulletin_winter15-16_web.pdf)
6. Coverage of our work as part of the International Livestock Vaccine Consortium (ILVAC)

ILVAC, Jul 19, 2016. “Discovery of CTL epitopes by peptide library screening of CTL lines from *Theileria parva* immune animals”, by Peter Ballantine (<https://ilvac.net/2016/07/19/ecf-keystone-svitek/>)

ILVAC, Nov 22, 2016. “Can cancer biology help us understand East Coast fever”, by Kyle Tretina and Joana Silva (<https://ilvac.net/2016/11/22/cancer-ecf/>)

ILVAC, Nov 29, 2016. “Can we remix the East Coast fever Muguga cocktail?”, by Joana Silva, Ivan Morrison, Dirk Geysen, George Chaka, Ine de Goeyse and Kyle Tretina (<https://ilvac.net/2016/11/29/muguga-cocktail-remix/>)

Major Invited Speeches

Local

1. *The roles of horizontal transfer and selection in the long-term survival of P transposable elements*. NCBI, NIH, Bethesda, MD. May 20, 2000
2. *Evolution of mammalian Plasmodium is contemporaneous with that of its hosts*. University of Maryland Baltimore County, Baltimore, MD. Sept 7, 2011
3. *Apicomplexan parasites: model systems for evolutionary genomics and disease*. United States Department of Agriculture, Agricultural Research Service, Beltsville, MD. Nov 1, 2011
4. *Plasmodium Nuclear Proteins Tick by the Clock: Implications for the Age of Malaria Parasites*. Carnegie Institution, Baltimore, Maryland. Apr 22, 2013
5. *Characterization of genomic diversity in hard-to-culture pathogens*. The Role of Genomics Research in Global Health. NIH Global Health Interest Group 2014 Symposium. NIH. Bethesda. Feb 6, 2014
6. *Genomics research to inform vaccine design*. Oct 18, 2016. George Mason University.
7. *Genomics research to inform the development of whole organism vaccines*. Naval Medical Research Center (NMRC), US Navy, Silver Spring MD. Dec 19, 2016
8. *Genomic characterization of Plasmodium falciparum vaccine and challenge strains*. 2nd Human Challenge Trials in Vaccine Development. International Alliance for Biological Standardization. Rockville, MD. Sept 28-30, 2017
9. *Using Genomics to Advance Vaccine Development*. International PfSPZ Consortium meeting. Baltimore, MD. Nov 10, 2017
10. *Comparative genomics to interpret vaccine efficacy in CHMI and field studies*. International PfSPZ Consortium Meeting. Rockville, MD. Nov 18, 2019
11. *Why CHMI with sporozoites of 7G8 is such a stringent test of vaccine efficacy in Africa*. International PfSPZ Consortium Meeting. Virtual. Dec. 9-10, 2020.
12. *Global genomics of PfSPZ-based vaccinology*. Malaria Vaccine Branch, Walter Reed Army Institute of Research. Silver Spring, MD. Feb 28, 2022
13. *Controlled Human Infection Model: Considerations on the Choice of Challenge Strains*. Frontiers in Vaccinology Symposium, Center for Vaccine Development and Global Health, University of Maryland School of Medicine. Sept 2022
14. *At the Junction of Evolutionary Genomics and Vaccinology*. Frontiers in Genomics, a Celebration of the Institute for Genome Sciences' 15th Anniversary. University of Maryland School of Medicine, Baltimore, MD. Oct. 19, 2022
15. *Genome-wide sieve analysis of PfSPZ infections from efficacy field trials and E140 protein*. Naval Medical Research Center (NMRC), US Navy. Silver Spring, MD. Feb 10, 2023.
16. *Genome-wide sieve analysis: using population genetics principles in applied vaccinology*. The Journal of Molecular Evolution Advances Meeting, American University Campus, Washington, DC, USA. March 17-19, 2023
17. *Title TBD*. Laboratory of Malaria and Vector Research (LMVR), NIAID, NIH. April 10, 2023.

National

18. *Unusual molecular evolution patterns provide intriguing insights into the evolution of P transposable elements*. Women in Evolution: A Gathering of Scientific Perspectives. Sept 18-21, 1996. University of Arkansas, Fayetteville, AR.
19. *The repetitive component of the T. vaginalis genome*. The Genome and Biology of the Trichomonads. Dec 2-3, 2003. Pre-ASTMH meeting of the International Trichomonads Consortium, Philadelphia, PA

20. *Exploring the world of close relatives for correlates of selective constraint*. International Meeting on Genomics of Closely Related Organisms. Jan 12-14, 2006. The University of Arizona, Tucson, AZ.
21. *Optimization of gene order in the Apicomplexa?* Mar 30, 2007. Virginia Bioinformatics Institute. Virginia Tech, VA.
22. *IDEA (Interactive Display for Evolutionary Analyses): providing a bird's eye view of genome-wide molecular evolution analyses*. Comparative Genomics of Malaria Parasites, Sept. 21, 2007. American Museum of Natural History, New York, NY.
23. *IDEA – The Sugarcoat for PAML*. Genome Informatics. Nov. 1-5, 2007. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.
24. *Apicomplexan parasites: a model system for disease and for evolutionary genomics*. Gordon Research Conference on Evolutionary & Ecological Functional Genomics. July 12-17, 2009. Tilton School. Tilton, NH.
25. *Phylogenomics and the age of speciation events: dating the origin of mammalian Plasmodium parasites*. Apr 13, 2012. University of Wisconsin, Madison.
26. *Generation of population genomics resources for Theileria parva*. Jun 4, 2012. United States Department of Agriculture, Agricultural Research Service, Pullman, WA.
27. *Parasite genetic variation and vaccine efficacy*. Oct 7, 2016. Network Dynamics and Simulation Science Laboratory, Biocomplexity Institute, Virginia Tech, Blacksburg, VA.
28. *Genomic epidemiology to inform vaccine design*. Oct 20, 2016. Huck Center for Malaria Research, The Pennsylvania State University, University Park, PA.
29. *Genomics of an anthroponotic Cryptosporidium parvum strain*. Nov 1, 2018. Cummings Veterinary Medicine School, Tufts University.
30. *Genomic studies of vaccine design and efficacy*. Keynote presentation at the Vaccine Development Center of San Antonio Conference. November 11, 2021. Virtual.

International

31. *Variabilidade e divergência em sequências de elementos P em Drosophilídeos*. Sept 2, 1996. Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil.
32. *On the nature of selective constraints in P transposable elements*. Aug 29, 1996. Universidade Estadual Paulista, São Paulo, Brazil.
33. *The Trichomonas vaginalis genome sequencing project*. International Conference on Anaerobic Protists. Sept 17-20, 2005. Alghero, Italy.
34. *Decomplexing the Apicomplexa: genome evolution and host-parasite interactions*. Cologne Spring Meeting 2007: Evolution of Pathogens and Immunity. Feb 21-23, 2007. Institute for Genetics. University of Cologne, Germany.
35. *Evolution of genome size in eukaryotic intracellular parasites: inferences from comparative genomics*. Oct 23, 2009. Universidade Clássica de Lisboa, Faculdade de Ciências. Lisbon, Portugal.
36. *Genome evolution of eukaryotic intracellular parasites: inferences from comparative genomics*. Apr 26, 2010. International Livestock Research Institute (ILRI), Nairobi, Kenya.
37. *Divergence times within the genus Plasmodium revealed by a comparative genomics approach*. Dec 1, 2010. Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.
38. *Development of resources for reverse vaccinology of Theileria parva, a protist pathogen of cattle*. Oct 29, 2012. Center for Environmental Biology, University of Lisbon, Lisbon, Portugal.
39. *Generation of population genomics data for a parasite of nucleated host cells*. Infectious Disease Genomics and Global Health conference. Oct 16-18, 2013. Wellcome Trust Conference Centre, Hinxton, Cambridge, UK.
40. *Towards a comprehensive antigen map of T. parva: bioinformatics and evolutionary genetics approaches*. Workshop on Improved vaccines for the control of ECF in cattle in Africa. Jan 27-29, 2014. International Livestock Research Institute, Nairobi, Kenya.
41. *Genome re-annotation and putative antigens*. Workshop on Improved vaccines for the control of ECF in cattle in Africa. Feb 9-11, 2015. International Livestock Research Institute, Addis Ababa,

- Ethiopia.
42. *Genomic studies of vaccine design and vaccine efficacy in eukaryotic pathogens*. Jun 30, 2015. The Roslin Institute, University of Edinburgh, Edinburgh, UK.
 43. Silva J.C. *Genomic composition of P. falciparum isolates in PfSPZ Vaccine studies*. Spring PfSPZ Consortium meeting. Apr 30-May 1, 2016. Leiden, The Netherlands.
 44. *Genomic composition of the Muguga Cocktail Vaccine*. Workshop on Improved vaccines for the control of ECF in cattle in Africa. May 15-18, 2016. London, UK.
 45. *Genomics of Vaccine Efficacy: Lessons from the Buffalo Wildlife Reservoir of East Coast Fever*. Keystone Symposium on *New Approaches to Vaccines for Human and Veterinary Tropical Diseases*. May 22-27, 2016. Cape Town, South Africa.
 46. *Plasmodium falciparum genetic variation, vaccine efficacy and vaccine design*. July 6, 2017. Instituto de Higiene e Medicina Tropical, Universidade NOVA de Lisboa, Lisbon, Portugal.
 47. *Advances and Challenges in Parasite Genomics*. Keynote Speaker at the symposium *Envisioning the Future of Genome Research*. Khalifa Center for Genetic Engineering & Biotechnology, United Arab Emirates University. November 14, 2017. Al Ain, United Arab Emirates.
 48. *The ABC and D of parasite genomics: Apicomplexan Bioinformatics, genome sequence Capture and genetic Diversity*. Oct, 2018. Instituto de Higiene e Medicina Tropical, Universidade Nova de Lisboa, Lisbon, Portugal.
 49. *Theileria parva population structure and genetic variation*. Workshop on Improved vaccines for the control of ECF in cattle in Africa. Nov 6-8, 2018. Nairobi, Kenya.
 50. *Malaria vaccine efficacy and design through the lens of Plasmodium falciparum genetic and transcriptional variation*. Instituto de Medicina Molecular João Lobo Antunes. December 10, 2018. Lisbon, Portugal.
 51. *Comparative genomics of Pf infections from PfSPZ Vaccine field trials to identify the basis of vaccine-induced protection*. International PfSPZ Consortium Meeting, May 7, 2019. Oxford, UK.
 52. *Vaccine resistance: the case of malaria*. Global Health and Tropical Medicine, Instituto de Higiene e Medicina Tropical, Universidade NOVA de Lisboa. May 16, 2019. Lisbon, Portugal.
 53. *Genomics of whole organism-based vaccines*. German Center for Infection Research (DZIF), June 6, 2019. Heidelberg, Germany.
 54. JC Silva, KE Lyke. *Optimization of Heterologous Plasmodium falciparum Challenge Strains for Use in Controlled Human Malaria Infection and Their Utility*. Joint International Tropical Medicine Meeting, Virtual. Dec 15-18, 2020.
 55. *Leveraging allele-specific efficacy of whole organism vaccines to identify novel targets of vaccine-induced protection*. Lou Miller Journal Club. March 22, 2022. University of Alberta, CA
 56. *Leveraging allele-specific efficacy of a whole organism-based vaccine tested against field strains to identify candidate targets of vaccine-induced protection*. 16th Brazilian Malaria Research Meeting (XVI RNPM), April 23-28, 2022, Rio de Janeiro, Brazil.
 57. *Identification of parasite targets of PfSPZ Vaccine-induced protective immunity using population genomics*. Biennial Banff Conference on Infectious Diseases (BCID), May 17-21, 2023. Banff Alberta, Canada.

Published Abstracts – Talks (selection; presenter underlined)

1. **Silva, J.C.** Current fisheries research in Portugal, with emphasis on projects in Lisbon. Fifth Annual Northeast Fisheries Center Research Meeting, April 30-May 3, 1991, Woods Hole Oceanographic Institute, Woods Hole, MA.
2. **Silva, J.C.** Transposable Elements and Rates of Speciation in Cichlid Fishes: a Preview. 1994 Genetic Seminar Series, University of Arizona.
3. **Silva, J.C.** P-Element Evolution at the Molecular Level. 1995 Genetics Seminar Series, University of Arizona.
4. **Silva, J.C.**, J.B. Clark, and M.G. Kidwell. P Element Evolution at the Molecular Level. Joint Meetings of the Society of Systematic Biologists, Society for the Study of Evolution, American

- Society of Naturalists, Numerical Taxonomy Group, July 8-12, 1995, McGill University, Montreal, Quebec, Canada.
5. **Silva, J.C.** *Molecular Evolution in P-Elements: Snail's pace for a jumping gene?* 1997 Genetics Seminar Series, University of Arizona.
 6. **Silva, J.C.** *Molecular Evolution in P-Elements: Snail's pace for a jumping gene?* Joint Meetings of the Society of Systematic Biologists, Society for the Study of Evolution, American Society of Naturalists, Numerical Taxonomy Group, June 14-18, 1997, University of Colorado, Boulder, CO.
 7. **Silva, J.C.** and M.G. Kidwell. Population genetics of *D. willistoni*, a widespread New World Drosophilid. Joint Meetings of the Society of Systematic Biologists, Society for the Study of Evolution, American Society of Naturalists, June 22-26, 1999, University of Wisconsin, Madison, WI.
 8. Tanikawa A., H.-P. Yang, W.A. Van Voorhies, **J.C. Silva**, A.S. Kondrashov. Mutational evolvability: the impact of EMS on several fitness-related traits in *Drosophila melanogaster*. Joint Meetings of the Society of Systematic Biologists, Society for the Study of Evolution, American Society of Naturalists, June 22-26, 1999, University of Wisconsin, Madison, WI.
 9. Yang, H.-P., A. Tanikawa, W.A. Van Voorhies, **J.C. Silva**, A.S. Kondrashov. Artificial mutagenesis as a tool for studying spontaneous mutation. Joint Meetings of the Society of Systematic Biologists, Society for the Study of Evolution, American Society of Naturalists, June 22-26, 1999, University of Wisconsin, Madison, WI.
 10. **Silva, J.C.** Patterns of mutation inferred from human-baboon comparisons. National Center for Biotechnology Information Seminar Series. NCBI, NIH, Bethesda MD. 2002.
 11. **Silva, J.C.** Identification of *mariner* elements in a protist. Meetings of the Society for Molecular Biology and Evolution, Newport Beach, CA, June 26-29, 2003.
 12. **Silva, J.C.** The repetitive component of the *Trichomonas vaginalis* genome. ASTMH pre-meeting symposium on "The genome and biology of the Trichomonas", Philadelphia, PA, December 3rd, 2003.
 13. **Silva, J.C.** Recent Expansion of transposable elements leads to dramatic increase in genome size. "Genomes and Evolution 2004" conference, Meetings of the Society for Molecular Biology and Evolution, The Pennsylvania State University, State College, PA, June 17-20, 2004.
 14. **Silva, J.C.** Tandem repeats and transposable elements in *Tetrahymena thermophyla*. Two-day meeting of the Scientific Advisory Board of the *Tetrahymena* Genome Sequencing Project, TIGR, Rockville, MD, April 2004.
 15. **Silva, J.C.** *Genome evolution of apicomplexan parasites*. Meetings of the Society for Molecular Biology and Evolution, May 24-28, 2006. Arizona State University, Tempe, AZ.
 16. **Silva, J.C.** *Plasmodium proteins tick by the clock*. Meeting of Comparative Genomics of Eukaryotic Parasites. Oct 17-22, 2009. San Feliu de Guixols, Spain.
 17. **Silva, J.C.** *Evolution of mammalian malaria: host transfer or co-evolution?* Meeting of the Society for the Study of Evolution, June 25-29, 2010, Portland, OR
 18. Takala Harrison S., T.G. Clark, M.P. Cummings, C.G. Jacob, O. Miotto, A.M. Dondorp, M.M. Fukuda, F. Nosten, H. Noedl, M. Imwong, D. Bethell, Y. Se, C. Lon, S. D Tyner, D. Saunders, D. Socheat, A. Pyae Phyo, P. Starzengruber, P. Swoboda, K. Stepniewska, J. Flegg, G.C. Cerqueira, **J.C. Silva**, C. Arze, S.M. Ricklefs, S.F. Porcella, M. Adams, L.J Kenefic, S. Campino, S. Auburn, M. Manske, B. MacInnis, D.P. Kwiatkowski, X-Z Su, N.J. White, P. Ringwald, C.V. Plowe. *ARC3: A genome-wide association study of the genetic basis of parasite clearance rate following treatment with artemisinins*. American Society of Tropical Medicine and Hygiene. December 4-8, 2011, Philadelphia, PA.
 19. **Silva, J.C.**, J. Orvis, J. Crabtree, R. Pelle, E. Awin³, A. Maroo, L. Tallon, C.A. Daubenberger, R.P. Bishop. *De novo genome assembly from DNA sequence capture of Theileria parva, an apicomplexan parasite of cattle in sub-Saharan Africa*. ApiCOWplexa: Apicomplexa in Farm Animals. October 25-28, 2012. Lisbon, Portugal.
 20. Cornillot, E., K. Hadj-Kaddour, A. Dassouli, A. Duclos, Y. Augagneur, S. Usmani-Brown, V. Brès, S. Delbecq, V. Barbe, A. Gorenflot, **J.C. Silva**, P. Krause, C. Ben Mamoun. *Development of genomics resources for Babesia microti, an emerging infectious disease agent in the United*

- States. American Society of Tropical Medicine and Hygiene. November 11-15, 2012. Atlanta, GA.
21. **Silva, J.C.**, R. Pelle, V. Nene, C.A. Daubenberger, R.P. Bishop. *Whole-genome capture of Theileria parva, an apicomplexan parasite of cattle in sub-Saharan Africa*. American Society of Tropical Medicine and Hygiene. November 11-15, 2012. Atlanta, GA.
 22. **Tretina, K., J.C. Silva**. Identification of transcriptional *cis*-regulatory motif in *Theileria parva*, an intracellular apicomplexan parasite of cattle in sub-Saharan Africa. American Society of Tropical Medicine and Hygiene. November 13-17, 2013. Washington, D.C.
 23. **Jacob, C.G.**, S. Takala-Harrison, **J.C. Silva**, et al. [35 authors]. Falciparum malaria in the greater Mekong sub-region: mapping gene flow and genomic signatures of drug resistance. American Society of Tropical Medicine and Hygiene. November 13-17, 2013. Washington, D.C.
 24. **Tretina K.**, H.T. Gotia, J. Orvis, O. Abolude, P.Kumari, V.M. Nene, R.P. Bishop, C. Daubenberger, **J.C. Silva**. RNA-seq-based structural annotation and regulatory motif discovery in *Theileria parva*, an apicomplexan parasite of cattle in sub-Saharan Africa. American Society of Tropical Medicine and Hygiene. November 2-6, 2014. New Orleans, LA.
 25. **Tretina K.**, H.T. Gotia, J. Orvis, O.O. Abolude, **J.C. Silva**. Identification of parasite-induced host cell transformation factors based on the re-annotation of the *Theileria parva* genome and on comparative genomics. American Society of Tropical Medicine and Hygiene. October 25-29, 2015. Philadelphia, PA.
 26. Takala-Harrison S, S. Agrawal, C. Jacob, L. Morton, M. Cummings, S. Chaorattanakawee, C. Lon, C. Parobek, J. Lin, **J.C. Silva**, J. Juliano, D. Saunders, and C.V. Plowe. A genome-wide association study of the genetic basis of piperazine resistance in *P. falciparum*. American Society of Tropical Medicine and Hygiene. October 25-29, 2015. Philadelphia, PA.
 27. **Silva, J.C.** Genomic tools to measure PfSPZ Vaccine-induced strain-specific immunity. Malaria Vaccines for the World. May 2-4, 2016. Leiden, The Netherlands.
 28. **Tretina K**, Haidar M, Pelle R, Orvis J, Gotia HT, Ifeonu OO, Chaussepied M, Kumari P, Iqbal SBA, Fry L, Knowles DP, Nene VM, Ginsberg D, Daubenberger C, Bishop RP, Langsley G, **Silva JC**. A *Theileria parva* protein with an LXCXE motif can induce bovine host cell proliferation and binds host DNA signaling adaptor protein STING. EMBO Symposium Innate Immunity in Host-pathogen Interactions, June 2016, Heidelberg, Germany.
 29. **Moser KA**, Ouattara A, Drabek EF, Koren S, Phillipy A, Adams M, Coulibaly D, Thera MA, Doumbo OK, Laufer MK, Laurens MB, Jongsakul K, Lon C, Saunders D, Han KT, Nyunt MM, Sauerwein RW, Sim BKL, Li T, Travassos MA, Takala-Harrison S, Hoffman SL, Plowe CV, **Silva JC**. Population genomics of *Plasmodium falciparum* to inform the design and efficacy of whole organism malaria vaccines. *American Society of Tropical Medicine and Hygiene*. November 13-17, 2016. Atlanta, GA.
 30. **Moser KA**, Dwivedi A, Stucke EM, Kalral G, Koren S, Phillipy A, Adams M, Ouattara A, Drabek EF, Coulibaly D, Doumbo OK, Thera MA, Nyunt MM, Laufer MK, Travassos MA, Takala Harrison S, Plowe CV, **Silva JC**. New *Plasmodium falciparum* genome assemblies from diverse endemic regions enables the comprehensive genomic and genetic characterization of clinical isolates. *American Society of Tropical Medicine and Hygiene*. November 5-9, 2017. Baltimore, MD.
 31. **Ifeonu OO**, Widmer G, Levine MM, Tzipori S, **Silva JC**. The genome sequence of anthroponotic *Cryptosporidium parvum*. *American Society of Tropical Medicine and Hygiene*. November 5-9, 2017. Baltimore, MD.
 32. **Moser KA**, Dwivedi A, Stucke EM, Kalral G, Koren S, Phillipy A, Adams M, Ouattara A, Drabek EF, Coulibaly D, Doumbo OK, Thera MA, Nyunt MM, Laufer MK, Travassos MA, Takala Harrison S, Plowe CV, **Silva JC**. New *Plasmodium falciparum* genome assemblies from diverse endemic regions enables the comprehensive genomic and genetic characterization of clinical isolates. *American Society of Tropical Medicine and Hygiene*. November 5-9, 2017. Baltimore, MD.
 33. **Harrison ST**, Shetty AC, Jacob CG, Machikas A, Agrawal A, Huang F, Li Y, Agrawal S, Saunders DL, Lon C, Fukuda MM, Ringwald P, Ashley EA, Han KT, Hlaing TM, Nyunt MM, **Silva JC**, Stewart KE, O'Connor TD, Plowe CV. Use of shared haplotypes that are identical-by-

- descent to infer population structure and parasite migration within southeast asia. *American Society of Tropical Medicine and Hygiene*. November 5-9, 2017. Baltimore, MD.
34. Palmateer NC, Daubenberger CA, Bishop RP, **Silva JC**. Characterization of Genetic Variation in Host-specific *Theileria parva* Populations. *American Society of Tropical Medicine and Hygiene*. Oct 28-Nov1, 2018. New Orleans, LA.
 35. **JC Silva**, A Dwivedi, KA Moser, M Sissoko, JE Epstein, S Healy, K Lyke, B Mordmüller, T Li, P Kremsner, PE Duffy, TL Richie, BKL Sim, SL Hoffman. *Genome, proteome, and immunone data explain why controlled human malaria infection with sporozoites of the Pf7G8 clone of Plasmodium falciparum is a rigorous predictor of the efficacy of the PfNF54-based PfSPZ Vaccine in Africa*. Talk. Annual meeting of the American Society of Tropical Medicine and Hygiene. Nov 15-19, 2020. Online.
 36. A Dwivedi, A Molina-Cruz, KA Moser, D Coulibaly, MA Thera, C Lon, D Lek, SD Tyner, DL Saunders, MM Nyunt, CV Plowe, MK Laufer, MA Travassos, S Takala-Harrison, C Barillas-Mury, **JC Silva**. *Adaptation to mosquito vector species impacts evolution of Plasmodium falciparum*. Talk. Annual meeting of the American Society of Tropical Medicine and Hygiene. Nov 15-19, 2020. Online.
 37. A Molina-Cruz, Ankit Dwivedi, GE Canepa, W Liu, N Raytselis, B Hahn, **JC Silva**, C Barillas-Mury. *Evolution of Pfs47 and the adaptation of ancestral Plasmodium falciparum to vectors of human malaria*. Talk. Annual meeting of the American Society of Tropical Medicine and Hygiene. Nov 17-21, 2021. Virtual.

Published Abstracts - Posters (selection; presenter underlined)

1. Carareto, C.M.A., W. Kim, M.F. Wojciechowski, P.M. O'Grady, A.V. Prokchorova, **J.C. Silva** and M.G. Kidwell. Using Transposable Elements to Drive Genes into Populations: I. Testing autonomous versus nonautonomous *P* element constructs in *Drosophila melanogaster*. Congress of Genetics, Sept. 1995, Brazil.
2. **Silva, J.C.**, J.B. Clark, and M.G. Kidwell. Patterns of molecular evolution in *P* transposable elements. Annual meeting of the Society for Molecular Biology and Evolution, June 8-11, 1996, Tucson, AZ.
3. **Silva, J.C.**, J.B. Clark and M.G. Kidwell. On the nature of selective constraints in *P* transposable elements. Abstract published at the 42th National Congress of Genetics, Sept. 4-7, 1996, Caxambu, Minas Gerais, Brazil.
4. Lyons, E.J., **J.C. Silva**, S.L. Bidwell and J.M. Carlton. A tandem repeats database for *Plasmodium vivax* with application to population genetic studies and targeted gene identification. Poster presented at Molecular Approaches to Malaria 2004, Feb. 1-5 2004, Lorne, Australia.
5. Guo, X., and **J.C. Silva**. Evolution of non-coding genomic regions in *Theileria*, a genus of cattle parasites of the phylum Apicomplexa. 9th Annual Conference on Computational Genomics, October 28-31, 2006, Baltimore, MD.
6. Egan, A., A. Mahurkar, and **J.C. Silva**. IDEA (Interactive Display of Evolutionary Analyses): a tool for setting up, managing and visualizing PAML analyses. 2007 Meeting of the Society for Molecular Biology and Evolution, June 24-28, 2007, Halifax, Canada.
7. Munro, J.B., C. Jacob, **J.C. Silva**. A Novel Clade of Eukaryotic Ribonucleotide Reductase R2 Subunits is Exclusive to Apicomplexan Parasites. American Society of Tropical Medicine and Hygiene. December 4-8, 2011, Philadelphia, PA.
8. Jacob, C.G., O. Miotto, S. Takala-Harrison, S., T.G. Clark, M.P. Cummings, A.M. Dondorp, M.M. Fukuda, F. Nosten, H. Noedl, M. Imwong, D. Bethell, Y. Se, C. Lon, S.D. Tyner, D. Saunders, D. Socheat, A. Pyae Phy, P. Starzengruber, P. Swoboda, G.C. Cerqueira, **J.C. Silva**, C. Arze, S.M. Ricklefs, S.F. Porcella, M. Adams, L.J. Kenefic, S. Campino, S. Auburn, M. Manske, B. MacInnis, D.P. Kwiatkowski, X-Z Su, N.J. White, P. Ringwald, C.V. Plowe. ARC3: Detecting recent positive selection in artemisinin resistant malaria parasites. American Society of Tropical Medicine and Hygiene. December 4-8, 2011, Philadelphia, PA.

9. Takala-Harrison, S., M. Imwong, C.G. Jacob, C. Arze, A.M. Dondorp, M.M. Fukuda, F. Nosten, H. Noedl, D. Bethell, Y. Se, C. Lon, S. D Tyner, D. Saunders, D. Socheat, A. Pyae Phyo, P. Starzengruber, P. Swoboda, K. Stepniewska, J. Flegg, G.C. Cerqueira, **J.C. Silva**, M. Adams, L.J Kenefic, J. Bailey, A. Niangaly, N.J. White, P. Ringwald, C.V. Plowe. *ARC3: Associations between candidate gene polymorphisms and parasite clearance rate following treatment with artemisinin*. American Society of Tropical Medicine and Hygiene. December 4-8, 2011, Philadelphia, PA.
10. Jacob, C.G., **J.C. Silva**, O. Miotto, M. Manske, A.M. Dondorp, M.M. Fukuda, H. Noedl, M. Imwong, D. Bethell, Y. Se, C. Lon, S.D. Tyner, D. Saunders, D. Socheat, P. Starzengruber, H.-P. Fuehrer, P. Swoboda, G. Maslen, S. Auburn, S. Campino, B. MacInnis, D.P. Kwiatkowski, N.J. White, P. Ringwald, S. Takala-Harrison, and C.V. Plowe. *SNPs Reveal Genome-Wide Differences Between Two Populations From Southeast Asia*. Genome Epidemiology of Malaria 2012. June 10-13, 2012. Wellcome Trust Genome Campus, Hinxton, Cambridge, UK.
11. Munro, J.B., M. Posavi, J. Orvis, K. Abolude, S. Nadendla, M. Borntrager, G.W. Gelembiuk, C.E. Lee, **J.C. Silva**. Chemosensory and sex determination in the copepod *Eurytemora affinis*. 2013 Meeting of the Society for Molecular Biology and Evolution. July 7-11. Chigago. IL.
12. Silva, M.C., Q. Su, S. Daugherty, M. Coelho, **J.C. Silva**. Evolution of olfaction in tubenose seabirds. 2013 Meeting of the Society for Molecular Biology and Evolution. July 7-11. Chigago. IL.
13. Gotia, H.T., **J.C. Silva**. Development of a qPCR-based method to quantify the ratio of host-to-parasite DNA in *Theileria parva*-infected host lymphocytes. American Society of Tropical Medicine and Hygiene. November 13-17, 2013, Washington, D.C.
14. Takala Harrison, S., C. Pepin, Cummings MP, Jacob CG, Arze C, Dondorp AM, Fukuda MM, Hien TT, M.P. Kyaw, Nyunt MH, Nyunt MM, Mayxay M, Newton PN, Nosten F, Noedl H, Imwong M, Bethell D, Y Se, Lon C, Tyner SD, Saunders DL, Socheat D, Phyo AP, Starzengruber P, Swoboda P, Fuehrer H-P, Clark TG, **Silva JC**, Adams M, Tan JC, Ferdig MT, Miotto O, Manske M, MacInnis B, Kwiatkowski DP, White NJ, Ringwald P, and Plowe CV. A replication genome-wide association study of the genetic basis of delayed parasite clearance following treatment with artemisinin. American Society of Tropical Medicine and Hygiene. November 13-17, 2013, Washington, D.C.
15. Drábek EF, AL Delcher, M Travassos, Q Su, A. Dara, D Coulibaly, M Daou, A Dembele, I Diarra, AK Kone, B Kouriba, MB Laurens, A Niangaly, K Traore, Y Tolo, CM Fraser, MA Thera, AA Djimde, OK Doumbo, CV Plowe, **JC Silva**. Novel algorithm to reconstruct complete *var* gene exons from clinical samples. Genomic Epidemiology of Malaria 2014. June 8-12, 2014. Wellcome Trust Genome Campus, Hinxton, Cambridge, UK.
16. Moser K.A., M Travassos, A. Ouattara, E. Drábek, C. Arze, C.M. Fraser, K.L. Sim S.L. Hoffman, O.K. Doumbo, M.A. Thera, S. Takala-Harrison, **J.C. Silva**, C.V. Plowe. A genomic epidemiology approach to assessing and improving strain-specific whole organism vaccine efficacy. American Society of Tropical Medicine and Hygiene. November 2-6, 2014. New Orleans, LA.
17. Ifeonu O., R. Simon, S.M. Tennant, A.S. Sheoran, J.C. Kissinger, G. Widmer, M.M. Levine, S. Tzipori, **J.C. Silva**. Identification of five novel *Cryptosporidium* vaccine candidates using reverse vaccinology. The Atlantic Vaccines & Immunotherapeutics Summit May 7-8, 2015. Bethesda, MD.
18. Moser K.A., E.F. Drábek, A. Ouattara, C. Arze, B.K.L. Sim, R. Sauerwein, S.L. Hoffman, C.V. Plowe, **J.C. Silva**. Methods for the comparison of genetic diversity in *Plasmodium falciparum* isolates in the context of the whole-organism PfSPZ Vaccine. The Atlantic Vaccines & Immunotherapeutics Summit May 7-8, 2015. Bethesda, MD.
19. Ifeonu OA, R Simon, SM Tennant, AS Sheoran, JC Kissinger, G Widmer, M.M. Levine, S Tzipori, JC Silva. Identification of five novel *Cryptosporidium* vaccine candidates using reverse vaccinology. 64th Annual American Society of Tropical Medicine and Hygiene Meeting, October 25-29, 2015, Philadelphia, PA. Poster #1152
20. Moser KA, Drábek EF, Ouattara A, Arze C, Sim BKL, Hoffman SL, Epstein JE, Plowe CV, **Silva JC**. The NF54-based whole-organism PfSPZ Vaccine in the context of global genetic diversity of *Plasmodium falciparum*: Implications for selection of vaccine and challenge strains. *American Society of Tropical Medicine and Hygiene*. October 25-29, 2015. Philadelphia, PA.

21. Moser KA, Drábek EF, Adams M, Hampton S, Ouattara A, Nagraj S, Travassos M, Fraser CM, Sim BKL, Hoffman SL, Plowe CV, **Silva JC**. Genomic characterization of NF54, the *Plasmodium falciparum* strain in the whole-organism malaria PfSPZ vaccine. *American Society of Tropical Medicine and Hygiene*. October 25-29, 2015. Philadelphia, PA.
22. Moser KA, Drabek EF, Ouattara A, Korsen S, Phillippy Adam, Nagraj S, Adams M, Sauerwein RW, Sim BKL, L Ti, Takala Harrison S, Hoffman SL, Plowe CV, **Silva JC**. Genomic characterization of NF54, the *P. falciparum* isolate in the PfSPZ Vaccine, and comparison to vaccine challenge strains from different geographic regions. *Genomic Epidemiology of Malaria*. June 5-8, 2016. Cambridge, UK.
38. Tretina K, Moser KA, Ifeonu OO, Munro JB, **Silva JC**. Turning back the clock: a history of apicomplexan species divergence. *American Society of Tropical Medicine and Hygiene*. November 5-9, 2017. Baltimore, MD.
39. Agrawal S, Huang F, Shrestha B, Adams M, Ott S, Sadzewicz L, Liu H, Serre D, Harrison ST, Nyunt MM, **Silva JC**, Plowe CV. Whole genome sequencing to measure complexity of infection and genetic diversity in *Plasmodium vivax* clinical isolates from the China-Myanmar border. *American Society of Tropical Medicine and Hygiene*. Oct 28-Nov1, 2018. New Orleans, LA.
23. Shah Z, Moser KA, Adams M, Buchwald A, Seydel K, Serre D, Laufer MK, **Silva JC**, Harrison ST. genome-wide differences in plasmodium falciparum parasites in Malawian children and adults. *American Society of Tropical Medicine and Hygiene*. Oct 28-Nov1, 2018. New Orleans, LA.
24. Stucke EM, Dara A, Dwivedi A, Hodges T, Coulibaly D, Kone AK, Traore K, Guindo B, Tangara BM, Niangaly A, Daou M, Diarra I, Tolo Y, Laurens MB, Ouattara A, Kouriba B, Duoumbo OK, Harrison, ST, Thera M, Plowe CV, Travassos MA, **Silva JC**. A novel method for identifying predominantly expressed vars from whole blood clinical samples. *American Society of Tropical Medicine and Hygiene*. Oct 28-Nov1, 2018. New Orleans, LA.
25. Dwivedi A, Moser KA, Molina-Cruz A, Barillas-Mury C, **Silva JC**. Investigating the selection of artemisinin resistance as the background of evolving pfs47 locus. *American Society of Tropical Medicine and Hygiene*. Oct 28-Nov1, 2018. New Orleans, LA.
26. Ifeonu O, Palmateer N, Tretina K, Knowles D, Nene V, Daubenberger CA, **Silva JC**. The *Theileria parva* Gene Catalog. *American Society of Tropical Medicine and Hygiene*. Oct 28-Nov1, 2018. New Orleans, LA.
27. Moser KA, Dwivedi A, Hodges T, Matsumura J, Crabtree J, Shah Z, Adams M, O'Connor TD, Thera MA, Taylor TE, Doumbo OK, Travassos MA, Laufer MK, Plowe CV, Harrison ST, **Silva JC**. African populations of *P. falciparum* undergo fluctuations in allele frequencies across the genome over time. *American Society of Tropical Medicine and Hygiene*. Oct 28-Nov1, 2018. New Orleans, LA.
28. Mbambo G, Moser KA, Travassos M, Berry A, Harrison AT, **Silva JC**. Utilizing *in silico* tools to perform B cell epitope prediction in *Plasmodium falciparum*. *American Society of Tropical Medicine and Hygiene*. Oct 28-Nov1, 2018. New Orleans, LA.
29. Hodges T, J Matsumura, A Dwivedi, KA Moser, AA Berry, S Takala-Harrison, J Crabtree, **JC Silva**. *In silico* capture and assembly of highly variable loci. *American Society of Tropical Medicine and Hygiene*. Nov 19-24, 2019. Washington DC.
30. Stucke EM, A Dara, A Dwivedi, T Hodges, D Coulibaly, AK Kone, K Troaore, B Guindo, B Tangara, A Niangaly, M Daou, I Diarra, Y Tolo2, M Sissoko, AE Zhou, MB Laurens, A Ouattara, B Kouriba, OK Duombo, S Takala-Harrison, D Serre, MA Thera, CV Plowe, MA Travassos, JC Silva. Identification of expressed vars in whole blood clinical samples with a custom capture array versus RNA enrichment methods. *American Society of Tropical Medicine and Hygiene*. Nov 19-24, 2019. Washington DC.
31. Shah Z, A Boleda, K Moser, M Adams, A Buchwald, K Seydel, D Mathanga, D Serre, MK Laufer, M Cummings, **JC Silva**, S Takala-Harrison Whole-genome analysis of Plasmodium falciparum to understand clinical immunity to malaria. *American Society of Tropical Medicine and Hygiene*. Nov 19-24, 2019. Washington DC.
32. Ouattara AM, A Niangaly, M Adams, D Coulibaly, AK Kone, K Traore, MB Laurens, Y Tolo, B Kouriba, DA Diallo, OK Doumbo, CV Plowe, MA Thera, S Takala-Harrison, MK Laufer, **JC Silva**. Epitope-based sieve analysis of Plasmodium falciparum sequences to assess FMP2.1/AS02A is

- consistent with differential vaccine efficacy against immunologically relevant AMA1 variants. *American Society of Tropical Medicine and Hygiene*. Nov 19-24, 2019. Washington DC.
33. NC Palmateer, JB Munro, R Pelle, L Steinaa, V Nene, RP Bishop, DP Knowles, I De Goeysen, D Geysen, I Morrison, **JC Silva**. Evolution of the *Theileria parva* repeat (*Tpr*) gene family is consistent with adaptation to mammalian host species. *American Society of Tropical Medicine and Hygiene*. Nov 19-24, 2019. Washington DC.
 34. A Dwivedi, A Molina-Cruz, G Carpi, KA Moser, C Barillas-Mury, JC Silva. Global genetic diversity and population structure of *Plasmodium falciparum* transmission vaccine targets Pfs47, Pfs48/45 and Pfs230. *American Society of Tropical Medicine and Hygiene*. Nov 19-24, 2019. Washington DC.
 35. Mbambo G, A Dwivedi, KE Lyke, and **JC Silva**. Characterization of differences in host immune gene expression profile in malaria-protected and malaria-susceptible children. *American Society of Tropical Medicine and Hygiene*. Nov 19-24, 2019. Washington DC.
 36. G Mbambo, A Dwivedi, D Coulibaly, AK Kone, AB Guindo, MA Thera, KE Lyke, **JC Silva**. Differential gene expression analysis of PBMCs from Malian children reveals molecular mechanisms associated with varying susceptibility to clinical malaria disease. Poster. Annual meeting of the American Society of Tropical Medicine and Hygiene. Nov 15-19, 2020. Virtual.
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