

# Marco Salemi, Ph.D.

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**Citizenship: USA**

**Primary Languages: Italian, English**

**Other Languages: Spanish (Intermediate), Portuguese (Intermediate), French (Beginner), Dutch (Beginner).**

## CURRENT AFFILIATION

University of Florida College of Medicine (UF-COM), Dept. Pathology, Immunology & Laboratory Medicine, Emerging Pathogens Institute, P.O. Box 103633, 2055 Mowry Rd, Gainesville, FL 32610, Phone/fax +1 352 273 8288/8284.

## DEGREES

- Ph.D. in Science. 1999. Catholic University, Leuven, Belgium.
- Post-graduate school in Biotechnology Application. 1995. University of Milan, Italy.
- B.S. with full marks in Chemistry, 1991. University of Pavia, Italy.

## SCIENTIFIC APPOINTMENTS

- 2019-current. Holloway and McClamma Endowed Chair in Chronic and Infectious Diseases. Department of Pathology Immunology and Laboratory Medicine. University of Florida, Gainesville, FL, USA
- 2017-current. Full Professor with Tenure. Department of Pathology Immunology and Laboratory Medicine. University of Florida, Gainesville, FL, USA
- 2015-2017. Associate Professor with Tenure. Department of Pathology Immunology and Laboratory Medicine. University of Florida, Gainesville, FL, USA.
- 2013-2014. Associate Professor. Department of Pathology Immunology and Laboratory Medicine. University of Florida, Gainesville, FL, USA.
- 2010-2012. Assistant Professor. Department of Pathology Immunology and Laboratory Medicine. University of Florida, Gainesville, FL, USA.
- 2004-2009. Research Assistant Professor. Department of Pathology, University of Florida (UF), Gainesville, Florida, U.S.A.
- 2002-2004. Postdoctoral Researcher. Laboratory of Prof. Walter Fitch, University of California Irvine (UCI), Irvine, California, U.S.A.
- 1999-2002, Postdoctoral scientist. Laboratory of Prof. Anne-Mieke Vandamme, Rega Institute, Catholic University of Leuven, Belgium.
- 1996-1999. Mary Curie Fellow. Laboratory of Prof. Anne-Mieke Vandamme, Rega Institute, Catholic University of Leuven, Belgium.
- 1991-1996. Postgraduate fellow. Laboratory of Prof. Umberto Bertazzoni, "Istituto di Genetica Biochimica ed Evoluzionistica" (Institute of Genetics, Biochemistry and Evolution) of CNR (National Research Center), Pavia, Italy.

## RESEARCH INTERESTS

As a Marie-Curie Fellow at the Rega Institute (Leuven, Belgium), and post-doctoral scientist with Walter M. Fitch at the University of California, Irvine (USA), I have been trained in the field of molecular evolution of viruses and phylogenetic analysis. During the last fifteen years, as faculty at the University of Florida, Gainesville, my research interests have included molecular epidemiology, intra-host viral evolution, and the application of phylogenetic and population genetic methods to the study of human and simian pathogenic viruses (in particular HIV/SIV, HCV, HTLV and influenza). More recently, I have been applying the Bayesian coalescent framework to study molecular evolution and phylogeography of emergent and re-emergent bacterial pathogens, such as *MRSA*, *Neisseria Meningitidis* and *Vibrio cholerae*, using genome-wide SNPs. In addition, my laboratory has developed *ad hoc*

protocols for the generation of high-throughput sequence data (including DNA sequencing, transcriptomics, and miRNA expression profiles) and droplet digital PCR quantitative analyses of viral and bacterial pathogens, as well as several automated bioinformatic and machine learning pipelines for the analysis of large sequence data sets (big data).

### **HONORS & AWARDS**

- 2019. McClamma Endowed Chair and Holloway Endowed Chair for Chronic and Infectious Diseases Research.
- 2017. UF Term Professorships award.
- 2012. University of Florida Excellence Awards for Assistant Professors.
- 2008. *Honor Aedificanti* Award for his efforts in AIDS research, Kiwanis International Association, Caltanissetta, Italy, December 5<sup>th</sup> 2008.
- 2004. Distinguished International Educator of the Year Award, University of Florida, Gainesville, U.S.A.
- 2002. Award from the Catholic University of Leuven for the best PhD thesis in Science
- 2001. Award for best scientific paper originated in Ireland: **M. Salemi**, et al. Dating the common ancestor of SIVcpz and HIV-1 group M and the origin of HIV-1 subtypes using a new method to uncover clock-like molecular evolution. *The FASEB J.* **15**:267-268, 2000.
- 1999-2000. His biography has been included in Who's Who in the world as young scientist.
- 1999. Invited Speaker (HTLV and the molecular clock) at the Fourth European Conference on Experimental AIDS Research, ECEAR 99. Tampere, Finland, June 18-21.
- 1999. Young Researcher Award for the abstract: The evolutionary rate of HTLV-II in injecting drug users is 50 to 200 times faster compared to in endemically infected Amerindian and Pygmy tribes. **M. Salemi**, J. Desmyter, A-M. Vandamme. Ninth International Conference on Human Retrovirology: HTLV. Kagoshima, Japan, April 5-9.
- 1998. Best Congress contribution award for the abstract: Post-Colombian introduction of HTLV-I in Latin America. S. Van Dooren, **M. Salemi**, E. Gotuzzo, E. Audenaert, S. Duwe, H. Ellerbrok, R. Grassmann, J. Desmyter and A-M Vandamme. Third European Conference on Experimental AIDS Research. Munich, Germany, February 28-March 3.
- 1996. Awarded with Marie Curie Fellowship, European Union, for the project "Molecular investigation on the origin and genetic stability of Human T-lymphotropic viruses".

### **EDITORIAL REVIEWER**

*Nature, Nature Medicine, Science, Science Translational Medicine, P.N.A.S., PLoS Pathogens, PLoS Computational Biology, Bioinformatics, Molecular Biology and Evolution, Journal of Virology, Journal of Molecular Evolution, Molecular Phylogenetics and Evolution, Emerging Infectious Diseases, Retrovirology, BMC Evolutionary Biology, AIDS Research and Human Retroviruses, Journal of Infectious Diseases.*

### **EDITORIAL APPOINTMENTS**

Associate Editor of *PLoS ONE*; Academic Editor of *New Microbiologica*; Editorial Board of *Retrovirology*; Editorial Board of *Scientific Reports*.

### **SELECTED INVITED TALKS**

- Mar 2019 Multiscale phylodynamics of viral and bacterial pathogens: from pandemic spread to intra-host evolution. Invited Lecture. University of Tulane, New Orleans, LA, USA
- Oct 2018 The SIV macaque model of neuroAIDS: phylodynamics and pathogenesis. Invited Lecture. Tulane National Research Primate Center, Covington, LA, USA.
- Nov 2017 Understanding and predicting ZIKV epidemic: a phylogenetic and Deep Learning perspective. Invited Lecture. Zika Action Meeting, Emerging Pathogens Institute, Gainesville, FL, USA.

- May 2017 Viral phylodynamics of emerging epidemics in the Caribbean area. Invited Seminar. Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA.
- July 2016 SIV phylodynamic and pathogenesis in the macaque model of neuroAIDS. Invited Seminar. University of Hawaii, Honolulu, HI, USA.
- Apr 2016 SIV phyloanatomy in the macaque model of neuroAIDS: a new framework to study the interplay between viral evolution and pathogenesis. Invited Lecture. CFAR Seminar Series, University of Miami, FL, USA.
- Mar 2016 Phylodynamics and phylogeography of infectious diseases. Invited Speaker. Academician Nicolae Cajal Symposium of the Romanian Academy of Medical Sciences, Bucharest, Romania.
- Sep 2015 Phylodynamic analysis of viral and bacterial pathogens in the genomics era. Invited Speaker. 10<sup>th</sup> International Conference on Information Processing in Cells and Tissues. San Diego, CA, USA.
- Aug 2015 SIV intra-host population dynamics in peripheral blood and tissues. Invited Seminar. University of Miami CFAR Web-seminars, Miami, FL, USA.
- Jul 2015 Towards a genomic epidemiology of microbial pathogens. Invited Seminar. University Hospitals – Campus Bio-Medico, Rome, Italy.
- Jun 2015 Impact of evolution, selection, and spatial dispersion on Ebola Zaire Virus (EBOV) epidemic waves. Invited Seminar. University of Florida Emerging Pathogens Institute, Gainesville, FL, USA.
- Mar 2015 Genomic epidemiology of bacterial pathogens: from cutting-edge research to clinical practice. Invited Seminar. University Hospitals – Campus Bio-Medico, Rome, Italy.
- Feb 2015 The phylodynamics and phylogeography of infectious diseases. Invited Seminar. Boston College, Boston, MA, USA.
- Nov 2014 Phylodynamics of Clinical and Environmental Toxigenic *Vibrio cholerae* O1 in Haiti. Invited Seminar. Sanger Institute, Cambridge, UK.
- Oct 2014 Intra-host evolution and pathogenesis of human and simian immunodeficiency viruses. Invited Seminar. University of Missouri Kansas City (UMKC), Oct 23, 2014.
- May 2014 HIV-1 Evolutionary Dynamics in HLA-B\*5701 Subjects with Different Risk of Disease Progression. Invited Speaker. 21<sup>st</sup> Annual HIV Dynamics & Evolution Conference, Tucson, AZ, USA.
- April 2014 .Intrahost phylodynamics and phylogeography in the SIV macaque model of neuroAIDS. Invited Speaker. Center for Disease Control and Prevention, Atlanta, GA, USA.
- Nov 2013. Intra-host Bayesian Phylogeography Infers Tempo and Mode of Neuropathogenesis in SIVmac251 Infected CD8-lymphocyte Depleted Rhesus Macaques. Invited Speaker. 31<sup>st</sup> Annual Symposium on Nonhuman Primate Models for AIDS. Atlanta, GA, USA.
- Oct 2013 Intra-host phylogeography of SIV brain invasion in the rhesus macaque model of NeuroAIDS. Invited Speaker. HIV/SIV phylodynamics and neuroAIDS Discussion. Italian Institute of Health, Rome, Italy.
- July 2013 Viral Quasispecies from the data derived from Sequencing Techniques of Last Generation. Invited Teacher. First International Bioinformatics Workshop on Molecular Biology and Evolution of Viruses. Salvador de Bahia, Brazil.
- April 2013 Phylodynamic analysis of brain infection in the SIV infected macaque model of NeuroAIDS. Invited Speaker. 19<sup>th</sup> Society for NeuroImmune Pharmacology (SNIP) Conference. San Juan, Puerto Rico.
- Mar 2012 Themed discussion on “Molecular epidemiology: primate viruses and how they affect humans”. Discussant and Chairman. 19th Conference on Retroviruses and Opportunistic Infections (CROI). Seattle, WA, USA.
- Nov 2011 Phylogeography of human infectious diseases. Keynote Speaker. 12th Annual Symposium on Antiviral Drug Resistance: Targets & Mechanisms. Hershey, PA, USA.
- June 2011 HIV/SIV intra-host phylodynamics and neuropathogenesis. Invited Lecturer. Henry M. Jackson Foundation, Rockville, MD, USA.
- June 2011 Retrovirus evolution and molecular anthropology HTLV and Related Viruses. Invited Speaker. Tenth International Conference on Human Retrovirology. Trinity College, Dublin, Ireland.
- May 2010 HIV-1 Molecular Epidemiology and Pathogenesis: A Phylodynamic Approach. Invited Speaker. Aaron Diamond AIDS Research Center. New York, NY, USA.
- April 2010 Phylogenetic challenges in the retroviridae branch of the tree of life. Keynote Speaker. 1st Symposium on Reconstructing the Tree of Life: Computational Challenges and Solutions. Gainesville, FL, USA.
- Oct 2009 Investigating HIV-1 epidemic emergence in Africa by Landscape Phylodynamics: a framework integrating geospatial, anthropological and phylogenetic data. Invited Speaker. International USA-Russia Symposium on HIV prevention science. Moscow, Russia.

- Feb 2009 The evolution of infectious diseases. Plenary Lecture. Darwin Day. University of Ferrara and Museum of Natural History. Ferrara, Italy.
- Dec 2008 Inter- and intra-host phylodynamics of RNA viruses. Plenary Lecture. Workshop on Bioinformatics and Molecular Epidemiology of Pathogens. Italian Institute of Health. Rome, Italy.

#### **NATIONAL AND INTERNATIONAL TEACHING EXPERIENCE**

- 1997-2017. Co-organizer and Instructor at the Annual Workshop on *Virus Evolution and Molecular Epidemiology* (<http://regaweb.med.kuleuven.be/workshop>): Katholieke Universiteit Leuven, Belgium, 1997-2002; Stanford University, CA, USA, 2003; The Finnish National Public Health Institute, Helsinki, Finland, 2004; Institute of Health, Lisbon, Portugal, 2007; South African National Bioinformatics Institute, Cape Town, South Africa, 2008; Erasmus Medical Center, Rotterdam, The Netherlands, 2009; Johns Hopkins University, Baltimore, MD, USA, 2010; University of Belgrade, Serbia, 2012; University of Florida Gainesville, FL, USA, 2013; National Institute for Infectious Diseases "L. Spallanzani", Rome, Italy, 2014; University of the West Indies, Trinidad and Tobago, 2015).
- 2015-2017. Co-organizer and Instructor at the *3rd (2015) and 4th (2017) International Workshops "Bioinformatics for NextGen sequence analysis and phylodynamics of infectious diseases"*, Hospital Nacional de Pediatría "Juan P. Garrahan", Buenos Aires, Argentina.
- 2013-2017. Spring semester – 3 credits course – *Introduction to phylodynamics: a practical approach to molecular phylogenetics of pathogens*. University of Florida, Gainesville.
- 2012. Spring semester – 2 credits course – *Introduction to phylodynamics: a practical approach to molecular phylogenetics of pathogens*. University of Florida, Gainesville.
- 2010. Fall semester – 1 credit course – *Molecular evolution and phylogenetics journal club*. University of Florida, Gainesville.
- 2011. Instructor at the *Bioinformatics for Phylogenetic Reconstruction in Virology training course*, Hospital Nacional de Pediatría "Juan P. Garrahan", Buenos Aires, Argentina.
- 2002-2010. Instructor and co-Organizer of the *Yearly Italian Workshop on Virus Evolution and Molecular Epidemiology*, Istituto Superiore di Sanità (Italian Institute of Health), Roma, Italy.
- 2007. Instructor and Lecturer at the *Brazilian Workshop on Virus evolution and Data mining*, University of Fiocruz, Salvador de Bahia, Brazil.
- 2005. Instructor at the *Taiwan Workshop of Molecular Evolution*, Taipei, Taiwan.
- 2004. Instructor at the *Second Brazilian Workshop on Virus Evolution and Molecular Epidemiology*, Salvador de Bahia, Brazil.
- 2003. Instructor at the *South African Workshop on Viral Molecular evolution* at the Nelson Mandela School Medicine, Durban, South Africa.
- 2002. Instructor at the *First Brazilian Workshop on Virus Evolution and Molecular Epidemiology*, Salvador de Bahia, Brazil.

#### **PHD STUDENTS TEACHING/MENTORING**

- Taylor Paisie [Supervisor]
- Yaser Alasahafi [co-Supervisor], graduated in Dec 2018.
- Brittany Rife, IDP Medical Sciences [Supervisor]: graduated in Fall 2017.
- Taj Hassan Azarian, Epidemiology [Co-Supervisor]: graduated in spring 2015.
- Samantha Strickland, IDP Medical Sciences [Supervisor]: graduated in fall 2013.
- Cameron Browne, Applied Mathematics [Co-supervisor]: graduated in spring 2013.

#### **REVIEWING PANEL AND COMMITTEE APPOINTMENTS**

- Member of the N.I.H. *AIDS Research Review Charter Committee Study Section*, August 14-15 , 2019.
- Member of the N.I.H. *ZRG1 AARR-Q (50) Study Section*, June 12 , 2019.

- Member of the N.I.H. *ACE Study Section*, December 5 , 2018.
- Member of the N.I.H. *ACE Study Section*, July 31, 2018.
- Member of the N.I.H. *ACE Study Section*, March 22 , 2019.
- Member of the N.I.H. *ACE Study Section*, March 13 – 14, 2018.
- Member of the N.I.H. *HIV/AIDS Vaccine study section (VACC)*, November 7, 2017.
- Member of the N.I.H. *Study Section for PAR-17-048 – Phylodynamic tracking of HIV transmission*, June 22, 2017.
- Member of the N.I.H. *Study Section for PAR-14-041 – Centers for AIDS Research and Developmental Centers for AIDS Research (P30)*, December 12 – 13, 2016.
- Member of the N.I.H. study section for *AARRH52 Planning Grant for Global Infectious Disease Research Training Program*. Bethesda, MD, USA, December 11, 2015.
- Member of the N.I.H. *Special Emphasis for ZAI1-UKS-A-JI — Centers for AIDS Research (CFAR)*. Bethesda, MD, USA, October 26 – 27, 2015.
- Member of the N.I.H. *Special Emphasis Panel for AARR M 50, RFA-AI-14-057 — U.S.-China Program for Research Toward a Cure for HIV/AIDS*. Bethesda, MD, USA, March 24, 2015.
- Member of the N.I.H. *Special Emphasis Panel — Centers for AIDS Research (CFAR)*. Bethesda, MD, USA, November 17 – 19, 2014.
- Member of the N.I.H. *Special Emphasis Panel/Scientific Review Group 2014/01 ZRG1 AARR-E02 —HIV/AIDS*. Bethesda, MD, USA, April 9 – 10, 2014.
- Member of the N.I.H. *Special Emphasis Panel/Scientific Review Group 2014/01 ZRG1 AARR-E (03) M —HIV/AIDS*. Bethesda, MD, USA, December 18 – 19, 2013.
- Member of the N.I.H. *Study Section for ZRG1 AARR-D(50) — Eradication of HIV-1 from CNS reservoirs: implication for therapeutics (RFA)*. Bethesda, MD, USA, November 15, 2013.
- Member of the N.I.H. *Special Emphasis for PAR 11-108 — Centers for AIDS Research (CFAR)*. Bethesda, MD, USA, September 21 – 23, 2011.
- Member of the N.I.H. *Study Section for RFA-AI-10-009 — Martin Delaney Collaboratory: Towards an HIV-1 Cure (U19)*. Bethesda, MD, USA, April 4 – 6, 2011.
- Member of the *Natural History and Epidemiology Planning Group*, U.S. Department of Health and Human Services, NIH, Office of AIDS Research, 2011 – 2016.
- Member of *ICBR-Genomic Cores advisory group*, University of Florida Gainesville, 2015.
- Member of the *UFII Seed Grants Committee*, University of Florida Gainesville, 2015.
- Member of the *Computational Biology Advisory Committee*, University of Florida Gainesville, 2010 – 2013.
- Member of the *Computational Biology Seed Grants Committee*, University of Florida Gainesville, 2009.

## PUBLICATIONS

### Chief Editor and contributor of two major textbooks in the field of molecular evolution and phylogenetic analysis:

1. **M. Salemi** and A-M. Vandamme (eds.) *The Phylogenetic Handbook: A Practical Approach to DNA and protein phylogeny*. Cambridge University Press, New York, NY, USA, 2003.
2. P. Lemey, **M. Salemi**, A-M Vandamme (eds.) *The Phylogenetic Handbook: A Practical Approach to phylogenetic analysis and hypothesis testing*. Cambridge University Press, New York, NY, USA, 2009.

### Additional contribution to book chapters:

3. **M. Salemi**. Bioinformatics. *Telemedicine Glossary 3<sup>rd</sup> edition*, pp. 33-34. European Commission Directorate General, Brussels, 2001.

### Peer-reviewed papers:

1. G. M. Blohm, M. C, Márquez-Colmenarez, J. A. Lednický, T. S. Bonny, C. Mavian, **M. Salemi**, L. Delgado-Noguera, J. G. Morris, A. E. Paniz-Mondolfi. Isolation of Mayaro virus from a Venezuelan patient with febrile illness, arthralgias, and rash: further evidence of regional strain circulation and possible long-term endemicity. *American Journal of Tropical Medicine & Hygiene* 2019 Oct 7. doi: 10.4269/ajtmh.19-0357. [Epub ahead of print].
2. M. Prosperì, **M. Salemi**, T. Azarian, F. Milicchio, J. A. Johnson, M. Oliva. Unexpected predictors of antibiotic resistance in housekeeping genes of staphylococcus aureus. *ACM Conference in Bioinformatics, Computational*

- Biology and Biomedicine* pp. 259-268. doi: 10.1145/3307339.334213, 2019
3. R. Durães-Carvalho, L. F. Ludwig-Begall, **M. Salemi**, R. D. Lins, E. T. A. Marques. Influence of directional positive Darwinian selection-driven evolution on arboviruses Dengue and Zika virulence and pathogenesis. *Molecular Phylogenetics and Evolution* **140**:106607. doi: 10.1016/j.ympev.2019.106607, 2019.
  4. G. Blohm, M. A. Elbadry, C. Mavian, C. Stephenson, J. Loeb, S. White, T. Telisma, S. Chavannes, V. Madsen Beau De Rochars, **M. Salemi**, J. A. Lednicky, J. G. Morris Jr. Mayaro as a Caribbean traveler: Evidence for multiple introductions and transmission of the virus into Haiti. *International Journal of Infectious Diseases* **87**:151-155, 2019.
  5. E. Wilkinson, D. M. Junqueira, R. Lessells, S. Engelbrecht, G. van Zyl, T. de Oliveira, **M. Salemi**. The effect of interventions on the transmission and spread of HIV in South Africa: a phylodynamic analysis. *Scientific Reports* **9**(1):2640. doi: 10.1038/s41598-018-37749-3, 2019.
  6. J. A. Lednicky, S. K. White, C. N. Mavian, M. A. El Badry, T. Telisma, **M. Salemi**, B. A. O'Kech, V. M. Beau De Rochars, J. G. Morris Jr. Emergence of Madariaga virus as a cause of acute febrile illness in children, Haiti, 2015-2016. *PLoS Neglected Tropical Diseases* **13**(1):e0006972. doi: 10.1371/journal.pntd.0006972, 2019.
  7. S. Y. C. Lin, B. Rife Magalis, **M. Salemi**, H. F. Liu. Origin and dissemination of hepatitis B virus genotype C in East Asia revealed by phylodynamic analysis and historical correlates. *Journal of Viral Hepatitis* **26**(1):145-154, 2019.
  8. C. Mavian, M. Dulcey, O. Munoz, **M. Salemi**, A. Y. Vittor, I. Capua. Islands as Hotspots for Emerging Mosquito-Borne Viruses: A One-Health Perspective. *Viruses* **11**(1). pii: E11. doi: 10.3390/v11010011, 2018.
  9. D. Prakoso, M. J. Dark, A. F. Barbet, **M. Salemi**, K. L. Barr, J. J. Liu, N. Wenzlow, T. B. Waltzek, M. T. Long. Viral Enrichment Methods Affect the Detection but Not Sequence Variation of West Nile Virus in Equine Brain Tissue. *Frontiers of Veterinary Science* **5**:318. doi: 10.3389/fvets.2018.00318, 2018.
  10. M. Fogolari, C. Mavian, S. Angeletti, **M. Salemi\***, K. A. Lampel, A. T. Maurelli\*. Distribution and characterization of Shiga toxin converting temperate phages carried by *Shigella flexneri* in Hispaniola. *Infection Genetics and Evolution* **65**:321-328, 2018. \* Corresponding authors.
  11. M. N. Séraphin, X. Didelot, D. J. Nolan, J. R. May, M. S. R. Khan, E. R. Murray, **M. Salemi**, J. G. Morris, M. Lauzardo. Genomic investigation of a *Mycobacterium tuberculosis* outbreak involving prison and community cases in Florida, United States. *American Journal of Tropical Medicine & Hygiene* **99**(4): 867-874, 2018.
  12. B. Rife Magalis, S. L. Kosakovsky Pond, M. F. Summers, **M. Salemi**. Evaluation of global HIV/SIV envelope gp120 RNA structure and evolution within and among infected hosts. *Virus Evolution* **4**(1):vey018, 2018.
  13. S. K. White, C. Mavian, M. A. Elbadry, V. M. Beau De Rochars, T. Paisie, T. Telisma, **M. Salemi**, J. A. Lednicky, J. G. Morris Jr. Detection and phylogenetic characterization of arbovirus dual-infections among persons during a chikungunya fever outbreak, Haiti 2014. *PLoS Neglected Tropical Diseases* **12**(5):e0006505, 2018.
  14. G. Singh, B. D. Rife, B. Seufzer, **M. Salemi**, A. Rendahl, K. Boris-Lawrie. Identification of conserved, primary sequence motifs that direct retrovirus RNA fate. *Nucleic Acids Research* **46**(14):7366-7378, 2018.
  15. S. W. White, C. Mavian, **M. Salemi**, J. G. Morris Jr, M. A. Elbadry, B. A. O'kech, J. A. Lednicky, J. C. Dunford. A new "American" subgroup of African-lineage Chikungunya virus detected in and isolated from mosquitoes collected in Haiti, 2016. *PLoS One* **13**(5):e0196857, 2018.
  16. G. M. Blohm, J. A. Lednicky, S. W. White, C. Mavian, M. C. Márquez, K. P. González-García, **M. Salemi**, J. G. Morris Jr, A. E. Paniz-Mondolfi. Madariaga virus: identification of a Lineage III strain in a Venezuelan child with acute undifferentiated febrile illness, in the setting of a possible equine epizootic. *Clinical Infectious Diseases* **67**(4):619-621, 2018.
  17. R. Durães-Carvalho R, **M. Salemi**. In-depth phylodynamics, evolutionary analysis and in silico predictions of universal epitopes of Influenza A subtypes and Influenza B viruses. *Molecular Phylogenetics and Evolution* **121**:174-182, 2018.
  18. D. J. Nolan, R. Rose, P. H. Rodriguez, **M. Salemi**, E. J. Singer, S. L. Lamers, M. S. McGrath. The spleen is an HIV-1 sanctuary during combined antiretroviral therapy. *AIDS Research and Human Retroviruses* **34**(1):123-125, 2018.
  19. E. Cella, E. Riva, **M. Salemi**, S. Spoto, S. Vita, M. Fogolari, S. Angeletti, M. Ciccozzi. The new Chikungunya virus outbreak in Italy possibly originated from a single introduction from Asia. *Pathogens and Global Health* **12**(2):93-95, 2017.
  20. B. Rife Magalis, D. Nolan, P. Autissier, T. Burdo, K. Williams, **M. Salemi**. Insights into the impact of CD8+ immune modulation on HIV evolutionary dynamics in distinct anatomical compartments using SIV-infected macaque models of AIDS progression. *Journal of Virology* **91**(23), pii: e01162-17, 2017.
  21. M. A. Elbadry, S. K. White, J. C. Loeb, M. S. Tagliamonte, **M. Salemi**, V. M. Beau De Rochars, T. Telisma, M. Rashid, J. G. Morris Jr, J. A. Lednicky. Complete Genomic Sequence of Dengue Virus Serotype 4 Isolated from Plasma Collected from a Haitian Child in 2014. *Genome Announcement* **5**(40), 2017.

22. T. S. Bonny, J. P. Driver, T. Paisie, **M. Salemi**, J. G. Morris, L. A. Shender, L. Smith, C. Enloe, K. Oxenrider, J. A. Gore, J. C. Loeb, C. Y. Wu, J. A. Lednicky. Detection of Alphacoronavirus vRNA in the Feces of Brazilian Free-Tailed Bats (*Tadarida brasiliensis*) from a Colony in Florida, USA. *Diseases* **5**(1), 2017.
23. S. C. Claytor, K. Subramaniam, N. Landrau-Giovannetti, V. G. Chinchar, M. J. Gray, D. L. Miller, C. Mavian, **M. Salemi**, S. Wisely, T. B. Waltzek. Ranavirus phylogenomics: Signatures of recombination and inversions among bullfrog ranaculture isolates. *Virology* **511**, 330-343, 2017.
24. C. Mavian, B. D. Rife, J. J. Dollar, E. Cella, M. Ciccozzi, M. C. F. Prosperi, J. Lednicky, J. G. Morris, I. Capua, **M. Salemi**. Emergence of recombinant Mayaro virus strains from the Amazon basin. *Scientific Reports* **7**(1):8718, 2017.
25. G. M. Blohm, J. A. Lednicky, M. Márquez, S. K. White, J. C. Loeb, C. A. Pacheco, D. J. Nolan, T. Paisie, **M. Salemi**, A. J. Rodríguez-Morales, J. Glenn Morris Jr, J. R. C. Pulliam, A. E. Paniz-Mondolfi. Evidence for Mother-to-Child Transmission of Zika Virus Through Breast Milk. *Clinical Infectious Diseases*, doi 10.1093/cid/cix968, Dec 30, 2017 [Epub ahead of print].
26. M. Elbadry, S. White, J. Loeb, M. Tagliamonte, **M. Salemi**, J. V. M. Beau De Rochars, B. Okech, J. G. Morris Jr, J. Lednicky. Complete Genomic Sequence of Dengue virus 1, Isolated from Plasma Collected from a Haitian Child in 2014. *Genome Announcement* **5**(22), 2017.
27. G. M. Blohm, J. A. Lednicky, M. Márquez, S. K. White, J. C. Loeb, C. A. Pacheco, D. J. Nolan, T. Paisie, **M. Salemi**, A. J. Rodríguez-Morales, J. G. Morris Jr, J. R. C. Pulliam, A. S. Carrillo, J. D. Plaza, A. E. Paniz-Mondolfi. Complete Genome Sequences of Identical Zika virus Isolates in a Nursing Mother and Her Infant. *Genome Announcement* **5**(17), 2017.
28. E. Cella, M. Ciccozzi, A. Lo Presti, M. Fogolari, T. Azarian, M. Prosperi, **M. Salemi**, M. Equestre, F. Antonelli, A. Conti, M. Cesaris, S. Spoto, R. A. Incalzi, R. Coppola, G. Dicuonzo, S. Angeletti. Multi-drug resistant *Klebsiella pneumoniae* strains circulating in hospital setting: whole-genome sequencing and Bayesian phylogenetic analysis for outbreak investigations. *Scientific Reports* **7**(1):3534, 2017.
29. J. Mallard, E. Papazian, C. Soulas, D. J. Nolan, **M. Salemi**, K. C. Williams. A method for obtaining simian immunodeficiency virus RNA sequences from laser capture microdissected and immune captured CD68+ and CD163+ macrophages from frozen tissue sections of bone marrow and brain. *Journal of Immunological Methods* **442**:59-63, 2017.
30. V. Beau de Rochars, J. Lednicky, S. White, J. Loeb, M. Elbadry, T. Telisma, S. Chavannes, M. G. Anilis, E. Cella, M. Ciccozzi, B. Okech, **M. Salemi**, J. G. Morris Jr. Isolation of Coronavirus NL63 from blood from children in rural Haiti: Phylogenetic similarities with recent isolates from Malaysia. *American Journal of Tropical Medicine & Hygiene* **96**(1):144-147, 2017.
31. N. Iovine, J. Lednicky, K. Cherabuddi, H. Croke, S. K. White, J. C. Loeb, E. Cella, M. Ciccozzi, **M. Salemi**, J. G. Morris. Co-Infection with Zika and Dengue-2 Viruses in a Traveler Returning from Haiti, 2016: Clinical Presentation and Genetic Analysis. *Clinical Infectious Diseases* **64**(1):72-75, 2017.
32. S. Zhou, E. Cella, W. Zhou, W. H. Kong, M. Q. Liu, **M. Salemi**, M. Ciccozzi, X. Chen. Population dynamics of HCV subtypes in injection drug-users on methadone maintenance treatment in China associated with economic and health reform. *Journal of Viral Hepatitis* **24**(7):551-560, 2017.
33. D. J. Nolan, S. L. Lamers, R. Rose, J. J. Dollar, **M. Salemi**, M. S. McGrath. Single Genome Sequencing of Expressed and Proviral HIV-1 Envelope Glycoprotein 120 (gp120) and nef Genes. *Bio-protocol* **7**(12), 2017.
34. G. B. Fogel, E. S. Liu, D. J. Nolan, **M. Salemi**, A. E. Barbier, R. Rose, E. J. Singer, M. S. McGrath. Predicted coreceptor usage at end-stage HIV disease in tissues derived from subjects on antiretroviral therapy with an undetectable plasma viral load. *Infection Genetics and Evolution* **51**, 194-197, 2017.
35. B. Vorbach, D. Rotstein, N. Stacy, C. Mavian, **M. Salemi**, T. Waltzek, M. de Wit. Fatal Systemic Salmonellosis in a Florida manatee (*Trichechus manatus latirostris*). *Journal of Wildlife Diseases* **53**(4), 930-933, 2017.
36. B. D. Rife, C. Mavian, X. Chen, M. Ciccozzi, **M. Salemi**, J. Min, M. C. Prosperi. Phylodynamic applications in 21st century global infectious disease research. *Global Health Research and Policy* **2**:13, 2017.
37. K. Cherabuddi, N. M. Iovine, K. Shah, S. K. White, T. Paisie, **M. Salemi**, J. G. Morris JG Jr, J. A. Lednicky. Zika and Chikungunya virus co-infection in a traveler returning from Colombia: virus isolation and genetic analysis. *Journal of Molecular Medicine Case Reports* **3**(6):e005072, 2016.
38. T. Azarian, A. Ali, J. A. Johnson, M. Jubair, E. Cella, M. Ciccozzi, D. J. Nolan, W. Farmerie, M. A. Rashid, S. Sinha-Ray, M. T. Alam, J. G. Morris, **M. Salemi**. Non-toxigenic environmental *Vibrio cholerae* O1 strains from Haiti provide evidence of pre-pandemic Cholera in Hispaniola. *Scientific Reports* **6**:36115, 2016.
39. J. Min, E. Cella, M. Ciccozzi, A. Pelosi, **M. Salemi**, M. Prosperi. The global spread of Middle East Respiratory Syndrome: an analysis fusing traditional epidemiological tracing and molecular phylodynamics. *Global Health*

- Research and Policy* **1**(14):1-14, 2016.
40. J. Lednicky, V. Madsen Beau De Rochars, M. El Badry, J. Loeb, T. Telisma, S. Chavannes, G. Anilis, B. Okech, **M. Salemi**, J. G. Morris Jr. Isolation of Mayaro virus from a child with acute febrile illness in Haiti. *Emerging Infectious Diseases* **22**(11):2000-2002, 2016.
  41. T. Azarian, N. F. Maraqa, R. L. Cook, J. A. Johnson, C. Bailey, S. Wheeler, D. Nolan, M. H. Rathore, J. G. Morris Jr., **M. Salemi**. Genomic Epidemiology of Methicillin-resistant Staphylococcus aureus in a Neonatal Intensive Care Unit. *PLoS ONE* **11**(10):e0164397, 2016.
  42. S. L. Lamers, R. Rose, D. J. Nolan, G. B. Fogel, A. E. Barbier, **M. Salemi**, M. S. McGrath. HIV-1 Evolutionary Patterns Associated with Metastatic Kaposi's Sarcoma during AIDS. *Sarcoma* 4510483, 2016.
  43. M. C. Ngwa, T. Masalla, S. Esemu, F. F. Fumoloh, I. Kracalik, E. Cella, M. T. Alam, J. Akoachere, S. Liang, **M. Salemi**, J. G. Morris, A. Ali, L. M. Ndip. Genetic Studies of Vibrio cholerae in South West Cameroon—A Phylogenetic Analysis of Isolates from the 2010-2011 Epidemic. *PLOS Currents Outbreaks*. Edition 1, doi: 10.1371/currents.outbreaks.13b4e5e36a5c0831a1663fbd5713fe9, 2016.
  44. S. L. Lamers, R. Rose, E. Maidji, M. Agsalda-Garcia, D. J. Nolan, G. B. Fogel, **M. Salemi**, D. L. Garcia, P. Bracci, W. Yong, D. Commins, J. Said, N. Khanlou, C. H. Hinkin, M. Valdes Sueiras, G. Mathisen, S. Donovan, B. Shirimizu, C. A. Stoddart, M. S. McGrath, E. J. Singer. HIV DNA is frequently present within pathologic tissues evaluated at autopsy from cART-treated patients with undetectable viral load. *Journal of Virology* **90**(20):8968-83, 2016.
  45. R. Rose, S. L. Lamers, D. J. Nolan, E. Maidji, N. R. Faria, O. G. Pybus, J. J. Dollar, S. A. Maruniak, A. C. McAvoy, **M. Salemi**, C. Stoddart, E. Singer, M. S. McGrath. HIV maintains an evolving and dispersed population among multiple tissues during suppressive cART with periods of rapid expansion corresponding to the onset of cancer. *Journal of Virology* **90**(20):8984-93, 2016.
  46. T. Azarian, R. S. Daum, L. A. Pett, J. L. Steinbeck, Z. Yin, D. Nolan, S. Boyle-Vavra, W. P. Hanage, **M. Salemi**, M. Z. David. Intra-host evolution of Methicillin-resistant Staphylococcus aureus USA300 among individuals with reoccurring skin and soft tissue infections. *Journal of Infectious Diseases* **214**(6):895-905, 2016.
  47. D. Rife, D. J. Nolan, S. L. Lamers, P. Autissier, T. Burdo, K. C. Williams, **M. Salemi**. Evolution of neuroadaptation in the periphery and purifying selection in the brain contribute to compartmentalization of Simian Immunodeficiency Virus (SIV) in the brain of rhesus macaques with SIV-associated encephalitis. *Journal of Virology* **32**(8), 829-40, 2016.
  48. M. El Badry, J. Lednicky, E. Cella, T. Telisma, S. Chavannes, J. Loeb, M. Ciccozzi, B. Okech, V. Madsen Beau De Rochars, **M. Salemi**, J. Glenn Morris Jr. Isolation of an Enterovirus D68 from blood from a child with pneumonia in rural Haiti: Close phylogenetic linkage with New York strain. *Pediatric Infectious Disease Journal* **35**(9), 1048-50, 2016.
  49. S. L. Lamers, G. B. Fogel, E. S. Liu, **M. Salemi**, M. S. McGrath. On the Physicochemical and Structural Modifications Associated with HIV-1 Subtype B Tropism Transition. *AIDS Research and Human Retroviruses* **32**(8), 829-40, 2016.
  50. S. L. Lamers, R. Rose, L. C. Ndhlovu, D. J. Nolan, **M. Salemi**, E. Maidji, C. A. Stoddart, M. S. McGrath. The meningeal lymphatic system: a route for HIV brain migration? *Journal of Neurovirology* **22**(3), 275-81, 2016.
  51. J. Lednicky, V. M. Beau De Rochars, M. El Badry, J. Loeb, T. Telisma, S. Chavannes, G. Anilis, E. Cella, M. Ciccozzi, M. Rashid M, B. Okech, **M. Salemi**, J. G. Morris Jr. Zika virus outbreak in Haiti in 2014: molecular and clinical data. *PLoS Neglected Tropical Diseases* **10**(4):e0004687. doi: 10.1371/journal.pntd.0004687, 2016.
  52. E. Cella, I. Gabrielli, G. Zehender, M. Giovanetti, A. Lo Presti, A. Lai, G. Dicuonzo, S. Angeletti, **M. Salemi**, M. Ciccozzi. Phylogeny of Murray Valley Encephalitis Virus in Australia and Papua New Guinea. *Asian Pacific Journal of Tropical Medicine* **9**(4), 385-9, 2016.
  53. N. Jain, C. E. Morgan, B. D. Rife, **M. Salemi**, B. S. Tolbert. Solution structure of the HIV-1 Intron Splicing Silencer and its Interactions with the UP1 domain of hnRNP A1. *Journal of Biological Chemistry* **291**(5), 2331-44, 2016.
  54. **M. Salemi**, B. D. Rife. Phylogenetics and phyloanatomy of HIV/SIV intra-Host compartments and reservoirs: the key role of the central nervous system. *Current HIV Research* **14**(2), 110-20, 2016.
  55. G. B. Fogel, S. L. Lamers, E. S. Liu, **M. Salemi**, M. S. McGrath. Identification of dual-tropic HIV-1 using evolved neural networks. *Biosystems* **137**, 12-9, doi: 10.1016/j.biosystems.2015.09.007, 2015.
  56. P. A. Chan, J. W. Hogan, A. Huang, A. DeLong, **M. Salemi**, K. H. Mayer, R. Kantor. Phylogenetic investigation of a statewide HIV-1 epidemic reveals ongoing and active transmission networks among men who have sex with men. *Journal of Acquired Immunodeficiency Syndrome* **70**(4), 428-35, 2015.
  57. B. D. Rife, **M. Salemi**. Intra-host Bayesian phylogeography linking viral evolution and pathogenesis comes to an



- age. *British Journal of Virology* **2**(4), 58-61, 2015.
58. L. A. Santos, R. R. Gray, J. P. Monteiro-Cunha, E. S. Rodrigues, E. S. Santos, T. H. Araujo, M. S. Gonçalves, **M. Salemi**, L. C. Alcantara. Phylodynamics analysis of the Human Immunodeficiency Virus type 1 (HIV-1) envelope gene in mother and child pairs. *AIDS Research and Human Retroviruses* **31**(9), 913-20, 2015.
  59. S. L. Lamers, D. J. Nolan, B. D. Rife, G. B. Fogel, M. S. McGrath, T. H. Burdo, P. Autissier, K. C. Williams, M. M. Goodenow, **M. Salemi**. Tracking the emergence of host-specific SIV env and nef populations reveals nef early adaptation and convergent evolution in brain of naturally progressing Rhesus macaques. *Journal of Virology* **89**(16), 8484-96, 2015.
  60. S. C. Keane, X. Heng, K. Lu, S. Kharytonchyk, V. Ramakrishnan, G. Carter, S. Barton, A. Hosis, A. Florwick, J. Santos, N. Bolden, S. McCowin, D. A. Case, B. Johnson, **M. Salemi**, A. Telesnitsky, M. F. Summers. Structure of the HIV-1 RNA packaging signal. *Science* **348**(6237), 917-21, 2015.
  61. R. Durães-Carvalho, L. C. Caserta, A. C. S. Barnabé, M. C. Martini, P. V. M. Simas, M. M. B. Santos, **M. Salemi**, C. W. Arns. Phylogenetic and phylogeographic mapping of the avian coronavirus spike protein-encoding gene in wild and synanthropic birds. *Virus Research* **201**, 101-12, 2015.
  62. T. Azarian, A. Lo Presti, M. Giovanetti, E. Cella, B. Rife, A. Lai, G. Zehender, M. Ciccozzi, **M. Salemi**. Impact of spatial dispersion, evolution, and selection on Ebola Zaire Virus epidemic waves. *Scientific Reports* **5**, 10170, 2015.
  63. T. Azarian, R. L. Cook, J. A. Johnson, N. Guzman, Y. S. McCarter, N. Gomez, M. H. Rathore, J. G. Morris Jr., **M. Salemi**. Whole-genome sequencing for outbreak investigations of methicillin resistant *Staphylococcus aureus* in the neonatal intensive care unit: Time for routine practice? *Infection Control & Hospital Epidemiology* **36**(7), 777-85, 2015.
  64. B. T. Nowlin, T. H. Burdo, C. C. Midkiff, **M. Salemi**, X. Alvarez, K. C. Williams. SIVE lesions are comprised of CD163+ macrophages present in the CNS during early SIV infection and SIV+ macrophages recruited terminally with AIDS. *American Journal of Pathology* **185**(6), 1649-65, 2015.
  65. G. Cortés-Hinojosa, F. M. Gulland, T. Goldstein, S. Venn-Watson, R. Rivera, T. B. Waltzek, **M. Salemi**, J. F. Wellehan Jr. Phylogenomic characterization of California sea lion adenovirus-1. *Infection Genetics and Evolution* **31**, 270-6, 2015.
  66. B. D. Rife, **M. Salemi**. On the early dynamics and spread of HIV-1. *Trends in Microbiology* **23**(1), 3-4, 2015.
  67. **M. Salemi**, A-M. Vandamme. Bioinformatics tools for the investigation of viral evolution and molecular epidemiology. *Infection Genetics and Evolution* **28**, 349-50, 2014.
  68. T. Azarian, A. Ali, J. A. Johnson, D. Mohr, M. Prosperi, N. M. Veras, M. Jubair, S. Strickland, M. H. Rashid, M. T. Allam, T. A. Weppelmann, L. S. Katz, C. L. Tarr, R. R. Colwell, J. G. Morris Jr., **M. Salemi**. Phylodynamic analysis of clinical and environmental *Vibrio Cholerae* isolates from Haiti demonstrates population expansion and diversification driven by positive selection. *mBio* **5**(6), pii e01824-14, 2014.
  69. J. H. Campbell, E-M. Ratai, P. Autissier, D. J. Nolan, S. Tse, A. D. Miller, R. G. González, **M. Salemi**, T. H. Burdo, K. C. Williams. Anti- $\alpha 4$  antibody treatment blocks virus traffic to the brain and gut early, and stabilizes CNS injury late in infection. *PLoS Pathogens* **10**(12), e1004533, 2014.
  70. M. Rahman, M. Jubair, M. T. Alam, T. A. Weppelmann, T. Azarian, **M. Salemi**, I. A. Sakharuk, M. H. Rashid, J. A. Johnson, M. Yasmin, J. Glenn Morris Jr, A. Ali. High-frequency rugose exopolysaccharide production by *Vibrio cholerae* strains isolated in Haiti. *PLoS ONE* **9**(11), e112853, 2014.
  71. S. L. Strickland, B.D. Rife, S. L. Lamers, D. J. Nolan, N. M. Veras, M. C. F. Prosperi, T. H. Burdo, P. Autissier, B. Nowlin, M. M. Goodenow, M. A. Suchard, K. C. Williams, **M. Salemi**. Spatiotemporal Dynamics of SIV Brain Infection in CD8+ Lymphocyte-Depleted Rhesus Macaques with NeuroAIDS. *Journal of General Virology* **95**(Pt 12), 2784-95, 2014.
  72. G. Fogel, E. Liu, **M. Salemi**, S. L. Lamers, M. S. McGrath. Evolved Neural Networks for HIV-1 Co-receptor Identification. *IEEE Congress on Evolutionary Computation* 2778-84, doi: 10.1109/CEC.2014.6900628, 2014.
  73. M. M Norström, N. M. Veras, W. Huang, M. C. F. Prosperi, J. Cook, W. Hartogensis, F. M. Hecht, A. C. Karlsson, **M. Salemi**. Baseline CD4+ T cell counts correlates with HIV-1 synonymous rate in HLA-B\*5701 subjects with different risk of disease progression. *PLoS Computational Biology* **10**(9), e1003830, 2014.
  74. S. L. Lamers, G. B. Fogel, D. J. Nolan, M. S. McGrath, **M. Salemi**. HIV-Associated neuropathogenesis: a systems biology perspective for modeling and therapy. *BioSystems* **119C**, 53-61, 2014.
  75. P. A. Chan, M. B. Reitsma, A. DeLong, B. Boucek, A. Nunn, **M. Salemi**, R. Kantor. Phylogenetic and Geospatial Evaluation of HIV-1 Subtype Diversity at the Largest HIV Center in Rhode Island. *Infection Genetics and Evolution* **14**, S1567-1348, 2014.
  76. M. M. Norström, **M. Salemi**, F. M. Hecht, A. C. Karlsson. Functional avidity and IL-2/perforin production is linked

- to the emergence of mutations within HLA-B\*5701-restricted epitopes and HIV-1 disease progression. *Journal of Immunology* **192**(10), 4685-96, 2014.
77. C. C. Rollins, J. D. Levensgood, B. D. Rife, **M. Salemi**, B. S. Tolbert. Thermodynamic and phylogenetic insights into hnRNP A1 recognition of the HIV-1 exon splicing silencer 3 element. *Biochemistry* **53**(13), 2172-84, 2014.
  78. D. Hickman, M. K. Jones, S. Zhu, E. Kirkpatrick, D. A. Ostrov, X. Wang, M. Ukhanova, Y. Sun, V. Mai, **M. Salemi**, S. M. Karst. The Effect of Malnutrition on Norovirus Infection. *mBio* **5**(2), e01032-13, 2014.
  79. M. C. F. Prosperi, L. Yin, D. J. Nolan, A. D. Lowe, M. M. Goodenow **M. Salemi**. Empirical validation of viral quasispecies assembly algorithms: state-of-the-art and challenges. *Scientific Reports* **3**, 2837, doi: 10.1038/srep02837, 2013.
  80. S. L. Lamers, D. J. Nolan, S. L. Strickland, M. C. F. Prosperi, G. B. Fogel, M. M. Goodenow, **M. Salemi**. Longitudinal analysis of intra-host SIV recombination in varied tissues of the Rhesus macaque model for neuroAIDS. *Journal of General Virology* **94**(Pt 11), 2469-79, 2013.
  81. M. C. F. Prosperi, N. M. C. Veras, T. Azarian, M. Rathore, D. J. Nolan, K. Rand, R. L. Cook, J. A. Johnson, J. G. Morris Jr., **M. Salemi**. Molecular Epidemiology of Community-Associated Methicillin-resistant *Staphylococcus aureus* in the genomic era: a Cross-Sectional Study. *Scientific Reports* **3**, 1902, doi 10.1038/srep01902, 2013.
  82. W. Murillo, N. M. C. Veras, M. C. F. Prosperi, I. L. de Rivera, G. Paz-Bailey, S. Morales-Miranda, S. I. Juarez, C. Yang, J. Devos, J. P. Marín, M. Mild, J. Albert, **M. Salemi**. A single early introduction of HIV-1 subtype B into Central America accounts for most current cases. *Journal of Virology* **87**(13), 7463-70, 2013.
  83. M. Mild, R. R. Gray, A. Kvist, P. Lemey, M. M. Goodenow, E. M. Fenyö, J. Albert, **M. Salemi**, J. Esbjörnsson, P. Medstrand. High inpatient HIV-1 evolutionary rate is associated with CCR5-to-CXCR4 coreceptor switch. *Infection Genetics and Evolution* **13**, S1567-1348, 2013.
  84. **M. Salemi**. The intra-host evolutionary and population dynamics of human immunodeficiency virus type 1: a phylogenetic perspective. *Infectious Disease Reports* **5**, s1e3, 2013.
  85. J-H. Lin, S-C. Chiu, J-C. Cheng, H-W. Chang, Y-C. Lin, K-L. Hsiao, **M. Salemi** ‡, H-F. Liu. The Molecular Epidemiology and Evolutionary Dynamics of influenza A virus in Taiwan: a microcosm of flu pandemics. *PLoS ONE* **8**(4), e61957, 2013. ‡ Corresponding author
  86. L. Yin, L. Liu, Y. Sun, W. Hou, A. C. Lowe, B. P. Gardner, **M. Salemi**, W. G. Farmerie, J. W. Sleasman, M. M. Goodenow. High-resolution deep sequencing reveals biodiversity, population structure, and persistence of HIV-1 quasispecies within host ecosystems. *Retrovirology* **9**, 108, doi: 10.1186/1742-4690-9-108, 2013.
  87. A. J. Tatem, J. Hemelaar, R. R. Gray, **M. Salemi**. Spatial accessibility and the spread of HIV-1 subtypes and recombinants. *AIDS* **26** (18), 2351-60, 2013.
  88. M. Ciccozzi, G. Madeddu, A. Lo Presti, E. Cella, M. Giovanetti, C. Budroni, S. Babudieri, M. S. Mura, G. Zehender, **M. Salemi**. HIV type 1 origin and transmission dynamics among different risk groups in sardinia: molecular epidemiology within the close boundaries of an Italian island. *AIDS Research and Human Retroviruses* **29** (2), 404-10, 2013.
  89. S. L. Lamers, G. B. Fogel, E. J. Singer, **M. Salemi**, D. J. Nolan, L. C. Huysentruyt, M. S. McGrath. HIV-1 Nef in macrophage-mediated disease pathogenesis. *International Reviews of Immunology* **31** (6), 432-50, 2012.
  90. M. C. F. Prosperi, S. Meloni, I. Fanti, S. Panzeri, G. Ulivi, **M. Salemi**. Characterization of *de novo* assemblies of quasispecies from next-generation sequencing via complex network modeling. *Scientific Research and Essays* **7**(33), 2997-3009, 2012.
  91. M. M. Norström, M. Buggert, J. Tauriainen, W. Hartogensis, M. C. F. Prosperi, M. Wallet, F. M. Hecht, **M. Salemi** ‡, A. C. Karlsson. Combination of immune and viral factors distinguish low-risk versus high-risk HIV-1 disease progression in HLA-B\*5701 subjects. *Journal of Virology* **86**(18), 9802-16, 2012. ‡ Corresponding author.
  92. R. R. Gray, **M. Salemi**. Integrative molecular phylogeography in the context of infectious diseases on the human-animal interface. *Parasitology* **139** (14), 1939-51, 2012.
  93. R. R. Gray, S. L. Strickland, N. M. C. Veras, M. M. Goodenow, O. G. Pybus, S. M. Lemon, M. W. Fried, D. R. Nelson, **M. Salemi**. Unexpected Maintenance of Hepatitis C Viral Diversity Following Liver Transplantation. *Journal of Virology* **86**(16), 8432-9, 2012.
  94. M. M. Norström, M. C. F. Prosperi, R. R. Gray, A. C. Karlsson, **M. Salemi**. PhyloTempo: a set of R scripts for assessing and visualizing temporal clustering in genealogies inferred from serially sampled viral sequences. *Evolutionary Bioinformatics Online* **8**, 261-269, 2012.
  95. L. Prosperi, R. R. Gray, **M. Salemi**, M. C. F. Prosperi. On counting the frequency distribution of string motifs in molecular sequences. *International Journal of Biomathematics* **5**(6), 1250055 [19 pages], 2012.

96. M. M. Norström, A. C. Karlsson, **M. Salemi**. Toward a new paradigm linking virus molecular evolution and pathogenesis: experimental design and phylodynamic inference. *New Microbiologica* **35**(2), 101-111, 2012.
97. R. R. Gray, **M. Salemi**, P. Klenerman, O.G. Pybus. A new evolutionary model for hepatitis C virus chronic infection. *PLoS Pathogens* **8**(5), e1002656, 2012.
98. M. Akrim, S. Lemrabet, E. Elharti, R. R. Gray, J. C. Tardy, R. L. Cook, **M. Salemi**, P. Andre, T. Azarian, R. El Aouad. HIV-1 subtype distribution in Morocco based on national sentinel surveillance data 2004-2005. *AIDS Research and Therapy* **9**(1), 5, 2012.
99. S. Strickland, R. R. Gray, S. L. Lamers, T. H. Burdo, E. Huenink, D. J. Nolan, B. Nowlin, X. Alvarez, C. C. Midkiff, M. M. Goodenow, K. Williams, **M. Salemi**. Efficient transmission and persistence of low frequency SIVmac251 variants in CD8-depleted Rhesus macaques with different neuropathology. *Journal of General Virology* **93**(Pt 5), 925-38, 2012.
100. M. C. F. Prosperi, **M. Salemi**. QuRe: software for viral quasispecies reconstruction from next generation sequence data. *Bioinformatics* **28**(1), 132-3, 2011.
101. J-H. Lin, S-C. Chiu, J-C. Cheng, H-W. Chang, K-L. Hsiao, Y-C. Lin, H-S. Wu, **M. Salemi** ‡, H-F. Liu. Phylodynamics and molecular evolution of influenza A virus nucleoprotein genes in Taiwan between 1979 and 2009. *PLoS ONE* **6**(8), e23454, 2011. ‡ Corresponding author.
102. M. R. Khanani, M. Somani, S. S. Rehmani, N. M. C. Veras, **M. Salemi**, S. H. Ali. The Spread of HIV in Pakistan: bridging of the epidemic between populations. *PLoS ONE* **6**(7), e22449, 2011.
103. R. R. Gray, O. G. Pybus, **M. Salemi**. Measuring the temporal structure in serially-sampled phylogenies. *Methods in Ecology and Evolution* **2**, 437-455, 2011.
104. S. Strickland, R. R. Gray, S. L. Lamers, T. H. Burdo, E. Huenink, D. J. Nolan, B. Nowlin, X. Alvarez, C. C. Midkiff, M. M. Goodenow, K. Williams, **M. Salemi**. Significant genetic heterogeneity of the SIVmac251 viral swarm derived from different sources. *AIDS Research and Human Retroviruses* **27**, 1327-32, 2011.
105. N. M. C. Veras, M. M. Santoro, R. R. Gray, A. J. Tatem, A. Lo Presti, F. Olearo, G. Cappelli, V. Colizzi, D. Takou, J. Torimiro, G. Russo, A. Callegaro, R. Salpini, R. D'Arrigo, C. F. Perno, M. M. Goodenow, M. Ciccozzi, **M. Salemi**. Molecular epidemiology of HIV-1 CRF02\_AG in Cameroon and African patients living in Italy. *AIDS Research and Human Retroviruses* **27**, 1173-82, 2011.
106. N. M. C. Veras, R. R. Gray, L. F. de Macedo Brigido, R. Rodrigues, **M. Salemi**. High-resolution phylogenetics and phylogeography of HIV-1 subtype C epidemic in South America. *Journal of General Virology* **92**, 1698-709, 2011.
107. M. C. F. Prosperi, M. Ciccozzi, I. Fanti, F. Saladini, M. Pecorari, V. Borghi, S. Di Gianbenedetto, B. Bruzzone, A. Capetti, A. Vivarelli, S. Rusconi, M. C. Re, M. R. Gismondo, L. Sighinolfi, R. R. Gray, **M. Salemi**, M. Zazzi, A. De Luca on behalf of the ARCA collaborative group. A novel methodology for large-scale phylogeny partition: application to the Italian HIV-1 epidemic. *Nature Communications* **2**, 321, doi: 10.1038/ncomms1325, 2011.
108. R. R. Gray, J. Parker, P. Lemey, **M. Salemi**, A. Katzourakis, O. G. Pybus. The mode and tempo of hepatitis C virus evolution within and among hosts. *BMC Evolutionary Biology* **11**(1), 131, doi: 10.1186/1471-2148-11-131, 2011.
109. M. Ciccozzi, A. Ciccaglione, A. LoPresti, T. Yalcinkaya, M. Equestre, A. Costantino, R. Bruni, E. Ebranati, **M. Salemi**, R. R. Gray, G. Rezza, M. Galli, G. Zehender. Reconstruction of the evolutionary dynamics of the hepatitis C virus 1b epidemic in Turkey. *Infection Genetics and Evolution* **11**, 863-8, 2011.
110. R. R. Gray, A. J. Tatem, J. A. Johnson, A. V. Alexseyenko, O. G. Pybus, M. A. Suchard, **M. Salemi**. Testing spatiotemporal hypothesis of bacterial evolution using Methicillin-Resistant Staphylococcus aureus ST239 genome-wide data within a Bayesian framework. *Molecular Biology and Evolution* **28**(5), 1593-603, 2011.
111. A. Callegaro, V. Svirch, C. Alteri, A. Lo Presti, D. Valenti, A. Goglio, **M. Salemi**, E. Cella, C. F. Perno, M. Ciccozzi, F. Maggiolo. Epidemiological network analysis in HIV-1B infected patients diagnosed in Italy between 2000 and 2008. *Infection Genetics and Evolution* **11**(3), 624-3, 2011.
112. **M. Salemi**. Toward a robust monitoring of HIV-1 subtypes distribution worldwide. *AIDS* **25**(5), 713-714, 2011.
113. R. R. Gray, **M. Salemi**, A. Lowe, K. J. Nakamura, W. D Decker, M. Sinkala, C. Kankasa, C. J. Mulligan, D. Thea, L. Kuhn, G. Aldrovandi, Goodenow, MM. Multiple independent lineages of HIV-1 persist in breast milk and plasma. *AIDS* **25**(2), 143-52, 2011.
114. S. L. Lamers ‡. R. R. Gray ‡, **M. Salemi** ‡, L. Huysentruyt, M. S. McGrath. HIV-1 Phylogenetic analysis shows HIV-1 transits through the meninges to brain and peripheral tissues. ‡ Equally contributing authors. *Infection Genetics and Evolution* **11**(1), 31-37, 2011. [Epub ahead of print Nov 3, 2010]
115. M. C. F. Prosperi, A. De Luca, S. Di Giambenedetto, L. Bracciale, M. Fabbiani, R. Cauda, **M. Salemi**. The threshold bootstrap clustering: a new approach to find families or transmission clusters within molecular quasispecies. *PLoS ONE* **5**(10), e13619, 2010.

116. S. L. Lamers, **M. Salemi**, D.C. Galligan, A. Morris, R.R. Gray, G. B. Fogel, L. Zhao, M. S. McGrath. HIV-1 Evolutionary patterns associated with pathogenic processes in the brain. *Journal of Neurovirology* **16**(3), 230-41, 2010.
117. R. R. Gray, N. M. C. Veras, L. Santos, **M. Salemi**. Full genome molecular evolution of West Nile Virus. *Molecular Phylogenetics and Evolution* **56**, 195-200, 2010.
118. **M. Salemi**, S. L. Lamers, L. C. Huysentruyt, D. C. Galligan, R. G. Gray, A. Morris, M. S. McGrath. Distinct patterns of HIV-1 evolution within metastatic tissues in patients with non-Hodgkins lymphoma. *PLoS ONE* **4**(12), e8153, 2009.
119. R. R. Gray, A. J. Tatem, S. L. Lamers, W. Hou, O. Laeyendecker, D. Serwadda, N. Serwankambo, R. H. Gray, M. Wawer, T. C. Quinn, M. M. Goodenow, **M. Salemi**. Spatial phylogenetics of HIV-1 epidemic emergence in east Africa. *AIDS* **23**(14), F9-F17, 2009.
120. L. Zhao, D. C. Galligan, S. L. Lamers, S. Yu, L. Shagrún, **M. Salemi**, M. S. McGrath. High level HIV-1 DNA concentrations in brain tissues differentiate patients with post-HAART AIDS dementia complex or cardiovascular disease from those with AIDS. *Science China C Life Sciences* **52**, 651-6, 2009.
121. S. L. Lamers, **M. Salemi**, D. C. Galligan, T. de Oliveira, G. B. Fogel, S. C. Granier, L. Zhao, J. N. Brown, A. Morris, E. Masliah, M. S. McGrath. Extensive HIV-1 intra-host recombination is common in tissues with abnormal histopathology. *PLoS ONE* **4**(3), e5065, 2009.
122. W. M. Switzer, **M. Salemi**, S. H. Qari, H. Jia, R. R. Gray, A. Katzourakis, S. J. Marriott, K. N. Pryor, N. D. Wolfe, D. S. Burke, T. M. Folks, W. Heneine. Ancient, independent evolution and distinct molecular features of the novel human T-lymphotropic Virus type 4. *Retrovirology* **6**, 9, doi: 10.1186/1742-4690-6-9, 2009.
123. **M. Salemi**, R. R. Gray, M. M. Goodenow. An exploratory algorithm to investigate intra-host recombinant viral sequences. *Molecular Phylogenetics and Evolution* **49**, 618-628, 2008.
124. **M. Salemi**, M. M. Goodenow, S. Montieri, T. de Oliveira, M. M. Santoro, D. Beshkov, I. Alexiev, I. Elenkov, T. Yakimova, T. Varleva, G. Rezza, M. Ciccozzi. The HIV-1 epidemic in Bulgaria involves multiple subtypes and is sustained by continuous viral inflow from West and East European countries. *AIDS Research and Human Retroviruses* **24**, 771-779, 2008.
125. **M. Salemi**, T. de Oliveira, M. Ciccozzi, G. Rezza, M. M. Goodenow. High-resolution molecular epidemiology and evolutionary history of HIV-1 subtypes in Albania. *PLoS ONE* **3**(1), e1390, 2008.
126. S. L. Lamers, **M. Salemi**, M. S. McGrath, G. B. Fogel. Predicting HIV R5, X4 and Dual tropic phenotype using evolved neural network. *IEEE/ACM Transactions in Computational Biology and Bioinformatics* **5**, 291-300, 2008.
127. **M. Salemi**, B. Burkhardt, R. R. Gray, G. Ghaffari, J. W. Sleasman, M. M. Goodenow. Phylogenetics of HIV-1 in lymphoid and non-lymphoid tissues reveals a central role for the thymus in emergence of CXCR4-using quasispecies. *PLoS ONE* **2**(9), e950, 2007.
128. M. Ciccozzi, S. Montieri, **M. Salemi**, T. de Oliveira, M. Dorrucchi, A. Sinicco, A. De Luca, M. Giuliani, C. Balotta, G. Rezza. An outbreak of HIV-1 subtype G among Italian IDUs. *AIDS* **21**, 1213-1215, 2007.
129. T. de Oliveira, O. G. Pybus, A. Rambaut, **M. Salemi**, S. Cassol, M. Ciccozzi, G. Rezza, G. Castelli Gattinara, R. D'Arrigo, M. Amicosante, L. Perrin, V. Colizzi, C. F. Perno, Benghazi Study Group. Molecular Epidemiology: HIV-1 and HCV sequences from Libyan outbreak. *Nature* **444**, 836-837, 2006.
130. L. Campitelli, M. Ciccozzi, **M. Salemi**, F. Taglia, S. Boros, I. Donatelli, G. Rezza. H5N1 influenza virus evolution: a comparison of different epidemics in birds and humans. *Journal of General Virology* **87**, 955-960, 2006.
131. L. Cali, B. Wang, M. Mikhail, M. J. Gill, B. Beckthold, **M. Salemi**, D. A. Jans, S.C. Piller, N. K. Saksena. Evidence for host-driven selection of the HIV type 1 vpr gene in vivo during HIV disease progression in a transfusion-acquired cohort. *AIDS Research and Human Retroviruses* **8**, 728-233, 2005.
132. **M. Salemi**, S. L. Lamers, S. Yu, T. De Oliveira, W. M. Fitch, M. S. McGrath. Phylogenetic analysis of human immunodeficiency virus type 1 in distinct brain compartments provides a model for the neuropathogenesis of AIDS. *Journal of Virology* **79**, 11343-52, 2005.
133. W. M. Switzer, **M. Salemi**, V. Shanmugam, F. Gao, M. Cong, C. Kuiken, V. Bhullar, B. Beer, D. Vallet, A. Gautier-Hion, Z. Tooze, F. Villinger, E.C. Holmes, and W. Heneine. Ancient co-speciation of simian foamy viruses and primates. *Nature* **434**, 376-380, 2005.
134. **M. Salemi**, T. de Oliveira, M. A. Soares, O. G. Pybus, A. T. Dumans, A-M. Vandamme, A. Tanuri, S. Cassol, W. M. Fitch. Different epidemic potentials of HIV-1 B and C subtypes. *Journal of Molecular Evolution* **60**, 598-605, 2005.
135. S. Van Dooren, O. G. Pybus, **M. Salemi**, H-F. Liu, P. Goubau, C. Remondegui, A. Talarmin, E. Gotuzzo, L. C. J. Alcantara, B. Galvao-Castro, A-M. Vandamme. The low evolutionary rate of Human T-Cell Lymphotropic Virus

- type-1 confirmed by analysis of vertical transmission chains. *Molecular Biology and Evolution* **21**, 603-611, 2004.
- 136.T. De Oliveira, **M. Salemi**, M. Gordon, A-M. Vandamme, E. J. van Rensburg, S. Engelbrecht, A. Smith, S. Cassol. Mapping sites of positive selection and amino acid diversification in the HIV genome: an alternative approach to vaccine design? *Genetics* **167**, 1047-58, 2004.
- 137.**M. Salemi**, W. M. Fitch, M. Ciccozzi, M. J. Ruiz-Alvarez, G. Rezza, M. J. Lewis. SARS-CoV sequence characteristics and evolutionary rate estimate from maximum likelihood analysis. *Journal of Virology* **78**, 1602-03, 2004.
- 138.S.L. Lamers, S. Beason, R. Compton, L. Dunlap, **M. Salemi**. HIVbase: a PC/Windows-based software offering storage and querying power for locally held HIV-1 genetic, experimental, and clinical data. *Bioinformatics* **20**, 436-38, 2004.
- 139.P. Lemey, **M. Salemi**, B. Wang, M. Duffy, W.W. Hall, N. Saksena, A-M. Vandamme. Site stripping based on likelihood ratio reduction is a useful tool to evaluate the impact of non-clock-like behavior on viral phylogenetic reconstructions. *FEMS Immunology Medicine and Microbiology* **39**, 125-32, 2003.
- 140.D. Paraskevis, P. Lemey, **M. Salemi**, M. Suchard, Y. Van der Peer, A-M. Vandamme. Analysis of the evolutionary relationships of HIV-1 and SIVcpz sequences using Bayesian inference: implications for the origin of HIV-1. *Molecular Biology and Evolution* **20**, 1986-96, 2003.
- 141.L. C. Alcantara, N. Shindo, S. Van Dooren, **M. Salemi**, M. C. Costa, S. Kashima, D. T. Covas, A-M. Vandamme, B. Galvao-Castro. Brazilian HTLV type 2a strains from intravenous drug users (IDUs) appear to have originated from two sources: Brazilian Amerindians and European/North American IDUs. *AIDS Research and Human Retroviruses* **6**, 519-23, 2003.
- 142.**M. Salemi**, T. De Oliveira, V. Courgnaud, V. Moulton, B. Holland, S. Cassol, W. M. Switzer, A-M. Vandamme. Mosaic genomes of the six major Primate lentivirus lineages revealed by phylogenetic analyses. *Journal of Virology* **77**, 7202-7213, 2003.
- 143.K. E. Robbins, P. Lemey, O. G. Pybus, H. W. Jaffe, A. M. Saekhou, T. M. Brown, **M. Salemi**, A-M. Vandamme, M. L. Kalish. Characterization of Early U.S. HIV-1 Strains, Dating of the introduction of HIV-1 into the U.S. and estimation of population history of the U.S. epidemic. *Journal of Virology* **77**, 6359-6366, 2003.
- 144.P. Lemey, O. G. Pybus, B. Wang, N. K. Saksena, **M. Salemi**, A-M. Vandamme. Tracing the origin and history of HIV-2 epidemics. *Proceedings of the National Academy of Sciences USA* **100**, 6588-6592, 2003.
- 145.X. Xia, Z. Xie, **M. Salemi**, L. Chen, Y. Wang. An index of substitution saturation and its application. *Molecular Phylogenetics and Evolution* **26**, 1-7, 2003.
- 146.M. Duffy, **M. Salemi**, N. Sheehy, A-M. Vandamme, J. Hegarty, M. Curry, N. Nolan, D. Kelleher, S. McKiernan, W.W. Hall. Comparative rates of nucleotide sequence variation in the hypervariable region of E1/E2 and the NS5b region of hepatitis C virus in patients with a spectrum of liver disease resulting from a Common Source of Infection. *Virology* **301**, 354-364, 2002.
- 147.V. Courgnaud, **M. Salemi**, X. Pourrut, E. Mpoudi-Ngole, B. Abela, P. Auzel, F. Bibollet-Ruche, B. Hahn, A-M. Vandamme, E. Delaporte, M. Peeters. Characterization of a novel simian immunodeficiency virus with a vpu gene from greater spot-nosed monkeys (*Cercopithecus nictitans*) provides new insights into simian/human immunodeficiency virus phylogeny. *Journal of Virology* **76**, 8298-309, 2002.
- 148.M. J. Lewis, N. Sheehy, **M. Salemi**, A-M. Vandamme, W. W. Hall. Comparison of CREB- and NF-kappaB-mediated transactivation by human T lymphotropic virus type II (HTLV-II) and type I (HTLV-I) tax proteins. *Virology* **295**, 182-189, 2002.
- 149.P. Lemey, **M. Salemi**, L. Bassit, H. Heuverswyn, A-M. Vandamme. Phylogenetic classification of TT virus groups based on the N22 region is unreliable. *Virus Research* **85**, 47-59, 2002.
- 150.N. Shindo, L. C. J. Alcantara, S. Van Dooren, **M. Salemi**, M. C. R. Costa, S. Kashima, D. T. Covas, A. Teva, M. Pellegrini, I. Brito, A-M. Vandamme, B. Galvao-Castro. Human retroviruses (HIV and HTLV) in Brazilian Indians: seroepidemiological study and molecular epidemiology of HTLV type 2 isolates. *AIDS Research and Human Retroviruses* **18**, 71-77, 2002.
- 151.**M. Salemi**, A-M. Vandamme. Evolutionary patterns of hepatitis C virus studied through analysis of full genome sequences. *Journal of Molecular Evolution* **54**, 62-70, 2002.
- 152.S. Van Dooren, **M. Salemi**, X. Pourrut, M. Peeters, M. van Ranst, E. Delaporte, A-M. Vandamme. Evidence for a second simian T-cell lymphotropic virus type 3 in *Cercopithecus nictitans* from Cameroon. *Journal of Virology* **75**, 11939-11941, 2001.
- 153.S. Van Dooren, **M. Salemi**, A-M. Vandamme. Dating the origin of the African human T-cell lymphotropic virus type I (HTLV-I) subtypes. *Molecular Biology and Evolution* **18**, 661-71, 2001.

154. **M. Salemi**, K. Strimmer, W. W. Hall, M. Duffy, E. Delaporte, S. Mboup, M. Peeters, A-M. Vandamme. Dating the common ancestor of SIVcpz and HIV-1 group M and the origin of HIV-1 subtypes using a new method to uncover clock-like molecular evolution. *FASEB Journal* **15**, 267-268, 2001.
155. **M. Salemi**. Controversy on the origin of HIV. *AIDS Reviews* **2**, 119-120, 2000.
156. A-M. Vandamme, U. Bertazzoni, **M. Salemi**. Evolutionary strategies of human T-cell lymphotropic virus type II (HTLV-II). *Gene* **261**, 171-180, 2000.
157. M. J. Lewis, P. Novoa, R. Ishak, M. Ishak, **M. Salemi**, A-M. Vandamme, M. K. Kaplan, W. W. Hall. Isolation, cloning, and complete nucleotide sequence of a phenotypically distinct Brazilian isolate of human T-cell lymphotropic virus type 2 (HTLV-2) isolate. *Virology* **271**, 142-154, 2000.
158. J-P. Allain, Y. Dong, A-M. Vandamme, V. Moulton, **M. Salemi**. Evolutionary rate and genetic drift of hepatitis C virus are poorly correlated with the host immune response: studies of infected donor-recipient clusters. *Journal of Virology* **6**, 2541-2549, 2000.
159. **M. Salemi**, J. Desmyter, A-M. Vandamme. Tempo and mode of human and simian T-lymphotropic virus (HTLV/STLV) evolution revealed by analyses of full-genome sequences. *Molecular Biology and Evolution* **3**, 374-386, 2000.
160. A-M. Vandamme, W. W. Hall, M. J. Lewis, P. Goubau, **M. Salemi**. Origin of HTLV-I in South America. *Nature Medicine* **3**, 232-233, 2000.
161. **M. Salemi**, S. Van Dooren, A-M. Vandamme. Origin of human and simian T-cell lymphotropic viruses. *AIDS Reviews* **3**, 131-139, 1999.
162. **M. Salemi**, M. J. Lewis, J. F. Egan, W. W. Hall, J. Desmyter, A-M. Vandamme. Different population dynamics and evolutionary rates of human T-cell lymphotropic virus type II (HTLV-II) in injecting drug users compared to in endemically infected Amerindian and Pygmy tribes. *Proceedings of the National Academy of Sciences USA* **96**, 13253-13259, 1999.
163. **M. Salemi**, A-M. Vandamme, J. Desmyter, C. Casoli, U. Bertazzoni. The origin and evolution of human T-cell lymphotropic virus type II (HTLV-II) and the relationship with its replication strategy. *Gene* **234**, 11-21, 1999.
164. M. Van Brussel, **M. Salemi**, H-F Liu, P. Goubau, J. Desmyter, A-M. Vandamme. The discovery of two new divergent STLVs has implications for the evolution and epidemiology of HTLVs. *Reviews in Medical Virology* **9**, 155-170, 1999.
165. S. Van Dooren, E. Gotuzzo, **M. Salemi**, D. Watts, E. Audenaert, S. Duwe, H. Ellerbrok, R. Grassmann, J. Desmyter, A-M. Vandamme. Evidence for a Post-Colombian introduction of human T-cell lymphotropic virus in Latin America. *Journal of General Virology* **79**, 2695-2708, 1998.
166. A-M. Vandamme, **M. Salemi**, J. Desmyter. The simian origins of the pathogenic human T-cell lymphotropic virus type I. *Trends in Microbiology* **6**, 477-483, 1998.
167. H. Ellerbrok, C. Fleischer, **M. Salemi**, P. Reinhardt, W-D. Ludwig, A-M. Vandamme, G. Pauli. Sequence analysis of the first HTLV-I infection in Germany without relations to endemic areas. *AIDS Research and Human Retroviruses* **14**, 1199-1203, 1998.
168. A-M. Vandamme, **M. Salemi**, M. Van Brussel, H-F. Liu, K. Van Laethem, M. Van Ranst, L. Michels, J. Desmyter, P. Goubau. African origin of human T-lymphotropic virus type II (HTLV-II) supported by a new subtype HTLV-IIid in Zairean Bambuti Efe pygmies. *Journal of Virology* **72**, 4327-4340, 1998.
169. M. Van Brussel, **M. Salemi**, H-F Liu, P. Goubau, J. Desmyter, A-M. Vandamme. The Simian T-lymphotropic virus STLV-PP1664 from *Pan paniscus* is distinctly related to HTLV-2 but differs in genomic organization. *Virology* **243**, 366-379, 1998.
170. **M. Salemi**, S. Van Dooren, E. Audenaert, E. Delaporte, P. Goubau, J. Desmyter, A-M. Vandamme. Two new human T-lymphotropic virus type I subtypes in seroindeterminates, a Mbuti pygmy and a Gabonese, have closest relatives among African STLV-I strains. *Virology* **246**, 277-287, 1998.
171. **M. Salemi**, A-M. Vandamme, C. Gradozzi, K. Van Laethem, P. Ferrante, G. Taylor, C. Casoli, P. Goubau, J. Desmyter, U. Bertazzoni. Evolutionary rate and genetic heterogeneity of human T-cell lymphotropic virus type II (HTLV-II) using new isolates from European injecting drug users. *Journal of Molecular Evolution* **46**, 602-611, 1998.
172. **M. Salemi**, A-M. Vandamme, F. Guano, E. Cattaneo, C. Casoli, U. Bertazzoni. Complete nucleotide sequence of the Italian human T-cell lymphotropic virus type II (HTLV-II) isolate Gu and phylogenetic identification of a possible origin of South European epidemics. *Journal of General Virology* **77**, 1193-1201, 1996
173. **M. Salemi**, E. Cattaneo, C. Casoli, U. Bertazzoni. Identification of IIa and IIb molecular subtypes of human T-cell lymphotropic virus type II among Italian injecting drug users. *Journal of Acquired Immune Deficiency Syndrome* **8**,

516-520, 1995.

174. D. Zella, A. Cavicchini, **M. Salemi**, C. Casoli, P. Ferrante, F. Lori, G. Achill, E. Cattaneo, V. Landini, U. Bertazzoni. Molecular characterization of two isolates of human T-cell leukemia virus type II from Italian drug abusers and comparison of genome structure with other isolates. *Journal of General Virology* **74**, 437-444, 1993.

## RESEARCH SUPPORT

### CURRENT:

- **2019 UF Research Opportunity Fund – Single-cell sequencing of the citrus Huanglongbing pathogen, *Candidatus Liberibacter asiaticus*, to advance understanding of pathogen biology.**  
Role: co-Principal Investigator (Goss, PI)  
Dates 07/01/19 – 06/31/21  
Budget: \$ 85,000
- **UF Moonshot Award – Confronting the Threat of Emerging Pathogens and Eliminating Hospital-Acquired Drug Resistant Infections.**  
Role: co-Investigator (Morris, Lauzardo, MPIS)  
Dates 01/01/19 – 12/31/19  
Budget: \$ 265,332
- **UF Moonshot Award – Advanced Data Capabilities: Integrating Precision Public Health and Precision Medicine.**  
Role: co-Investigator (Hogan, Shenkman, MPIS)  
Dates 01/01/19 – 12/31/19  
Budget: \$ 501,150.
- **NIH R01 – Cholera persistence, transmission, and evolution in Goma, DRC.**  
Role: co-Investigator (Morris, PI)  
Dates 04/01/19 – 31/03/24  
Budget: \$ 3,767,458
- **NIH R01 NS063897-01A7 – Viral evolution in peripheral macrophages and brain during progression to AIDS.**  
Role: Principal Investigator  
Dates 09/22/17 – 06/30/22 (competitive renewal)  
Budget: \$ 3,794,832
- **NIH R21 AI138815 – HIV Dynamic Modelling for Identification of Transmission Epicenters (HIV-DYNAMITE)**  
Role: Principal Investigator (Salemi, Prosperi, MPIS)  
Dates 04/01/18 – 03/31/20  
Budget: \$419,375.
- **NIH R01 sub award – Monocyte Traffic and Neuropathogenesis of AIDS**  
Budget: \$141,868  
Role: co-Investigator (Williams, PI)  
Dates: 04/01/18 – 03/31/21
- **NIH R01 AI128750-01 – Cholera persistence, transmission and clinical illness in Haiti**  
Role: Co-Investigator (Morris, PI)  
Dates: 1/1/17 – 12/31/21  
Budget: \$490,000
- **NIH R01 AI126357-01 – Cholera transmission and evolution in Port-au-Prince, Haiti**  
Role: Co-Investigator (Morris, PI)  
Dates: 7/1/16 – 6/30/21  
Budget: \$494,290
- **NIH R01AI123657-01S1 – Transmission of Zika and other arboviruses in Haiti**  
Role: Co-investigator (Morris, PI)  
Dates 7/01/16 – 6/30/20

Budget: \$1,758,905

- **NIH R01 AI116770-01 – Regression, Phylogenetics, and Study Design in Infectious Disease Epidemiology**  
Role: Co-Investigator (Yang, PI)  
Dates: 01/01/16 – 12/31/20  
Budget: \$500,600

**PREVIOUS:**

- **UF Opportunity Funds – DeepPhylo: integrating Deep Learning and Bayesian Phylogenetic Inference to optimize and improve phylodynamic analyses using Zika Virus Epidemic data.**  
Role: Principal Investigator  
Dates: 08/15/17-08/15/18  
Budget: \$44,000
- **NIH P50 GM103297-01 – The Center for HIV RNA Studies (CRNA)**  
Role: Principal Investigator of Bioinformatics Core  
Dates 9/17/12 - 08/31/17  
Budget: \$823,808
- **NIH F31 AI126357-01 – Intra-host phylogeography and population dynamics of SIV in the rhesus macaque model of neuroAIDS**  
Role: Mentor/Principal Investigator  
Dates: 7/1/16 – 6/30/17  
Budget: \$75,530
- **NIH RO1MH100984 Molecular Features and Approach to the HIV CNS Reservoir Post cART**  
Role: Co-Principal Investigator  
Dates: 04/01/13-08/31/17  
Budget: \$555,957
- **US Department of Homeland Security. Mapping and modeling Bacillus anthracis and Clostridium botulinum across North Africa and the Middle East with high-resolution genetic sequencing and spatial analysis.**  
Role: Co-Investigator  
Dates: 6/1/16 – 5/31/17  
Budget: \$44,272
- **Florida Department of Health (FL DOH) – Whole Genome Sequencing of Neisseria meningitidis serogroup W135 Isolates Belonging to a Clone Emerging in Florida.**  
Role: Principal Investigator  
Dates 09/01/2014 - 08/31/16  
Budget: \$102,000
- **NIH R01 sub award – Monocyte Traffic and Neuropathogenesis of AIDS**  
Role: Investigator  
Dates 10/01/15 to 6/30/2016
- **NIH R01 AI097405 – Cholera transmission in Gressier region, Haiti.**  
Role: Co- Principal Investigator  
Dates 12/1/11-11/30/15
- **NIH R01AI097405-03– Cholera transmission in Gressier Region, Haiti - Supplement**  
Role: Principal Investigator of supplement  
Dates: 08/01/14 - 11/30/15
- **NIH R01 NS063897-01A2 - Viral evolution in peripheral macrophages and brain during progression to AIDS.**  
Role: Principal Investigator  
Dates 02/15/09 – 01/31/15
- **NIH R01 NS053359 – HIV-1 specific immune responses in Thai individuals with HIV dementia.**  
Role: Principal Investigator of UF subcontract  
Dates 08/11/10- 07/31/13
- **2011 UF Clinical and Translational Science Institute (CTSI) Pilot Award—Solving the puzzle of quasispecies reconstruction using next-generation sequencing technologies.**  
Role: Principle Investigator (no salary for faculty)



Dates: 05/01/11-09/30/12

- **2010 UF Research Opportunity Fund - Development of a phylogeographic framework to investigate the origin and spread of cholera pandemics.**  
Role: Co-Principal Investigator (no salary for faculty)  
Dates: 05/10-04/12.
- **EPI seed funding—Preliminary study on the phylogeography of hospital acquired methicillin-resistant staphylococcus aureus (HA-MRSA) in different North Florida hospitals using genome-wide data.**  
Role: Principal Investigator (no salary for faculty)  
Dates: 12/01/10-05/31/11
- **NIH R01 AI065265 - Role of HIV-1 *env* diversity in cellular tropism.**  
Role: Co-Investigator  
Dates: 02/15/06- 01/31/11
- **NIH Contract Award # 00075848 - Analysis of HIV sequence data.**  
Role: Principal Investigator  
Dates: 06/29/07- 04/30/10
- **FLORIDA CFAR seed grant - Molecular epidemiology and anthropological determinants of HIV-1 emerging epidemic in Southern Morocco.**  
Role: Principal Investigator  
Dates: 12/08-05/10.
- **UF Experimental Pathology Innovative Grant (EPIG) Award - Landscape Phylodynamics: a New Framework To Study Epidemics Of Emerging Pathogens.**  
Role: Principal Investigator  
Dates: 09/08-05/09.