

Marco Salemi, Ph.D.

Citizenship: Italy, USA

Primary Languages: Italian, English, Spanish and Portuguese (intermediate), 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.

(a) Professional Preparation

Catholic University of Leuven, Leuven BE: Ph.D. in molecular evolution (1996-1999)

University of Pavia, Pavia, IT: Specialty in Biotechnology (1993-1995)

University of Pavia, Pavia, IT: MS in Chemistry (1986-1991)

(b) Appointments

Holloway and McClamma Endowed Chair in Chronic and Infectious Diseases Department of Pathology Immunology and Laboratory Medicine. University of Florida (UF), Gainesville, FL, USA (2019-current).

Full Professor with Tenure. Department of Pathology Immunology and Laboratory Medicine. UF, Gainesville, FL, USA (2017-current).

Associate Professor with Tenure. Department of Pathology Immunology and Laboratory Medicine. UF, Gainesville, FL, USA (2015-2017).

Associate Professor. Department of Pathology Immunology and Laboratory Medicine. UF, Gainesville, FL, USA (2013-2014).

Assistant Professor. Department of Pathology Immunology and Laboratory Medicine. UF, Gainesville, FL, USA (2010-2012).

Research Assistant Professor. Department of Pathology, UF, Gainesville, FL, USA (2004-2009).

Catholic University of Leuven, Leuven, BE: Postdoctoral Scientist in Evolutionary Genetics (1999-2002)

University of California Irvine (UCI), Irvine, CA, USA: Postdoctoral Associate in Evolutionary Genetics (2002-2004)

(c) Research Activities

My research interests include molecular epidemiology, intra-host viral evolution, and the application of phylogenetic and population genetic methods to the study of human and simian pathogenic viruses (HIV/SIV, HCV, HTLV and influenza). I have also been applying the Bayesian coalescent framework to study molecular evolution and phylogeography of emergent and re-emergent bacterial pathogens, such as *MRSA*, and *Vibrio cholerae*, using genome-wide SNPs. More recently, as Holloway and McClamma chair in chronic and infectious diseases, my laboratory has been developing *ad hoc* protocols for the generation of high-throughput full genome sequence data of viral and bacterial pathogens, as well as automated bioinformatic pipelines and machine learning algorithms for the analysis of “big” omic data (genomic, transcriptomic and proteomics). My scientific production covers multiple areas of research in molecular evolution, phylogenetic analysis of pathogens, development of algorithms to investigate big “omic” data, and computational methods for molecular biology. My publication record (170+ peer reviewed articles) has overall been cited 8000 times (Google Scholar) in other peer-reviewed papers with an h-index of 44, and an i10-index of 130. I am *editor* of two of the main textbooks in applied phylogenetic inference (Salemi, Vandamme, The Phylogenetic Handbook – A Practical Approach to DNA and Protein

Phylogeny, Cambridge University Press, New York, 2003; Lemey, Salemi, Vandamme, The Phylogenetic Handbook – A Practical Approach to Phylogenetic analysis and hypothesis testing).

(d) Grants and Awards

My research has continuously been funded by extramural awards (for a total to date of ~\$20M). I am member of the American Association for the Advancement of Science (AAAS) and of several NIH *ad hoc* study sections for grant reviews. I am Associate Editor of *PLoS ONE*, member of the Editorial Board of *Retrovirology* and Nature's *Scientific Reports*, and reviewer for *Nature*, *Science* and *PNAS*. I was awarded as UF Distinguish International Educator in 2004. In 2008, I received the *Honor Aedificanti* Award for my efforts in AIDS research by the Kiwanis (Rotary) International Association. I received the UF Excellence Awards in 2012 and the Term Professorship Award in 2017.

(e) Selected Publication (out of 170 peer reviewed articles)

1. Wilkinson E, Junqueira DM, Lessells R, Engelbrecht S, van Zyl G, de Oliveira T, **Salemi M**. 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.
2. Rife Magalis B, Nolan D, Autissier P, Burdo T, Williams K, **Salemi M**. 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.
3. Rife B, Nolan D, Lamers S, Autissier P, Burdo T, Williams K, **Salemi M**. 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.
4. Keane SC, Heng X, Lu K, Kharytonchyk S, Ramakrishnan V, Carter G, Barton S, Hosic A, Florwick A, Santos J, Bolden NC, McCowin S, Case DA, Johnson BA, **Salemi M**, Telesnitsky A, Summers MF. RNA structure. Structure of the HIV-1 RNA packaging signal. *Science* **348**(6237):917-21. doi: 10.1126/science.aaa9266. PMID: 25999508; PMCID: PMC4492308, 2015.
5. Azarian T, Ali A, Johnson JA, Mohr D, Prospero M, Veras NM, Jubair M, Strickland S, Rashid MH, Allam MT, Weppelmann TA, Katz LS, Tarr CL, Colwell RRMorris Jr. JG, Salemi M. 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.
6. Prospero M, Ciccozzi M, Fanti I, Saladini F, Pecorari M, Borghi V, Di Giambenedetto S, Bruzzone B, Capetti A, Vivarelli A, Rusconi S, Re MC, Gismondo MR, Sighinolfi L, Gray RR, **Salemi M**, Zazzi M, De Luca A; ARCA collaborative group. A novel methodology for large-scale phylogeny partition. *Nature Communications* **2**, 321, 2011.
7. de Oliveira T, Pybus OG, Rambaut A, **Salemi M**, Cassol S, Ciccozzi M, Rezza G, Gattinara GC, D'Arrigo R, Amicosante M, Perrin L, Colizzi V, Perno CF; Benghazi Study Group. Molecular epidemiology: HIV-1 and HCV sequences from Libyan outbreak. *Nature* **444**(7121):836-7. PMID: 17171825, 2006
8. Switzer WM, **Salemi M**, Shanmugam V, Gao F, Cong ME, Kuiken C, Bhullar V, Beer BE, Vallet D, Gautier-Hion A, Tooze Z, Villinger F, Holmes EC, Heneine W. Ancient co-speciation of simian foamy viruses and primates. *Nature* **434**(7031):376-80. PMID: 15772660, 2005.
9. Vandamme AM, Hall WW, Lewis MJ, Goubau P, **Salemi M**. Origin of HTLV-I in South America. *Nature Medicine* **3**, 232-233, 2000.
10. **Salemi M**, Lewis MJ, Egan JF, Hall WW, Desmyter J, Vandamme AM. 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.