

CURRICULUM VITAE

PERSONAL DATA

Name: Philippe Lemey
Date of birth: 10 august, 1977 (Kortrijk, Belgium)
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EDUCATION

1989 – 1995: Secondary school: ASO Wet B, St-Jozefsinstituut, Kortrijk, Belgium.
Laureate in “Science-Mathematics” 1995.

1995 – 2000: Master in Pharmaceutical sciences, biopharmacy specialization, Faculty of Pharmaceutical Sciences, Katholieke Universiteit Leuven.
Magna Cum Laude.

Thesis: Association between Mannan Binding Lectin gene polymorphisms and Inflammatory Bowel Disease. Promoter: Prof. Dr. Marc Van Ranst, Laboratory for Clinical and Epidemiological Virology, Rega Institute, Katholieke Universiteit Leuven.

2001-2003: Master in Science of Bioinformatics, Faculty of Agricultural and Applied Biological Sciences, Katholieke Universiteit Leuven.
Magna Cum Laude.

Thesis: Bayesian co-estimation of divergence times and population parameters for HIV-1 group O. Promoter: Prof. Dr. Marc Van Ranst, Laboratory for Clinical and Epidemiological Virology, Rega Institute, Katholieke Universiteit Leuven.

2000 – 2005: PhD in Medical Sciences, Faculty of Medicine, Rega Institute, Laboratory for Clinical and Epidemiological Virology, Katholieke Universiteit Leuven.

PhD thesis: Molecular investigation of evolutionary and population genetic processes in human retroviruses. Promoter: Prof. Dr. Anne-Mieke Vandamme. Co-promotor: Prof. Dr. Marc Van Ranst.

RESEARCH POSITIONS

- 11/2007-present: Postdoctoral research assistant, Laboratory for Clinical and Epidemiological Virology, Department of Microbiology and Immunology, Katholieke Universiteit Leuven, Belgium.
- 6/2005-10/2007: Postdoctoral research assistant, Department of Zoology, University of Oxford, Oxford, United Kingdom.
- 10/2004-5/2005: Postdoctoral research assistant, Laboratory for Clinical and Epidemiological Virology, Department of Microbiology and Immunology, Katholieke Universiteit Leuven, Belgium. Funded by the Rega Foundation.
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FELLOWSHIPS, GRANTS and FUNDING

- FWO postdoctoral research mandate (November 2007 – present).
 - High-throughput sequencing experiment grant (2009), Genomics Core, Biomedical Sciences, K.U. Leuven
 - CREA project: “*A population genomic perspective on persistent viral infections*” (October 2008 - present)
 - Bill and Melinda Gates' Foundation Education Scholarship for attending the meeting on Molecular Evolution as a Driving Force in Infectious Diseases, Apr 8-13, 2008.
 - Marie Curie Intra European Fellowship (January – October 2007).
 - Fellow of the Phylogenetics programme, Isaac Newton Institute for Mathematical Sciences. Cambridge, UK (September - December 2007).
 - European Molecular Biology Organization (EMBO) long-term fellowship (2005-2006).
 - Royal Society Conference Grant (2006/R1) for attending the Genomes, Evolution, & Bioinformatics (GEB2006) conference, Tempe, Arizona, U.S.A, May 24-28, 2006.
 - Royal Society Research Grant (2006/R2). Population genomic analysis of viral diversity in an HIV transmission pair.
 - FWO Travel Grant (2004, C 17/5 – CVW. D5) for the 7th International meeting on molecular epidemiology and evolutionary genetics of infectious diseases. Valencia, July, 2004.
 - PhD Fellowship from the Flemish Institute for Promotion and Innovation through Science and Technology in Flanders (IWT-Vlaanderen) (2000-2004).
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TEACHING EXPERIENCE

- 9/2001: Assistant teacher at the 7th European Workshop on Virus Evolution and Molecular Epidemiology, Rega Institute, Catholic University Leuven, Belgium.
- 3/2002: Teacher at the First Brazilian Workshop on Virus Evolution and Molecular Epidemiology, Centro de Pesquisas Goncalo Moniz, Fundacao Oswaldo Cruz, Salvador Bahia, Brasil.
- 7/2002: Teacher at the First African Workshop on Virus Evolution and Molecular Epidemiology. Durban, South Africa.
- 9/2002: Teacher at the 8th European Workshop on Virus Evolution and Molecular Epidemiology, Rega Institute, Katholieke Universiteit Leuven, Belgium.
- 8/2003: Teacher at the 9th International Workshop on Virus Evolution and Molecular Epidemiology, Wallenberg Hall, Stanford University, Stanford, California, USA.
- 9/2004: Teacher at the 10th International Workshop on Virus Evolution and Molecular Epidemiology, The Finnish National Public Health Institute, Helsinki, Finland.
- 11/2004: Teacher at the 2nd Brazilian Workshop on Virus Evolution and Molecular Epidemiology, Centro de Pesquisas Goncalo Moniz, Fundacao Oswaldo Cruz, Salvador Bahia, Brasil.
- 9/2005: Teacher at the 11th International Workshop on Virus Evolution and Molecular Epidemiology, Petropolis, Brasil.
- 10-11/10/2005: Teacher at the "Highlights in Virus Evolution" Workshop, Rome, Italy.
- 2/3/2006: Teacher in the "genetics of vectors and pathogens study unit" at the London School for Hygiene and Tropical Medicine. "Molecular Epidemiology of Viruses".
- 6/2006: Teacher at the Marie Curie Gene Time workshop on ancient DNA. Oxford, UK.
- 9/2006: Teacher at the 12th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology, Athens, Greece.
- 1/3/2007: Teacher in the "genetics of vectors and pathogens study unit" at the London School for Hygiene and Tropical Medicine. "Molecular Epidemiology of Viruses".
- 9/2007: Teacher at the 13th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology, Lisbon, Portugal.
- 16/1/2008: Teacher at the Hotspot Workshop on Phylogenetic Reconstruction, University of Lausanne, Lausanne, Switzerland
- 28/2/2008: Teacher in the "genetics of vectors and pathogens study unit" at the London School for Hygiene and Tropical Medicine. "Molecular Epidemiology of Viruses".
- 6/2008: Teacher at the Bayesian Evolutionary Analysis Sampling Trees Workshop, University of Algarve, Faro, Portugal.

- 9/2008: Teacher and Advanced Module organizer at the 14th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology, University of The Western Cape, Cape Town, South Africa.
- 5/3/2009: Teacher in the “Research Progress and Applications Unit” at the London School for Hygiene and Tropical Medicine. “Molecular Epidemiology of Viruses”.
- 6-7/2009: Invited teacher at the Summer Institute in Statistics and Modeling of Infectious Diseases, University of Washington, Seattle, U.S.A.
- 9/2009: Teacher and Advanced Module organizer at the 15th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology, Erasmus Medical Center, Rotterdam, The Netherlands.
- 6/2010: Invited teacher at the second Summer Institute in Statistics and Modeling of Infectious Diseases, University of Washington, Seattle, U.S.A.
- 2008-present: Teaching assistant for B-KUL-I0D53A Bio-informatics: Evolutionary and Quantitative Genetics, and B-KUL-E02N3A Bioinformatics and Systems Biology: Sequence, Structure & Evolution, KU Leuven.

Training and advising researcher for undergraduate students:

- 2001-2002: Darek Krzywania, "Licentie Informatica". "Datamining in HIV-onderzoek".
- 2001-2002: Anneleen Vanassche, "Licentie Informatica". "Datamining in HIV-onderzoek".
- 2002-2003: Stephanie Dumont, “Industrieel Ingenieur”, De Naeyer Instituut, St. Kathelijne Waver, Belgium. “Reconstructie van een HIV-1 transmissieketen met behulp van moleculair biologische technieken”.
- 2003-2004: Steve Vermeulen, “Licentie biomedische wetenschappen”. “Karakterisatie van een HIV-1 transmissieketen aan de hand van genetische informatie”.
- 2006-2007: Ailsa McLean, M. Sc. Project on “Investigating the rate of RNA virus evolution”. University of Oxford, U.K.
- 2009: Nuno Miguel Faria, Medical Biology M. Sc. Project on “Spatio-temporal history of HIV-2 revealed by Bayesian phylogeography”. University of Amsterdam, The Netherlands.

Tutorials for PhD students

- 2005-2006: Peter Burlinson (New College) and Ioannis Hodges-Mameletzis (St. Peter's College). Tutorial in phylogenetics. University of Oxford, U.K.

Promoter or (Co-)supervisor of PhD students:

- 2006-2007: Co-supervisor of Gabrielle Harrison. PhD project on “The molecular epidemiology of Hepatitis B virus in the Pacific”. University of Oxford, U.K.
- 2007-2010: Co-promoter of Jannick Verbeeck. PhD project on “*The molecular epidemiology of Hepatitis C genotype 5a*”. Katholieke Universiteit Leuven, Belgium.
- 2010-present: Co-promoter of Nuno Miguel Faria. PhD project on “*Uncovering the patterns of gene flow in viral epidemic history*”. Katholieke Universiteit Leuven, Belgium.
- 2008-present: Co- promoter of Bram Vrancken. PhD project on “*A population genomic perspective on persistent viral infections*”. Katholieke Universiteit Leuven, Belgium.
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SEMINARS AND INVITED LECTURES

- ‘Bayesian backbone analysis of HIV intrahost evolution’, research talk at Phylogroup IV 21/10/2005, University College London, London, UK
 - ‘The devil’s backbone: statistical analysis of HIV intrahost evolution’, Infectious Diseases Seminar 9/11/2005, Peter Medawar Building for Pathogen Research, Oxford University, Oxford, UK.
 - ‘Phylogenetics: Unifying the Evolutionary and Epidemiological Dynamics of Pathogens’, invited Lecturer at the Summerschool “Approaches to Viral and Bacterial Pathogenesis” 4-6/10/2005, Hannover, Germany.
 - ‘The Bayesian backbone: statistical analysis of HIV intrahost evolution’, Computational Biology Seminar 01/06/2005, University of East Anglia, Norwich, UK
 - ‘Basic science of phylogenetic analysis’, invited speaker at the 10th Annual Resistance Meeting ‘Which Resistance Matters’. 21/09/2006, London, UK
 - ‘Recombination detection in human and primate immunodeficiency virus genomes using a quartet scanning approach’, research talk Phylogroup VII 28/09/2007, Cambridge, UK
 - ‘Molecular Phylogenetics’, Invited lecture at the Molecular Medicine Postgraduate School 16/5/2008, Erasmus Medical Center, Rotterdam, The Netherlands.
 - ‘Tracing the origins, evolution and epidemic histories of viruses using phylogeographic analysis: insights into rabies, influenza & HIV’. Research Seminar at the University of the West Indies 4/10/2008, Trinidad and Tobago.
 - ‘The spatial phylogenetics of HIV-1 and HIV-2’, invited speaker at the ‘HIV/AIDS: Closing the Gap between Basic Research and Clinical Practice’ meeting, 22-23/01/2010, Instituto de Medicina Molecular (IMM), Lisbon, Portugal.
 - ‘The early spread of HIV-1 in the DRC, invited speaker at the International Symposium on ‘Simian viruses and emerging diseases in humans. Virology, epidemiology and medical history.” 9-10/05/2010, Hôpital St-Louis, Paris, France.
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CONFERENCE & WORKSHOP ORGANIZATION / CHAIRING

- Invited Chair of the discussion session: "How old is HIV?". MEEGID VIII, Bangkok, Thailand, 30/11-2/12/2006.
 - 2008 – present: organizer of the 'Advanced Module' at the yearly International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology.
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PUBLICATIONS

ARTICLES IN PEER-REVIEWED JOURNALS

1. Rector A., **Lemey P.**, Laffut W., Keyaerts E., Struyf F., Wollants E., Vermeire S., Rutgeerts P. & Van Ranst M. Mannan Binding Lectin (MBL) Gene Polymorphisms in Ulcerative Colitis and Crohn's Disease. *Genes and Immunity*, 2001, 2 (6): 323-328.
2. Leyssen P., Charlier N., Billoir F., **Lemey P.**, Vandamme A.-M., de Lamballerie X., De Clercq E. & Neyts J. Complete Genome Sequence, Taxonomic Assignment, and Comparative Analysis of the Untranslated Regions of the Modoc Virus, a Flavivirus with No Known Vector. *Virology*, 2002, 293: 125-140.
3. **Lemey P.**, Salemi M., Leda Bassit & Vandamme A.-M. Phylogenetic classification of TT virus groups based on the N22 region is unreliable. *Virus Research*, 2002, 85 (1): 47-59.
4. Charlier N., Leyssen P., Billoir F., **Lemey P.**, Vandamme A.-M., de Lamballerie X., De Clercq E. & Neyts J. Complete genome Sequence of the Montana Myotis Leukoencephalitis Virus; Phylogenetic Analysis and Comparative Study of the 3' Untranslated Region of flaviviruses with No Known Vector. *Journal of General Virology*, 2002, 83: 1875-1885.
5. **Lemey P.**, Pybus O.G., Wang B., Saksena N.K., Salemi M., & Vandamme A.-M. Tracing the origin and history of the HIV-2 epidemic. *Proceedings of the National Academy of Sciences of the United States of America*, 2003, 100 (11): 6588-6592.
6. Thoelen I., **Lemey P.**, Van Der Donck I., Beuselinck K., Lindberg A.M., & Van Ranst M. Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000. *Journal of Medical Virology*, 2003, 70 (3): 420-429.
7. Robbins K.E., **Lemey P.**, Pybus O.G., Jaffe H.W., Youngpairoj A.S., Brown T.M., Salemi M., Vandamme A.-M., & Kalish M.L. U.S. Human immunodeficiency virus type 1 epidemic: date of origin, population history, and characterization of early strains. *Journal of Virology*, 2003, 77 (11): 6359-6366. Portrayed in *Nature*, 20 May 2003, News: HIV's history traced.
8. Paraskevis D., **Lemey P.**, Salemi M., Suchard M., Van Der Peer Y., & Vandamme A.-M. 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*, 2003, 20 (12): 1986-1996.
9. **Lemey P.**, Salemi M., Wang B., Duffy M., Hall W.H., Saksena N.K., & Vandamme A.-M. 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 and Medical Microbiology*, 2003, 39 (2): 125-132.
10. Thoelen I., Moës E., **Lemey P.**, Mostmans S., Wollants E., Lindberg A.M., Vandamme A.-M., & Van Ranst, M. Analysis of the serotype/genotype correlation of VP1 and the 5' noncoding region of the human enterovirus B. *Journal of Clinical Microbiology*, 2004, 42 (3): 963-971.
11. Zlateva K.T., **Lemey P.**, Vandamme A.-M., & Van Ranst, M. Molecular evolution and circulation patterns of Human Respiratory Syncytial Virus subgroup A: positively selected sites in the attachment G glycoprotein. *Journal of Virology*, 2004, 78 (9): 4675-4683.
12. Keyaerts E., Ghijsels E., **Lemey P.**, Maes, P., Zachee P., Daelemans R., Vervoort T., Mertens G., Van Ranst M., & Clement J. Plasma exchange-associated immunoglobulin m-negative hantavirus disease after a camping holiday in southern France. *Clinical Infectious Diseases*, 2004, 38 (10): 1350-1356.

13. Potter S.J., **Lemey P.**, Achaz G., Chew C.B., Vandamme A.-M., Dwyer D.E. & Saksena N.K. HIV-1 compartmentalisation in diverse leukocyte populations during antiretroviral therapy. *Journal of Leukocyte Biology*, 2004, 76(3): 562-750.
14. **Lemey P.**, Pybus O.G., Rambaut A., Drummond A.J., Robertson D.L., Roques P., Worobey M., & Vandamme A.-M. The molecular population genetics of HIV-1 group O. *Genetics*, 2004, 167: 1059-1068.
15. Paraskevis D., Magiorkinis E., Magiorkinis G., Kiosses V.G., **Lemey P.**, Vandamme A.-M., Rambaut A., & Hatzakis A. Phylogenetic reconstruction of a known HIV-1 CRF04_cpx transmission network using maximum likelihood and Bayesian methods. *Journal of Molecular Evolution*, 2004, 59: 709-717.
16. Paraskevis D., Deforche K., **Lemey P.**, Magiorkinis G., Hatzakis A., & Vandamme A.-M. SlidingBayes: exploring recombination using a sliding window approach based on Bayesian phylogenetic inference. *Bioinformatics*, 2004, 21(7): 1274-1275.
17. Hens K., **Lemey P.**, Macours N., Francis C., & Huybrechts R. Cyclorraphan yolk proteins and lepidopteran minor yolk proteins originate from two unrelated lipase families. *Insect Molecular Biology*, 2004, 13(6): 615-623.
18. Van Laethem K., Schrooten Y., **Lemey P.**, Van Wijngaerden E., De Witt S., Van Ranst M., & Vandamme A.-M. A genotypic resistance assay for the detection of drug resistance in the HIV-1 envelope gene. *Journal of Virological Methods*, 2005, 123: 25-34.
19. **Lemey P.**, Van Dooren S., & Vandamme A.-M. Evolutionary dynamics of human retroviruses investigated through full genome scanning. *Molecular Biology and Evolution*, 2005, 22(4): 942-951.
20. Vijgen L., Keyaerts E., Moës E., Thoelen I., Wollants E., **Lemey P.**, Vandamme A.-M., & Van Ranst M. Complete genomic sequence of human coronavirus OC43: molecular clock analysis suggests a relatively recent zoonotic coronavirus transmission event. *Journal of Virology*, 2005, 79(3): 1595-1604.
21. Vijgen, L., **Lemey P.**, Keyaerts E., & Van Ranst M. Genetic variability of human respiratory coronavirus OC43. *Journal of Virology*, 2005, 79(5): 3223-3225.
22. **Lemey P.**, Pybus O.G., Van Dooren S., & Vandamme A.-M. A Bayesian statistical analysis of Human T-cell Lymphotropic Virus evolutionary rates. *Infection, Genetics and Evolution*, 2005, 5: 291-298.
23. Vijgen L., Keyaerts E., **Lemey P.**, Moës E., Li S., Vandamme A.-M., & Van Ranst M. Circulation of genetically distinct contemporary human coronavirus OC43 strains. *Virology*, 2005, 337(1): 85-92.
24. Van Dooren S., Meertens L., **Lemey P.**, Gessain A., & A.-M. Vandamme. Full genome analysis of a highly divergent Simian T-cell Lymphotropic Virus type-1 (STLV-1) strain in *Macaca arctoides*. *Journal of General Virology*, 2005, 86(7): 1953-1959.
25. Rector A., Van Doorslaer K., Bertelsen M., Barker I.K., Olberg R.-A., **Lemey P.**, Sundberg J.P., & Van Ranst M. Isolation and cloning of the raccoon (*Procyon lotor*) papillomavirus type 1 by using degenerate papillomavirus-specific primers. *Journal of General Virology*, 2005, 86(7): 2029-2033.
26. Mikhail M., Wang B., **Lemey P.**, Beckthold B., Vandamme A.-M., Gill J.M., & Saksena N.K. Role of viral evolutionary rate in HIV-1 disease progression in a linked cohort. *Retrovirology*, 2005, 2(1): 41.
27. Mikhail M., Wang B., **Lemey P.**, Beckthold B., Vandamme A.-M., Gill J.M., & Saksena N.K. Longitudinal analysis of Full-length HIV genomes demonstrating transmission of HIV-1 from a

non-progressing donor to two recipients who progressed to AIDS. *AIDS Res. Hum. Retroviruses*, 2005, 21(6): 575-579.

28. Zlateva K.T., **Lemey P.**, Moës E., Vandamme A.-M., & Van Ranst M. Genetic variation and molecular evolution of subgroup B Human Respiratory Syncytial Virus. *Journal of Virology*, 2005, 79(14): 9157-9167.
29. **Lemey P.**, & Vandamme A.-M. Exploring full-genome sequences for phylogenetic support of HIV-1 transmission events. *AIDS*, 2005, 19(14): 1551-1552.
30. **Lemey P.**, Derdelinckx I., Rambaut A., Van Laethem K., Dumont S., Vermeulen S., Van Wijngaerden E., & Vandamme A.-M. Molecular footprint of drug selective pressure in a human immunodeficiency virus transmission chain. *Journal of Virology*, 2005, 79(18): 11981-11989.
31. **Lemey P.**, Van Dooren S., Derdelinckx I., Schrooten Y., Van Wijngaerden E., & Vandamme A.-M. Molecular testing of multiple HIV-1 transmissions in a criminal case. *AIDS*, 2005, 19(15): 1649-1658.
32. Potter S.J., **Lemey P.**, Dyer W.B., Sullivan, J.S., Chew C.B., Vandamme A.-M., Dwyer D.E. & Saksena N.K. Genetic analyses reveal structured HIV-1 populations in serially sampled T lymphocytes of patients receiving HAART. *Virology*, 2006, 348(1): 35-46.
33. Verbeeck J., Maes P., **Lemey P.**, Pybus O.G., Wollants E., Song E., Nevens F., Van der Merwe S. & Van Ranst M. Investigating the origin and spread of hepatitis C virus genotype 5a. *Journal of Virology*, 2006, 80(9): 4220-4226.
34. Vijgen L., Keyaerts E., **Lemey P.**, Maes P., Van Reeth K., Nauwynck H., Pensaert M. & Van Ranst M. Evolutionary history of the closely related group 2 coronaviruses: porcine hemagglutinating encephalomyelitis virus, bovine coronavirus, and human coronavirus OC43. *Journal of Virology*, 2006, 80(14): 7270-7274.
35. **Lemey P.**, Rambaut A. & Pybus O.G. HIV evolutionary dynamics within and among hosts. *AIDS Reviews*, 2006, 8: 125-140.
36. **Lemey P.**, Kosakovsky Pond S.L., Drummond A.J., Pybus O.G., Shapiro B., Barroso H., Taveira N. & Rambaut A. Synonymous substitution rates predict HIV disease progression as a result of underlying replication dynamics. *PLoS Computational Biology*, 2007, 3(2): e29.
37. Resik S., **Lemey P.**, Ping L.-H., Kouri V., Joanes J., Perez J., Vandamme A.-M. & Swanstrom R. Limitations To Contact Tracing and Phylogenetic Analysis In Establishing HIV-1 Transmission Networks In Cuba. *AIDS Research and Human Retroviruses*, 2007, 23(3): 347-356.
38. Rector A., **Lemey P.**, Tachezy R., Mostmans S., Ghim S.-J., Van Doorslaer K., Roelke M., Bush M., Montali R.J., Joslin J, Burk R.D., Bennett Jenson A., Sundberg J.P., Shapiro B. & Van Ranst M. Ancient Papillomavirus-host Co-speciation in Felidae. *Genome Biology*, 2007, 8(4): R57.
39. Abecasis A.B., **Lemey P.**, Vidal N., de Oliveira T., Peeters M., Camacho R., Shapiro B., Rambaut A. & Vandamme A.-M. Recombination confounds the early evolutionary history of human immunodeficiency virus type 1: subtype G is a circulating recombinant form. *Journal of Virology*, 2007, 81(16): 8543-8551.
40. Deforche K., Camacho R., Van Laethem K., Shapiro B., Moreau Y., Rambaut A. , Vandamme A.-M & **Lemey P.** Estimating the relative contribution of dNTP pool imbalance and APOBEC3G/3F editing to HIV evolution in vivo. *Journal of Computational Biology*, 2007, 14(8): 1105-1114.
41. Deforche K., Camacho R., Van Laethem K., **Lemey P.**, Rambaut A., Moreau Y. & Vandamme A.-M. Estimation of an in vivo Fitness Landscape experienced by HIV-1 under Drug Selective

Pressure useful for Prediction of Drug Resistance Evolution during Treatment. *Bioinformatics*, 2008, 24(1): 34-41.

42. Matheï C., Van Dooren S., **Lemey P.**, Van Damme P., Buntinx F., Vandamme A.-M. The epidemic history of hepatitis C among injecting drug users in Flanders, Belgium. *J Viral Hepat.*, 2008, 15(6): 399-408.
43. Hoffmann F.G., He X., West J.T., **Lemey P.**, Kankasa C. & Wood C. Genetic variation in mother-child acute seroconverter pairs from Zambia. *AIDS*, 2008, 22(7): 817-824.
44. Rector A., Stevens H., Lacave G., **Lemey P.**, Mostmans S., Salbany A., Vos M., Van Doorslaer K., Ghim S.-J., Rehtanz M., Bossart G.D., Jenson A.B. & Van Ranst M. Genomic Characterization of Three Novel Dolphin Papillomaviruses Provides Indications for Recombination within the Papillomaviridae. *Virology*, 2008, 378(1): 151-161.
45. Ross R.S., Verbeeck J., Viazov S., **Lemey P.**, Van Ranst M. & Roggendorf M. Evidence for a Complex Mosaic Genome Pattern in a Full-length Hepatitis C Virus Sequence. *Evol Bioinform Online*, 2008, 4: 249-254.
46. Pybus O.G., Barnes E., Taggart R., **Lemey P.**, Markov P., Rasachak B., Syhavong B., Phetsouvanah R., Sheridan I., Humphreys I.S., Lu L., Newton P.N. & Klenerman P. Genetic History of Hepatitis C Virus In East Asia, *J. Virol.*, 2009, 83(2): 1071-1082.
47. Canducci F., Marinozzi M.C., Sampaolo M., Berrè S., Bagnarelli P., Degano M., Gallotta G., Mazzi B., **Lemey P.**, Burioni R. & Clementi M. Dynamic features of the selective pressure on the human immunodeficiency virus type 1 (HIV-1) gp120 CD4-binding site in a group of long term non progressor (LTNP) subjects. *Retrovirology*, 2009,15;6: 4.
48. Machado E.S., Adriana O. Afonso A.O., Nissley D.V., **Lemey P.**, Cunha S.M., Oliveira R.H. & Soares M.A. Emergency of primary NNRTI resistance mutations without antiretroviral selective pressure in a HAART-treated child. *PLoS One*, 2009, 4(3): e4806.
49. **Lemey P.**, Lott M., Martin, D. & Moulton V. Identifying recombinants in human and primate immunodeficiency virus sequence alignments using quartet scanning, *BMC Bioinformatics*, 2009, 10: 126.
50. Tsoa F.Y., Hoffmann F.G., Tully D.C., **Lemey P.**, Rasmussen R.A., Zhang H., Ruprecht R.M. & Wood C. *AIDS*, 2009, 23(14): 1817-1828. A comparative study of HIV-1 clade C env evolution in a Zambian infant with an infected rhesus macaque during disease progression.
51. Pourkarim M.R., Verbeeck J., Rahman M., Amini-Bavil-Olyaei S., Forier A.M., **Lemey P.**, Maes P. & Van Ranst M. *J Clin Virol*, 2009, 46(1): 61-88. Phylogenetic analysis of hepatitis B virus full-length genomes reveals evidence for a large nosocomial outbreak in Belgium.
52. **Lemey P.**, Rambaut A., Drummond A.J. & Suchard M. Bayesian phylogeography finding its roots, *PLoS Computational Biology*, 5(9):e1000520.
53. McDonald S.M., Matthijnssens J., McAllen J.K., Hine E., Overton L., Wang S., **Lemey P.**, Zeller M., Van Ranst M., Spiro D.J. & Patton J.T. Evolutionary Dynamics of Human Rotaviruses: Balancing Reassortment with Preferred Genome Constellations. *PLoS Pathogens*, 2009, 5(10):e1000634.
54. Abecasis A.B., A.-M. Vandamme & **Lemey P.** Quantifying differences in the tempo of HIV-1 subtype evolution. *Journal of Virology*, 2009, 83(24): 12917-12924.
55. **Lemey P.**, Suchard M. & Rambaut, A. Reconstructing the initial global spread of a human influenza pandemic: A Bayesian spatial-temporal model for the global spread of H1N1pdm. *PLoS Currents: Influenza*. 2009 Sep 2:RRN1031.

56. Pourkarim M.R., **Lemey P.**, Amini-Bavil-Olyaei S., Maes P. & Van Ranst M. Novel hepatitis B virus subgenotype A6 in African-Belgian patients. *Journal of Clinical Virology*, 2010, 47(1): 93-96.
57. Pourkarim M.R., Amini-Bavil-Olyaei S., **Lemey P.**, Maes P. & Van Ranst M. Are hepatitis B virus "subgenotypes" defined accurately? *J Clin Virol*, 2010 Feb 12. [Epub ahead of print].
58. Pourkarim M.R., Amini-Bavil-Olyaei S., Verbeeck J., **Lemey P.**, Zeller M., Rahman M., Maes P., Nevens F. & Van Ranst M. Molecular evolutionary analysis and mutational pattern of full-length genomes of hepatitis B virus isolated from Belgian patients with different clinical manifestations. *J Med Virol*, 2010, 82(3): 379-389.
59. **Lemey P.**, Rambaut A., Welch J.J. & Suchard M.A. Phylogeography takes a relaxed random walk in continuous space and time. *Mol Biol Evol*, 2010, Mar 4. [Epub ahead of print].
60. Campos P.F., Willerslev E., Shapiro B., Sher A., Axelsson E., Tikhonov A., Aaris-Sørensen K., Greenwood A., Kahlke R.-D., Kosintsev P., Krakhmalnaya T., Kuznetsova T., **Lemey P.**, MacPhee R., Matheus P., Norris C.A., Shepherd K., Suchard M.A., Zazula G.D. & Gilbert M.T.P. Ancient DNA analyses exclude humans as the driving force behind late Pleistocene musk ox (*Ovibos moschatus*) population dynamics. *Proceedings of the National Academy of Sciences of the United States of America*, 2010, Mar 8. [Epub ahead of print].
61. Sousa J.D., Müller V., **Lemey P.** & Vandamme A.-M. High GUD incidence in the early 20th century created a particularly permissive time window for the origin and initial spread of epidemic HIV strains, *PLoS One*, 2010, 5(4): e9936.
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63. Siebenga J., **Lemey P.**, Kosakovsky Pond S., H. Vennema H. & Koopmans M.P.G. Phylodynamic Reconstruction Reveals Norovirus GII.4 Epidemic Expansions and their Molecular Determinants. *PLoS Pathog.* 2010, 6(5): e1000884.
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