



## Curriculum vitae



École Pratique des Hautes Études

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## EMPLOYMENT HISTORY

Accreditation to direct Research (HDR), University Paris-Sud XI, UFR Scientifique d'Orsay (2006).

- 2006–present Full Professor EPHE/Museum of Natural History, Paris
- 2004-2006 Assistant Professor at Konstanz University (Chair of Zoology and Evolution).
- 2000-2004 Postdoctoral fellow at the Max-Planck Institute for Infectious Diseases, Berlin, Germany
- 1998-2000 Postdoctoral fellow at the University Laval, Québec, Canada
- 1994-1998 PhD at the University Basel, Switzerland.

## FIELD OF STUDY

Researcher and Professor in evolutionary genomics, with proven expertise in molecular epidemiology of bacterial pathogens, focusing on epidemicity estimation and prediction using machine learning technology and Bayesian statistics. Other research incorporated the rise of antibiotic resistance and secondary compensatory mutations in MDR strains.

Extensive investigations also included, the coalescent, demography and origin of major human disease agents (*Mycobacterium tuberculosis*, *Helicobacter pylori*, *Staphylococcus aureus* and *Yersinia pestis*), including the effects of globalisation and human migrations in the dissemination of the pathogens.

Domain of expertise: Evolutionary Biology, Microbiology, Population Genomics, Molecular Epidemiology, ABC Computation, Modeling and Signatures of Selection.

## AWARDS & GRANTS

- Swiss National Fonds support – CRSNG/FCAR (Canada). German DFG (100 k€), CORALSPOT project, Labex Corail (project MICRODIV – 25k€), ATM Muséum “Biodiversity and role of micro-organisms in past and present ecosystems” - 420 k€, ANR IM-model@coralfish - 135 k€, EUROPE-ASPIRE (Pfizer company), GENOSCOPE (project Evo-metagenomics), ANR TB-Emerge 600 k€, ANR ResisTrack 620 k€.

## PUBLICATIONS & BOOK CHAPTERS

- 66 publications, 8 book chapters and participation to 60 international conferences (invited 41 times). Hirsch = 39 in Google Scholar; ISI WEB of KNOWLEDGE citation index = 6,412. Average citation per item = 97 times.

## SCIENTIFIC and ADMINISTRATIVE RESPONSABILITIES

- Member of the scientific council of *Paris Sciences et Lettres* (PSL) – 2016/2020
- Member of the scientific council at the Ecole Pratique des Hautes Etudes – 2018/2021
- Member of the Board of Directors (EPHE) – 2014/2017
- Head of the “Speciation and Systematics” department at the Natural History Museum (UMR 7205) – 2015/2018
- Section Editor in Chief for the International Journal “Genes” 2015- present (IF = 4.07)
- Editor for *Infection, Genetics and Evolution*, 2016 – 2020
- Referee for > 20 different scientific journals (including *Science, Nature, Nature Genetics, Nature Microbiology, Nature Communications, Genome Research, PloS Pathogens*,)
- Referee for > 30 different scientific journals (including *Science, Nature, Nature Genetics, Nature Microbiology, Nature Communications, Genome Research, PloS Pathogens*)
- External expert of the European Union, the Institut Pasteur (France), the Agropolis Foundation, the French Research Agency ANR, the French HCERES, the Netherland Genomics Initiative, the Central Finance and Contracting Agency (CFCA) of the Republic of Latvia, the National Centre of Science and Technology Evaluation Republic of Kazakhstan and the Medical Research Council (UK).

## SCIENCE DISSEMINATION

- Publications on tuberculosis and plague were covered by different media: *Le Point, Le Nouvel Observateur, Le Monde, Libération, France Culture, le Magazine de la Santé (TV5), the New-York Times, the Scientist, Nature News, Research Highlight Nature* and the *New-Scientist*.
- Military Service at the Louis Pasteur Hospital (CHA) in Berlin, Germany, 1990-1991.
- Cited in *Who’s Who in Medicine and Healthcare 2006-2009*
- Cited in *Who’s Who in the World 2019*.

### Online attention



#### Altmetric score (what's this?)

- Tweeted by 43
- On 7 Facebook pages
- Mentioned in 3 Google+ posts
- Picked up by 22 news outlets
- Blogged by 1

#### This Altmetric score means that the article is:

- in the 99 percentile (ranked 1,014th) of the 174,366 tracked articles of a similar age in all journals
- in the 98 percentile (ranked 1st) of the 66 tracked articles of a similar age in *Nature Genetics*

*Nature Genetics*



### MICROBIOLOGY

## Tuberculosis has history in its DNA

Key historical events such as the First World War drove the global spread of a strain of tuberculosis-causing bacteria that is prone to becoming resistant to drugs.

Thierry Wirth of the National Museum of Natural History in Paris and his colleagues collected 4,987 samples of the Beijing strain of *Mycobacterium tuberculosis*, isolated from patients from 99 countries, and analysed the microbe's DNA to trace its ancestry. They found that the strain originated in East Asia 6,600 years ago with the rise of agriculture. From there, it spread throughout the

world, increasing in prevalence when the human population grew in the nineteenth century, as well as when people were vulnerable to infection during the First World War and after HIV began to spread as epidemics. The drug-resistant strains that now affect Asia appeared when the Soviet Union — and its health system — collapsed in the 1990s. *Nature Genetics* <http://dx.doi.org/10.1038/ng.3195> (2015)

22 JANUARY 2015 | VOL 517 | NATURE | 415

### RESEARCH HIGHLIGHTS THIS WEEK



## INVITED LECTURES

- October 2018: "From genomes to biology: the power of population studies", Congress of the French Society of Microbiology, Paris, France.
- August 2018: "Niche specialization and spread of multidrug-resistant *Staphylococcus capitis* clone involved in neonatal sepsis", International Symposium on Staphylococci and Staphylococcal Infections, ISSSI, Copenhagen, Denmark.
- December 2017: "Mycobacterium tuberculosis Beijing lineage: an emerging pathogen", 37<sup>ième</sup> réunion interdisciplinaire de Chimiothérapie Anti-Infectieuse, RICAI, Paris, France.
- May 2017: "Host-pathogen coevolution" 2<sup>ième</sup> colloque la microbiologie dans tous ses états, Paris
- January 2017: "Inferring evolutionary history of pathogens based on genome data" at the Leibniz Centre Infection Symposium 2017, "Evolution & Infection", Hamburg, Germany.
- December 2016: "Origin, Spread and Demography of Major Human Bacterial Diseases in a Globalizing World", 8<sup>ième</sup> édition des Journées Infections Nosocomiales, Lyon Biopôle-FINNOVI.
- December 2016: "Dispersion and demography of Mycobacterium tuberculosis in a globalizing world", Colloque International INRAP Archéologie de la Santé, Anthropologie du Soins, Paris, France.
- May 2016: Plenary talk "Origin, spread and demography of major human bacterial diseases in a globalizing world" at the 13<sup>th</sup> International Conference on Molecular Epidemiology and Evolutionary genetics of Infectious Diseases, Antwerp, Belgium.
- March 2016: William H. Telfer Endowed Lectureship recipient, University of Pennsylvania, USA.
- March 2015: "Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage", 11<sup>th</sup> Congress of the French Society of Microbiology, Institut Pasteur, Paris, France.
- October 2014: "Out of Africa, evolutionary history of the community acquired ST80". SYMPOSTAPH 2014, Lyon, France.
- July 2014: "Coalescence and demogenetical analyses based on full genome data". ESCMID Postgraduate Education Course in Molecular Typing methods for Pathogens, Lyon, France.
- October 2013: "A tribute to Mark Achtman: Impact of his scientific contribution in the fields of molecular epidemiology and evolutionary microbiology". The International Meeting on Microbial Epidemiological Markers – IMMEDI, Paris.
- May 2013: "Micro and macro evolution of the Mycobacterium tuberculosis complex" MYCOCLUB Congress, Toulouse.
- November 2012: Conference on bacterial pathogens at the third Darwin Days, Institut Poincaré, Paris.
- September 2012: "Population Genetics: from bacteria to humans". Congress Adaptation, Persistence, Extinction, MNHN/UNESCO, Paris.
- March 2012: "Rôle des guerres et des camps de réfugiés dans la dissémination de la fièvre de Lassa en Afrique de l'ouest". Colloque international sur la transmission. Institut Thématique Multi Organisme Microbiologie et Maladies Infectieuses (IMMI). Abbaye des Vaux de Cernay.
- January 2012: "Tuberculosis through times" International Conference on Drug Therapy in TB Infection, Edinburgh, Scotland.
- October 2011: "Of bugs and Men: from past migrations to recent epidemics", International Congress, Microorganisms facing their environment. Paris – MNHN/CNRS.
- January 2011: Inaugural conference "Des bactéries et des hommes: des migrations du Paléolithique supérieur aux vagues épidémiques récentes" au congrès de la Société d'Anthropologie de France sur le thème Coévolution Hommes – maladies (infectieuses et non infectieuses) - Paris.
- June 2010: "Guns, germs and rats: lessons from Lassa Hemorrhagic fever". Congress of the French Society of Microbiology, Marseille.
- October 2009: "Discovering human history from our bugs: review and perspectives". Congress "Darwin's legacy: New Insights into Human Evolution", University Paris-Diderot, Paris.
- May 2009: "Sélection et neutralisme: évolution des pathogènes et biologie de la santé". Colloque EPHE, Théorie de l'évolution et religions de 1859 à nos jours. Paris, Lycée Henri IV.
- December 2009: Chairman and speaker "Evolution and microbial diversity: impact of next generation sequencing", Institut Pasteur, Paris.
- May 2008: "Sex and virulence in bacteria, phylodynamics and demographics". Workshop on phylogeny and genetics in microbiology and virology, Erasmus MC postgraduate school of Molecular Medicine, Rotterdam, the Netherlands.
- May 2007: "Sex and virulence in bacteria: empirical evidence and experimental perspectives". VIII<sup>th</sup> National Congress of the French Society of Microbiology, Nantes.

October 2006: "Recent advances in bacterial population genomics". Workshop on microbial systematics, population genetics and epidemiology, Charité Hospital, Berlin.

June 2006: "Bacterial evolution and population genetics: from sex and virulence to human migrations". Après-midi d'Evolution (AME), Natural History Museum, Paris.

November 2005: "Invasive species and host parasite interactions: the eel paradigm". National University of Ireland, Galway.

August 2005: "Deciphering human origins and migrations by means of their microbial pathogens", 10th Congress of the European Society for Evolutionary Biology (ESEB 2005). Cracow, Poland.

May 2005: "Eel population genetics and hybridization". Workshop "Biological basis of the management of diadromous fish in temperate and tropical regions" à La Rochelle (University La Rochelle).

February 2005: "Eel population genetics: a review". Fourth International Symposium on Ecological Genetics. Antwerp, Belgium.

November 2004: "Revisiting Escherichia coli biology and population genetics". Workshop of the Deutsche Gesellschaft für Hygiene und Mikrobiologie. "Bacterial systematics, Population Genetics and Infection Epidemiology".

July 2004: Chairman du Symposium "Molecular epidemiology of bacteria". VII International Meeting on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, Valencia, Spain.

November 2001: "Escherichia coli population genetics". Third Workshop on microbial systematics, population genetics and Epidemiology, Berlin.

October 2001: "Clones identification, recombination parameters and population genetics in Escherichia coli: three facets of an MLST approach." Prof J. Hacker, Institut for Molecular Infectious Biology, University Würzburg (Germany).

## E CONFERENCES

ESCMID Conference on Coronavirus Disease (ECCVID) - September 2020. SARS-Cov-2 phylodynamics differentiates the effectiveness of non-pharmaceutical interventions. Top rated abstract.

## ORAL CONFERENCES

International Conference of the Society for Molecular Biology and Evolution, SMBE, (2018, Yokohama, Japan) - Conf. of the European Society of Clinical Microbiology and Infectious Diseases, ECCMID, (2018, Madrid, Spain) – Sixth International Conference of Infectious Disease Dynamics, EPIDEMICS6 (2017, Sitges, Spain) - XIIth International conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (Bangkok, Thailand, 2014) – The International Meeting on Microbial Epidemiological Markers – IMMEM, Paris - XIVth Congress of the European Society for Evolutionary Biology, ESEB (2013, Lisbon, Portugal) – Vth World Congress on Leishmaniasis (2013, Recife, Brazil) – IVth World Congress on Leishmaniasis (2009, Lucknow, India) – Helicobacter pylori Symposium (2008, Max-Planck Institut for infectious Disease, Berlin, Germany) – Jacques Monod Conference, Evolutionary genomics (2007, Roscoff, France) – VIIth International Meeting on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (2004, Valencia, Spain) –SMBE meetings (2002, Sorrento, Italy) - Gordon Research Conference (2001, Williamston, Massachusetts) – Evolution meetings (2000, Bloomington, Indiana)

## POSTER COMMUNICATIONS AT CONFERENCES

SMBE meetings (2016, Brisbane, Australia) - XIVth Congress of the European Society for Evolutionary Biology, ESEB (2013, Lisbon, Portugal) - 6th World Fisheries Congress (2012, Edinburgh, UK) - Jacques Monod Conference, (2011, Roscoff France) – Canadian Conference for Fisheries Research CCFFR (2000, Fredericton, New-Brunswick) - XXth International Congress of Entomology (1996, Florence, Italy) – SMBE meetings (1994, Athens, USA).



## TEN SIGNIFICANT PUBLICATIONS

- **Wirth T** (2021). When specialized clones go global. *Nature Microbiology* (in press). **IF = 17.74.**
- **Wirth T**, Bergot. M, Rasigade JP, Pichon B, Barbier M, Martins-Simoes P, Jacob L, Pike R, Tissières P, Picaud JC, Kearns A, Supply P, Butin M, Laurent F (2020). Niche specialization and spread of *Staphylococcus capitis* involved in neonatal sepsis. *Nature Microbiology* 5:735-745. **IF = 17.74**
- **Wirth T** (2015) Massive lineage replacements and cryptic outbreaks of *Salmonella* Typhi in eastern and southern Africa. *Nature Genetics* 47: 565-567. **IF = 38.33**
- Merker M, Blin C, Mona S, Duforet-Frebourg N, Lecher S, Willery E, Blum M, Rüscher-Gerdes S, Mokrousov I, Aleksic E, Allix-Béguec C, Antierens A, Augustynowicz-Kopeć E, Ballif M, Barletta F, Beck HP, Barry III CE, Bonnet M, Borroni E, Campos-Herrero I, Cirillo D, Cox H, Crowe S, Crudu V, Diel R, Drobniewski F, Fauville-Dufaux M, Gagneux S, Ghebremichael S, Hanekom M, Hoffner S, Jiao WW, Kalon S, Kohl TA, Kontsevaya I, Lillebæk T, Maeda S, Nikolayevskyy V, Rasmussen M, Rastogi N, Samper S, Sanchez-Padilla E, Savic B, Chola Shamputa I, Shen A, Sng LH, Stakenas P, Toit T, Varaine F, Vukovic D, Wahl C, Warren R, Supply P, Niemann S & **Wirth T** (2015). Evolutionary history and global spread of the *Mycobacterium tuberculosis* Beijing lineage. *Nature Genetics* 47: 242-249. **IF = 38.33. Highly cited = 283**
- Roetzer A, Diel R, Kohl TA, Rückert C, Nübel U, Blom J, **Wirth T**, Jaenicke S, Schuback S, Rüscher-Gerdes S, Supply P, Kalinowski J & Niemann S (2013). Whole genome sequencing versus traditional genotyping for investigation of a *Mycobacterium tuberculosis* outbreak : A longitudinal molecular epidemiological study. *PloS Medicine* 10: e1001387. **IF = 11.07. Highly cited = 316**
- **Wirth, T**, Stegger M, Andersen PS, Skov RL, De Grassi A, Simoes PM, Tristan A, Petersen A, Aziz M, Kiil K, Cirkovic I, Udo EE, del Campo R, Vuopio-Varkila J, Ahmad N, Tokajian S, Peters G, Schaumburg F, Olsson-Liljequist B, Givskov M, Driebe EE, Vigh HE, Shittu A, Ramdani-Bougessa N, Rasigade JP, Price LB, Vandenesch F, Larsen AR & Laurent F (2014). Origin and evolution of European community acquired methicillin-resistant *Staphylococcus aureus*. *Mbio* 5: e01044-14. **IF = 7.87.**
- Morelli M, Song Y, Mazzoni CJ, Eppinger M, Roumagnac P, Wagner DM, Feldkamp M, Kusecek B, Vogler AJ, Li Y, Cui Y, Thomson N, Leblois R, Lichtner P, Rahalison L, Peterson JM, Keim P, **Wirth T**, Ravel J, Yang R, Carniel E & Achtman M (2010). *Yersinia pestis* genome sequencing identifies patterns of global phylogenetic diversity. *Nature Genetics* 42: 1140-1147. **IF = 38,33. Highly cited: 339**
- **Wirth, T.**, Hildebrand F., Allix-Béguec C. et al (2008). Origin, spread and demography of the *Mycobacterium tuberculosis* complex. *PloS Pathogens* 4: e1000160. **IF = 6.82. Highly cited = 281**
- **Wirth T.**, Wang X., Linz B. et al. (2004) Distinguishing human ethnic groups by means of sequences from *Helicobacter pylori*: Lessons from Ladakh. *Proc. Natl. Acad. Sci. USA* 101: 4746-4751. **IF = 10.70**
- Falush D., **Wirth, T.**, Linz B. et al (2003) Traces of human migration in *Helicobacter pylori*. *Science* 299: 1582-1585. **IF = 47.73. Highly cited = 669**