

Personal Data

Name WIRTH Thierry, Prof. Dr. rer. nat. habil.
Place/Date of Birth Mulhouse, France / 08.08.1966

Affiliation

Institution Natural History Museum, EPHE, Paris
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Education/Training

1988 - 1989 Licence Populations and organisms biology, University Rennes 1.
1989 - 1990 Master Populations and organisms biology, University Rennes 1.
1990 - 1991 Military service at the Louis Pasteur Hospital, Berlin, Germany.
1991 - 1992 DEA at Rennes 1 University.
1994 - 1998 PhD in Zoology at the University Basel (Switzerland) entitled "Molecular Genetics and its Significance for Conservation Biology".
2006 Habilitation HDR, "From population genetics to population genomics", Univ. Paris-Sud XI, Orsay.

Research Experience/Academic Appointments

1998 - 2000 Postdoctoral fellow, Dpt. Of Biology, University Laval, Québec, Canada
2000 - 2004 Postdoctoral fellow, Max-Planck Institute for Infectious Diseases, Berlin.
2004 - 2006 Assistant Professor, Dpt. of Biology, University Konstanz, Konstanz.
Since 2006 Full Professor at Natural History Museum, EPHE, Paris
2015 - 2018 Head of the "Speciation and Systematics" department at the Natural History Museum (UMR 7205) – 2015/2018
Since 2018 - Team Leader at the ISYEB (team integrative biology and molecular evolution).
- Exceptional class Professor
2018 - 2020 Director of the EPHE laboratory "Integrative Population Biology and Molecular Evolution"

Important Scientific Prizes/Functions

2007- 2017 Lecturer and teaching coordinator at the Ecole Normale de Lyon (Bioscience Master)
2013 - 2017 Member of the strategic committee (UMR-CNRS 7205) at the Natural History Museum
2014 Evaluator and expert for the Medical Research Council, UK
2014 - 2017 Member of the Board of Directors (EPHE)
2015 Named member of the Scientific evaluation committee, ANR ASTRID - French Defence Procurement Agency
2015 External expert (named): Member of the French Research evaluation committee– UMR-SAVE, Bordeaux
Since 2015 Section Editor in Chief "Microbial Genetics and Genomics" for the International Journal "Genes" 2015 - present. IF = 4.10
2015 - 2017 Evaluator and expert for the Pasteur Institute INCEPTION program and International Network
2016 William H. Telfer Endowed Lectureship recipient (March 2016), University of Pennsylvania, USA
2016 - 2018 Member of the Department and Unit Councils (UMR-CNRS 7205) at the Natural History Museum
2016 - 2019 Editor for the international journal "Infection, Genetics and Evolution"
2016 - 2020 Member of the Scientific Council of Paris Sciences et Lettres (PSL)
2016 - 2021 Lecturer and teaching coordinator at the Ecole Normale de Paris (Imalis Master)
2018 - 2022 Member of the Scientific Council at the Ecole Pratique des Hautes Etudes
2018 - 2022 Member of the scientific politic commission at the EPHE
2019 Expert and evaluator for the ESCMID Study Group Research Grants
2019 - 2024 Elected member of the Migrations Institute

Curriculum Vitae Prof. Dr. Thierry WIRTH

2020	Expertise and project evaluations for the Central Finance and Contracting Agency (CFCA) of the Republic of Latvia; the National Centre of Science and Technology Evaluation Republic of Kazakhstan
2021	Acting member of the French Research Evaluation Committee (HCERES), UMR Ecobio Rennes

Key indicators

Cumulative IF (life time): > 550	H-factor: 33 (WOS), 40 (Google Scholar) Mean citation per article in WOS > 84
Researcher ID: B-4915-2008	Public Grants (2012-2020): appr. 2 Mio. €

Current Projects (selection)

2009 - 2013	Museum Transverse Action (ATM-MNHN) – Biodiversity and role of microorganisms in present and past ecosystems (PI). 600 k€
2017 - 2021	ANR Blanc, TBemerg, Birth of a killer: genetic factors and metabolic adaptations required for the emergence of epidemic tuberculosis bacilli - 598k€
2021 - 2024	ANR Blanc, Resitrack, Controlling antibiotic resistance in the hospital - 620 k€ - Partner WP5 (modelling and Bayesian inferences).

Ten Main Publications (75 original papers, 5 reviews und editorials, 8 book chapters)

1. **Wirth T** (2021). When specialized clones go global. *Nature Microbiology* 6: 1215-1216. IF = 17.74
2. Moura A, Lefrancq N, **Wirth T** et al. (2021). Emergence and global spread of *Listeria monocytogenes* main clinical clonal complex. *Science Advances* 7: eabj9805. IF = 14.14
3. **Wirth T**, Bergot M, Rasigade JP, Pichon B, Barbier M, Martins-Simoes P, Jacob L, Pike R, Tissieres 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
4. **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
5. Merker M, Blin C, Mona S, Duforet-Frebourg N, Lecher S, Willery E, Blum M, Rüscher-Gerdes S, Mokrousov I, Aleksic E, Allix-Béguet 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, Drobniowski 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.
6. 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 = 13.58.
7. 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
8. **Wirth, T**, Hildebrand F, Allix-Béguet C et al (2008). Origin, spread and demography of the Mycobacterium tuberculosis complex. *PloS Pathogens* 4: e1000160. IF = 6.82.
9. **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 = 11.20
10. Falush D, **Wirth, T**, Linz B. et al (2003) Traces of human migration in *Helicobacter pylori*. *Science* 299: 1582-1585. IF = 41.84.

Patent