

Thierry Wirth Publications

→ Liste complète

- 64. Kohl TA, Kranzer K, Andres S, **Wirth T**, Niemann S, Moser I (2020). Population structure of *Mycobacterium bovis* in Germany: a long-term study using whole-genome sequencing combined with conventional molecular typing methods. *Journal of Clinical Microbiology* 58: e01573. IF = 5.90.
- 63. **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 = 15.54.
- 62. **Wirth T**, Wong V, Vandenesch F, Rasigade JP (2020). Applied phyloepidemiology: Detecting drivers of pathogen transmission from genomic signatures using density measures. *Evolutionary Applications* 13: 1513-1525. IF = 4.01.
- 61. Franssen SU, Durrant C, Stark O, Moser B, Downing T, Imamura H, Dujardin JC, Sanders M, Mauricio I, Miles M, Schnur L, Jaffe CL, Nasereddin A, Schalgig H, Yeo M, Bhattacharyya T, Alam MZ, Berriman M, **Wirth T**, Schoenian G, Cotton JA (2020). Global genome diversity of the Leishmania complex. *eLife* 9: e51243. IF = 7.62.
- 60. Arandjelovic I, Merker M, Richter E, Kohl TA, Savic B, Soldatovic I, **Wirth T**, Vukovic D, Niemann S (2019). Longitudinal Outbreak of Multidrug-Resistant Tuberculosis in a Hospital Setting, Serbia. *Emerging Infectious Diseases* 25: 555-558. IF = 7.42.
- 59. Bal A, Sabatier M, **Wirth T**, Coste-Burel M, Lazrek M, Stefic K, Brengel-Pesce K, Morfin F, Lina B, Schuffenecker I, Josset L (2019). Emergence of enterovirus D68 clade D1, France, August to November 2017. *Eurosurveillance* 24: 8-12. IF = 7.13.
- 58. Rasigade JP, Hollandt F, **Wirth T** (2018) Genes under positive selection in the core genome of pathogenic *Bacillus cereus* group members. *Infection Genetics and Evolution* 65: 55-64. IF = 2.77.
- 57. Merker M, Barbier M, Cox H, Rasigade JP, Feuerriegel S, Kohl TA, Diel R, Borrell S, Gagneux S, Nikolayevskyy V, Andres S, Nuble U, Supply P, **Wirth T**, Niemann S (2018). Compensatory evolution drives multidrug-resistant tuberculosis in Central Asia. *Elife* 7: e38200. IF = 7.62.
- 56. Kramer R, Sabatier M, **Wirth T**, Pichon M, Lina B, Schuffenecker I, Josset L (2018) Molecular diversity and biennial circulation of enterovirus D68: a systematic screening in Lyon, France, 2010 to 2016. *Eurosurveillance* 23: 12-21. IF = 7.13.
- 55. Gustave CA, Tristan A, Martins-Simoes P, Stegger M, Benito Y, Skytt Andersen P, Bes M, Le Hir Y, Diep BA, Uhlemann AC, Glaser P, Laurent F, **Wirth T**, Vandenesch F (2018). Demographic fluctuation of community-acquired antibiotic-resistant *Staphylococcus aureus* lineages: potential role of flimsy antibiotic exposure. *ISME Journal* 12: 1879-1894. IF = 9.66.
- 54. Barbier M, Dumitrescu O, Pichat C, Carret G, Ronnaux-Baron AS, Blasquez G, Godin-Benhaim C, Boisset S, Carricajo A, Giacomo V, Fredenucci I, Pérouse de Montclos M, Genestet C, Flandrois JP, Ader F, Supply P, Lina G, **Wirth T** & Rasigade JP (2018). Changing patterns of human migrations shaped the global population structure of *Mycobacterium tuberculosis* in France. *Scientific Reports* 8: 5855. IF = 5.23.
- 53. Quarrell SR, Arabi J, Suwalski A, Veuille M, **Wirth T** & Allen GR (2018). The invasion biology of the invasive earwig, *Forficula auricularia* in Australasian ecosystems. *Biological Invasions* 20:1553-1565. IF = 2.47

- 52. Hussen KA, Manh TPV, Guimiot F, Nelson E, Chabaane E, Delord M, Barbier M, Berthault C, Dulphy N, Alberdi AJ, Burlen-Defranoux O, Socie G, Bories JC, Larghero J, Vanneaux V, Verhoeyen E, **Wirth T**, Dalod M, Gluckman JC, Cumano A, Canque B (2017). Molecular and Functional Characterization of Lymphoid Progenitor Subsets Reveals a Bipartite Architecture of Human Lymphopoiesis. *Immunity* 47: 680-696. IF = 22.84.
- 51. Rasigade JP, Barbier M, Dumitrescu O, Pichat C, Carret G, Ronnaux-Baron AS, Blasquez G, Godin-Benham C, Boisset S, Carricajo A, Jacomo V, Fredenucci I, Pérouse de Montclos M, Flandrois JP, Ader F, Supply P, Lina G & **Wirth T** (2017). Strain-specific estimation of epidemic success provides insights into the transmission dynamics of tuberculosis. *Scientific Reports* 7:45326. IF = 5.23.
- 50. Barbier M & **Wirth T** (2016). The evolutionary history, demography and spread of the *Mycobacterium tuberculosis* complex. *Microbiology Spectrum*. 4 : TBTB2-0008-2016. IF = 4.51.
- 49. Glaser P, Martins-Simoes P, Villains A, Barbier M, Tristan A, Bouchier C, Ma L, Bes M, Laurent F, Guillemot D, **Wirth T** & Vandenesch F (2016). Demography and intercontinental spread of the USA300 community-acquired Methicillin-resistant *Staphylococcus aureus* lineage. *Mbio* 7: e02183-15 IF = 6.79.
- 48. Sapriel G, Konjek J, Orgeur M, Bouri L, Frezal L, Roux AL, Dumas E, Brosch R, Bouchier C, Brisse S & **Wirth T** (2016). Genome-wide mosaicism within *Mycobacterium abscessus*: evolutionary and epidemiological implications. *BMC Genomics* 17: 118. IF = 3.99.
- 47. **Wirth T** (2015). Massive lineage replacements and cryptic outbreaks of Salmonella Typhi in Eastern and South Africa (News and Views). *Nat. Genet.* 47: 565-567. IF = 29.65.
- 46. Huber B, Whibley A, Poul YL, Navarro N, Martin A, Baxter S, Shah A, Gilles B, **Wirth T**, McMillan WO & Joron M (2015). Conservatism and novelty in the genetic architecture of adaptation in *Heliconius* butterflies. *Heredity* 114: 515-524. IF = 3,80.
- 45. 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, 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. *Nat. Genet.* 47: 242-249. IF = 29.65. [Highly cited = 248](#)
- 44. Stegger M, **Wirth, T**, 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 = 6.79.
- 43. Wielgoss S, Gilabert A, Meyer A & **Wirth T** (2014). Introgressive hybridisation and latitudinal admixture clines in North Atlantic eels. *BMC Evol. Biol.* 14 : 61. IF = 3.41.
- 42. Cantinelli T, Chenal-Francois V, Diancourt L, Frezal L, Leclercq, A, **Wirth, T**, Lecuit M & Brisse S (2013). Epidemic clones of *Listeria monocytogenes* are widespread and ancient clonal groups. *J. Clin. Microbiol.* 51: 3770-3779. IF = 4.23.
- 41. Kuhls K, Cupolillo E, Silva SO, Schweynoch C, Boite MC, Mello MN, Mauricio IL, Miles M, **Wirth T** & Schönian G (2013). Population structure and evidence for both clonality and recombination among Brazilian strains of the subgenus *Leishmania* (Viannia). *PloS Neglect. Trop. D.* 5: e1155. IF = 4.49.

- 40. Roetzer A, Diel R, Kohl TA, Rückert C, Nübel U, Blom J, **Wirth T**, Jaenicke S, Schuback S, Rüsck-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 Med.* 10: e1001387. IF = 14.00. [Highly cited = 288](#)
- 39. Lalis A, Leblois R, Lecompte E, Denys C, ter Meulen J & **Wirth T** (2012). The impact of human conflict on the genetics of *Mastomys natalensis* and Lassa virus in West-Africa. *PloS One* 7: e37068. IF = 3.53.
- 38. Supply P, Niemann S & **Wirth T** (2011). On the mutation rates of spoligotypes and variable number of tandem repeat loci of *Mycobacterium tuberculosis*: Continued-when tuning matters. *Infect. Genet. Evol.* 11: 251-252. IF = 3.26.
- 37. Leblois R, Kuhls K, François O, Schönian G & **Wirth T** (2011). Guns, germs and dogs: on the origin of *Leishmania chagasi*. *Infect. Genet. Evol.* 11: 1091-1095. IF = 3.26.
- 36. Kuhls K, Alam MZ, Cupolillo E, Ferreira, GEM., Mauricio IL, Oddone R, Feliciangeli MD, **Wirth T**, Miles MA & Schönian G (2011). Comparative microsatellite typing of New World *Leishmania infantum* reveals low heterogeneity among populations and its recent Old-World origin. *PloS Neglect. Trop. D.* 5: e1155. IF = 4.49.
- 35. Supply P, Niemann S & **Wirth T** (2011). On the mutation rates of spoligotypes and variable number of tandem repeat loci of *Mycobacterium tuberculosis*. *Infect. Genet. Evol.* 11: 251-252. IF = 3.26.
- 34. 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 = 29.65.
- 33. Wielgoss S, Hollandt F, **Wirth T** & Meyer A (2010). Genetic signatures in an invasive parasite of *Anguilla anguilla* correlate with differential stock management. *J. Fish Biol.* 77: 191-210. IF = 1.73.
- 32. Nübel U, Dordel J, Kurt K, Strommenger B, Westh H, Shukla SK, Berger-Bächi B, Žemličková H, Leblois R, **Wirth T**, Jombart T, Balloux F & Witte W (2010). A timescale for evolution of methicillin-resistant *Staphylococcus aureus*: genome variation traces an ongoing epidemic of hospital infections. *PloS Path.* 6: e1000855. IF = 8.06.
- 31. Elmer KR, Reggio C, **Wirth T**, Verheyen E, Salzburger W & Meyer A (2009). Pleistocene dessication in East Africa bottlenecked but did not extirpate the adaptive radiation of Lake Victoria haplochromine cichlid fishes. *Proc. Natl. Acad. Sci. USA* 106: 13404-13409. IF = 9.81.
- 30. Wielgoss S, **Wirth T** & Meyer A (2008). Isolation and characterization of 12 dinucleotide microsatellites in the European eel, *Anguilla anguilla* L., and tests of amplification in other species of eels. *Mol. Ecol. Resour.* 8: 1382-1385. IF = 5.63
- 29. **Wirth, T**, Hildebrand F, Allix-Béguec C et al (2008). Origin, spread and demography of the *Mycobacterium tuberculosis* complex. *PloS Path.* 4: e1000160. IF = 8.06.
- 28. Ragon M, **Wirth T**, Hollandt F et al (2008). A new perspective on *Listeria monocytogenes* evolution. *PloS Pathogens* 4: e1000146. IF = 8.06.
- 27. Al-Jawabreh A, Diezmann S, Muller M, **Wirth T**, Schnur LF et al (2008). Identification of geographically distributed sub-populations of *Leishmania major* by microsatellite analysis. *BMC Evol. Biol.* 8: 183. IF = 3.41.
- 26. Wielgoss S, Taraschewski H, Meyer A & **Wirth T** (2008). Population structure of the parasitic nematode *Anguillicola crassus*, an invader of declining North Atlantic eel stocks. *Mol. Ecol.* 17: 3478-3495. IF = 5.84.

- 25. **Wirth T**, Morelli G, Kusecek B et al (2007). The rise and spread of a new pathogen: seroresistant *Moraxella catarrhalis*. *Genome Research* 17: 1647-1656. IF = 13.85.
- 24. Rattei T, Ott S, Gutacker M, Rupp J, Maass M, Schreiber S, Solback W, **Wirth T** & Gieffers J. (2007). Genetic diversity of the obligate intracellular bacterium *Chlamydophila pneumoniae* by genome-wide analysis of single nucleotide polymorphisms: evidence for highly clonal population structure. *BMC Genomics* 8: 355-361. IF = 4.04.
- 23. Wielgoss S, Sanetra M, Meyer A & **Wirth T** (2007). Isolation and characterization of short tandem repeats (STR) in an invasive swimbladder nematode, parasitic in Atlantic freshwater eels, *Anguillicola crassus*. *Mol. Ecol. Notes* 7: 1051-1053. IF = 1.63
- 22. **Wirth T**, Falush D, Lan R, Colles F, Mensa P, Wieler L, Karch H, Reeves P, Maiden P, Ochman H & Achtman M (2006). Sex and virulence in *Escherichia coli*: an evolutionary perspective. *Mol. Mic.* 60: 1136-1151. IF = 5.03. **Highly cited = 1199**
- 21. Perez-Losada M, Browne EB, Madsen A, **Wirth T**, Viscidi RP & Krandall KA (2006). Population genetics of microbial pathogens estimated from Multilocus Sequence Typing (MLST) data. *Infect. Genet. Evol.* 6: 97-112. IF = 3.26.
- 20. Gu W, Gibert Y, **Wirth T**, Elischer A, Bloch W et al (2005). Applying expression and evolutionary analysis to predict genes related to human diseases. *FASEB Journal* 19: A1510. IF = 6.51.
- 19. Schwenkenbecher JM, **Wirth T**, Schnur LF, Jaffe CH, Schallig H, Al-Jawabreh A, Hamarsheh O, Azmi K, Pratlong F & Schoenian G (2006). Microsatellite analysis reveals genetic structure of *Leishmania tropica*. *Int. J. Parasitol.* 36: 237-246. IF = 3.40.
- 18. Gu W, Gibert Y, **Wirth T**, Elischer A, Bloch W, Meyer A, Steinlein OK & Begemann G (2005). Using gene-history and expression analyses to assess the involvement of LGI genes in human disorders. *Mol. Biol. Evol.* 22: 2209-2216. IF = 14.31.
- 17. **Wirth T**, Meyer A & Achtman M (2005). Deciphering host migrations and origins by means of their microbes. *Mol. Ecol.* 14: 3289-3306. IF = 5.84.
- 16. Achtman M, Morelli G, Zhu P, **Wirth T**, Diehl I, Kusecek B, Vogler AJ, Wagner DM, Allender CJ, Easterday WR, Chenal-Francisque V, Worsham P, Thomson NR, Parkhill J, Lindler LE, Carniel E & Keim P (2004). Microevolution and history of the plague bacillus, *Yersinia pestis*. *Proc. Natl. Acad. Sci. USA* 101: 17837-17842. IF = 9.81. **Highly cited = 316**
- 15. **Wirth T**, Wang X, Linz B, Novick RP, Lum, JK, Blaser M, Morelli G, Falush D & Achtman M (2004). Distinguishing human ethnic groups by means of sequences from *Helicobacter pylori*: Lessons from Ladakh. *Proc. Natl. Acad. Sci. USA* 101: 4746-4751. IF = 9.81.
- 14. **Wirth T** & Bernatchez L (2003). Decline of North-Atlantic eels: a fatal synergy? *Proc. R. Soc. Lond. B* 270: 681-688. IF = 5.29.
- 13. Haase M, Misof B, **Wirth T**, Baminger H & Baur B (2003). Mitochondrial differentiation in a polymorphic landsnail: evidence for a Pleistocene survival within the boundaries of permafrost. *J. Evolution. Biol.* 16: 415-428. IF = 3.48.
- 12. Falush D, **Wirth T**, Linz B, Pritchard JK, Stephens M, Kidd M, Blaser MJ, Graham DY, Vacher S, Perez-Perez GI, Yamaoka Y, Mégraud F, Otto K, Reichard U, Katzowitsch E, Wang X, Achtman M & Suerbaum S (2003). Traces of human migration in *Helicobacter pylori*. *Science* 299: 1582-1585. IF = 31.48. **Highly cited = 584**
- 11. Gagneux S, **Wirth T** et al. (2002). Clonal grouping in serogroup X *Neisseria meningitidis*. *Emerg. Infect. Dis.* 8: 462-466. IF = 7.33.
- 10. Gagneux S, Hodgson A, Smith T, **Wirth T** et al. (2002). Prospective study of a serogroup X *Neisseria meningitidis* outbreak in Northern Ghana. *J. Infect. Dis.* 185: 618-626. IF = 5.78.

- 9. **Wirth T** & Bernatchez L (2001). Genetic evidence against panmixia in the European eel. *Nature* 409 : 1037-1040. IF = 42.35.
- 8. **Wirth T** (2000). Isolation and characterization of variable microsatellite markers in the land snail *Helicella itala*, and cross species amplification within the family Helicidae. *Mol. Ecol.* 9: 501-502. IF = 5.84.
- 7. Leclerc D, **Wirth T** & L. Bernatchez (2000). Isolation and characterization of variable microsatellite markers in the yellow perch (*Perca flavescens*), and cross species amplification within the family Percidae. *Mol. Ecol.* 9: 995-997. IF = 5.84.
- 6. Jäggi C, **Wirth T** & B Baur (2000). Genetic variability in subpopulations of the asp viper (*Vipera aspis*) in the Swiss Jura mountains: implications for a conservation strategy. *Biol. Cons.* 94: 69-77. IF = 4.04.
- 5. **Wirth T**, Leguellec R & M Veuille (1999). Directional substitution and evolution of nucleotide content in the cytochrome oxidase II in earwigs (Dermapteran insects). *Mol. Biol. Evol.* 16: 1645-1653. IF = 14.31.
- 4. **Wirth T**, Saint-Laurent R & L Bernatchez (1999). Isolation and characterization of microsatellite loci in the walleye (*Stizostedion vitreum*), and cross-species amplification within the family Percidae. *Mol. Ecol.* 8: 1961-1963. IF = 5.84.
- 3. **Wirth T**, Oggier P & B Baur (1999). Effect of road width on dispersal and genetic population structure in the land snail *Helicella itala*. *J. Nat. Conserv.* 8: 23-29. IF = 1.83.
- 2. **Wirth T**, Leguellec R, Vancassel M & M Veuille (1998). Molecular and reproductive characterization of two sibling species in the European earwig (*Forficula auricularia*). *Evolution* 52: 260-265. IF = 4.66.
- 1. **Wirth T**, Baur A & B Baur (1997). Mating system and genetic variability in the simultaneously hermaphroditic terrestrial gastropod, *Balea perversa* on the Baltic island of Öland, Sweden. *Hereditas* 126: 199-209. IF = 1.07.

→ **Liste complète (chapitres de livres)**

- Auteur de "Dispersion et démographie de *Mycobacterium tuberculosis* dans un contexte de globalisation", dans *Archéologie de la santé, anthropologie du soin*, Édité par Alain Froment et Hervé Guy, La découverte Edition. (2019).
- Auteur de "Globalization and Infectious Diseases" dans *Biodiversity and Evolution*, Edité par Philippe Grandcolas et Marie-Christine Maurel, ISTE Edition - Elsevier (2018).
- Co-auteur (deux auteurs - Lalis A & **Wirth T**), "Mice and Men : an Evolutionary History of Lassa Fever" dans *Biodiversity and Evolution*, Edité par Philippe Grandcolas et Marie-Christine Maurel, ISTE Edition - Elsevier (2018).
- Co-auteur (deux auteurs – Barbier M & **Wirth T**), "The evolutionary history, demography and spread of the *Mycobacterium tuberculosis* complex (MTBC)" dans *Tuberculosis and the Tubercle Bacillus*, 2nd Edition, American Society for Microbiology Press (2018).
- Co-auteur (trois auteurs - Gilabert A, Rasigade JP & **Wirth T**), "Microbes as tracers of past human demography and migrations" dans *Genetics and Evolution of Infectious Diseases*, 2nd Edition, Edité par Michel Tibayrenc, Elsevier (2017).
- Auteur de "Selection and neutralism: pathogens evolution and health biology". Veuille, Portier et Willaime edt, Editions Riveneuve, (2011).
- Co-auteur (deux auteurs - Gilabert A & **Wirth T**), "Elucidating human migration by means of their pathogens" dans *Genetics and Evolution of Infectious Diseases*, Edité par Michel Tibayrenc, Elsevier (2011).
- Co-auteur (deux auteurs – Bunje P & **Wirth T**), "Inferring patterns of migration" dans *Methods in Molecular Biology, Bioinformatics (Volume 1)*, Humana Press (2008).
- Auteur de "Eels phylogenetic relationships and population genetics" dans *The eel (F. Tesch)*, Blackwell, Oxford (2006).

→ Conférencier invité

- Octobre 2018: "From genomes to biology: the power of population studies", Congress of the French Society of Microbiology, Paris, France.
- Août 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.
- Décembre 2017: "*Mycobacterium tuberculosis* Beijing lineage: an emerging pathogen", 37ième réunion interdisciplinaire de Chimiothérapie Anti-Infectieuse, RICAI, Paris, France.
- Mai 2017: "Host-pathogen coevolution" 2ième colloque la microbiologie dans tous ses états, Paris
- Janvier 2017: "Inferring evolutionary history of pathogens based on genome data" at the Leibniz Centre Infection Symposium 2017, "Evolution & Infection", Hamburg, Germany.
- Décembre 2016: "Origin, Spread and Demography of Major Human Bacterial Diseases in a Globalizing World", 8ième édition des Journées Infections Nosocomiales, Lyon Biopôle-FINNOVI.
- Décembre 2016: "Dispersion and demography of *Mycobacterium tuberculosis* in a globalizing world", Colloque International INRAP Archéologie de la Santé, Anthropologie du Soins, Paris, France.
- Mai 2016: Plenary talk "Origin, spread and demography of major human bacterial diseases in a globalizing world" at the 13th International Conference on Molecular Epidemiology and Evolutionary genetics of Infectious Diseases, Antwerp, Belgium.
- Mars 2016: William H. Telfer Endowed Lectureship recipient, University of Pennsylvania, USA.
- Mars 2015: "Evolutionary history and global spread of the *Mycobacterium tuberculosis* Beijing lineage", 11th Congress of the French Society of Microbiology, Institut Pasteur, Paris, France.
- Octobre 2014: "Out of Africa, evolutionary history of the community acquired ST80". SYMPOSTAPH 2014, Lyon, France.
- Juillet 2014: "Coalescence and demogenetical analyses based on full genome data". ESCMID Postgraduate Education Course in Molecular Typing methods for Pathogens, Lyon, France.
- Octobre 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 – IMMEM, Paris.
- Mai 2013: "Micro and macro evolution of the *Mycobacterium tuberculosis* complex" MYCOCLUB Congress, Toulouse.
- Novembre 2012: Conference on bacterial pathogens at the third Darwin Days, Institut Poincaré, Paris.
- Septembre 2012: "Population Genetics: from bacteria to humans". Congress Adaptation, Persistence, Extinction, MNHN/UNESCO, Paris.
- Mars 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.
- Janvier 2012: "Tuberculosis through times" International Conference on Drug Therapy in TB Infection, Edinburgh, Scotland.
- Octobre 2011: "Of bugs and Men: from past migrations to recent epidemics", International Congress, Microorganisms facing their environment. Paris – MNHN/CNRS.
- Janvier 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.

- Juin 2010: "Guns, germs and rats: lessons from Lassa Hemorrhagic fever". Congress of the French Society of Microbiology, Marseille.
- Octobre 2009: "Discovering human history from our bugs: review and perspectives". Congress "Darwin's legacy: New Insights into Human Evolution", University Paris-Diderot, Paris.
- Mai 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.
- Decembre 2009: Chairman and speaker "Evolution and microbial diversity: impact of next generation sequencing", Institut Pasteur, Paris.
- Mai 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.
- Mai 2007: "Sex and virulence in bacteria: empirical evidence and experimental perspectives". VIIIth National Congress of the French Society of Microbiology, Nantes.
- Octobre 2006: "Recent advances in bacterial population genomics". Workshop on microbial systematics, population genetics and epidemiology, Charité Hospital, Berlin.
- Juin 2006: "Bacterial evolution and population genetics: from sex and virulence to human migrations". Après-midi d'Evolution (AME), Natural History Museum, Paris.
- Novembre 2005: "Invasive species and host parasite interactions: the eel paradigm". National University of Ireland, Galway.
- Août 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.
- Mai 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).
- Février 2005: "Eel population genetics: a review". Fourth International Symposium on Ecological Genetics. Antwerp, Belgium.
- Novembre 2004: "Revisiting *Escherichia coli* biology and population genetics". Workshop of the Deutsche Gesellschaft für Hygiene und Mikrobiologie. "Bacterial systematics, Population Genetics and Infection Epidemiology".
- Juillet 2004: Chairman du Symposium "Molecular epidemiology of bacteria". VII International Meeting on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, Valencia, Spain.
- Novembre 2001: "*Escherichia coli* population genetics". Third Workshop on microbial systematics, population genetics and Epidemiology, Berlin.
- Octobre 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-conférences

Conférence ESCMID sur le SARS-Cov-19 (ECCVID) - Septembre 2020. SARS-Cov-2 phylodynamics differentiates the effectiveness of non-pharmaceutical interventions. Top rated abstract.

→ Communications orales (CONFERENCES)

International Conference of the Society for Molecular Biology and Evolution, SMOBE, (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)

➔ **Posters (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 CCFR (2000, Fredericton, New-Brunswick) - XXth International Congress of Entomology (1996, Florence, Italy) – SMBE meetings (1994, Athens, USA).