

I have a background that spans conventional microbiology to genomic techniques, allowing me to apply these skills in food microbiology, environmental risk assessment, control of zoonotic infections and public health.

## CIVIL STATUS

**Personal address:** Via Trento e Trieste, 33, 64100 Teramo TE (Italy).

**Professional address:** IZSAM-NRC-GENPAT, via Campo Boario 64100 Teramo TE (Italy).

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**Professional contact:** +39 0861 3321, [n.radomski@izs.it](mailto:n.radomski@izs.it).

**Citizenship:** French citizen, permanent resident in Canada, resident currently in Italy, living in a common-law union.

**Language:** French (mother tongue), English (read, write, speak), German (notions).

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## DISCIPLINES/SPECIALITY and SPECIFIC SKILLS

Cellular biology, biology of populations and ecology, biology of organisms.

Food microbiology, environmental risk assessments, control of zoonotic infections.

Conventional microbiology, molecular biology, bacterial genomic.

Bacterial genomics, statistics, bioinformatics.

## CURRENT POSITION

Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "Giuseppe Caporale" (IZSAM).

National Reference Centre (NRC) for Whole Genome Sequencing of microbial pathogens: data-base and bioinformatics analysis (GENPAT).

Senior Bioinformatics Expert in Genomics of Microorganisms.

## PROFESSIONAL EXPERIENCES

- |                        |  |
|------------------------|--|
| 2020                   | <b>Senior Bioinformatics Expert in Genomics of Microorganisms</b> - Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "Giuseppe Caporale" (IZSAM), National Reference Centre (NRC) for Whole Genome Sequencing of microbial pathogens: data-base and bioinformatics analysis (GENPAT) - Teramo, Italy:<br><br>Technical support of scientists to analyze next generation sequencing data (NGS) coming from diverse platforms, development of bioinformatics workflows for the NRC platform GENPAT, collaborate in the drafting and presentation of project proposals in response to national and European calls, support the national and international training activities carried out by IZSAM in the field of bioinformatics - A. Di Pasquale (GENPAT-NRC-IZSAM). |
| 2015-20<br>(66 months) | <b>Scientific officer in bacterial genomics</b> - French agency for food, environmental and occupational health and safety (ANSES), Laboratory of food safety (LSAL) - Team genome analysis modelling risk (GAMeR) - Maisons-Alfort, France:<br><br>Implementation of high throughput sequencing, building of Linux network to store and process sequencing data, Linux training for lab teams, bacterial genomic (detection of variants, genetics, <i>de novo</i> assembly, molecular mechanisms of virulence and host adaptation, molecular epidemiology, association study, antimicrobial resistance, mobilome), recruitment and integration of students and colleagues each 6 months (INRA-ANSES), certification to manage research (HDR) – M.Y. Mistou (ANSES-INRAE).         |
| 2015<br>(1 month)      | <b>Teaching assistant</b> - École des ponts ParisTech (ENPC) - Engineering course - Marne-la-Vallée, France:<br><br>Theories in bacterial genomics, using of Linux command-line, setting of programs, execution of programs, organization of successive bioinformatic tasks – F.S. Lucas (LEESU).  |
| 2011-15<br>(43 months) | <b>Postdoctoral fellow</b> - Research institute of McGill university health center (RI MUHC) - Montréal QC, Canada:<br><br>Care and handling of laboratory animals and biosafety level-3 laboratory, installation of software and programs of lab management and statistical analyses, phylogenetic analyses, comparison of sequences and genomes, management of high throughput sequencing, molecular detection and quantification of mycobacterial pathogens during experimental infection, development and application of a bioinformatics pipeline for high-throughput sequencing projects of tuberculosis molecular epidemiology - M.A. Behr (RI MUHC).   |
| 2007-11<br>(39 months) | <b>PhD student</b> - École des ponts ParisTech (ENPC) - Laboratory water environment and urban systems UMR MA-102 (LEESU) - Marne-la-Vallée, France:<br><br>Implementation of bacteriology and molecular biology lab, harmonization of mycobacteriological   |

	isolation methods from environmental sources, development of quantitative real-time PCR methods, genotyping of isolates by Multilocus Sequencing Analysis and genome comparison for molecular target improvement - R. Moilleron, F.S. Lucas (LEESU).
2008-10 (160 hours)	<b>Teaching assistant</b> - Undergraduate degree of biological analysis and biochemistry (ABB) and master of applied microbiology and biology (MAGB) in Paris-Est university (IUT UPEC) and Paris Diderot (Paris-Sud) - Créteil and Orsay, France : In charge of courses and small group teaching on classification, identification and characterization of pathogenic bacteria ( <i>Vibrionaceae</i> , <i>Pseudomonadaceae</i> , <i>Micrococcaceae</i> , <i>Streptococcaceae</i> , <i>Mycobacteriaceae</i> , <i>Nisseriaceae</i> ) for undergraduate and master students - F. Odelin (IUT UPEC), C. Rousseau (IUT UPEC), C. Sola (Paris-Sud).
2010 (3 months)	<b>PhD training</b> - Virginia polytechnic institute (VirginiaTech) - Department of biology - Blacksburg VA, USA : Study of non-tuberculous mycobacteria sources in a watershed of Virginia by quantitative real-time PCR, writing of book chapter - J.O. Falkinham III (VirginiaTech) - R. Moilleron, F.S. Lucas (Lab. Water Environment and Urban Systems).
2007 (6 months)	<b>Master training</b> - French agency of food safety (AFSSA) - Unit of bacterial zoonoses (UZB) - Maisons-Alfort, France: Genetic diversity of <i>Mycobacterium avium</i> subsp. from human and animal origin by Variable Number of Tandem Repeats and Mycobacterial Interspersed Repetitive Unit (VNTR-MIRU) and Restriction Fragments Length Polymorphism (RFLP) - M.L. Boschioli (UZB).
2006-07 (6 months)	<b>Project manager</b> - Pasteur Institute of Lille - Center of molecular typing (IPL-CTM) - Lille, France: In charge of audits (Quality and Safety), supervision of project about the typing of <i>Listeria monocytogenes</i> by serotyping, ribotyping and pulsotyping - J.P. Vincent (IPL-CTM).
2006 (6 months)	<b>Bachelor training</b> - Pasteur Institute of Lille - Center of molecular typing (IPL-CTM) - Lille, France: Organization of database management of strains collection of <i>Listeria monocytogenes</i> characterized by serotyping, ribotyping, and pulsotyping - J.P. Vincent (IPL-CTM).
2005 (2 months)	<b>Laboratory technician</b> - French agency of food safety (AFSSA) - Laboratory of food safety (LSAL) (Boulogne sur Mer, France): In charge of analyses: total volatile acid base, Kjeldhal, standardized microbiology, Random Amplified Polymorphism DNA (RAPD), Polymerase Chain reaction (PCR) - G. Bourdin (LSAL).
2005 (2 months)	<b>Undergraduate student</b> - French agency of food safety (AFSSA) - Laboratory of food safety (LSAL) (Boulogne sur Mer, France): Study of <i>Listeria monocytogenes</i> growth in salmon by challenge test at different temperatures - G. Bourdin (LSAL).
2002-04 (2 years)	<b>Hygienist technician</b> - Pasteur institute of Lille, service of microbiology and food hygiene (ILP-SERMHA) - Caen, France: In charge of sampling (water and food), Hazard Analyses Critical Control Point (HACCP) audits, interpretation of microbiological analyses, and control of food oils quality - J.P. Vincent (IPL-SERMHA).
2002 (2 months)	<b>Undergraduate training</b> - University of Caen – Team of research in physico-chemistry and biotechnology (ERPCB) - Caen, France: Growth study of <i>Pseudomonas putida</i> and development of sugar and intermediate acid elements by high performance liquid chromatography HPLC - D. Corrolier (ERPCB).

## DIPLOMA

2023	<b>Registered in the Register of the Order of Biologists of Lazio and Abruzzo</b> (Rome, Italy): National Federation of Orders of Biologists (FNBO), Order of Biologists of Lazio and Abruzzo (17/04/2023, n. AA_100199).
2020	<b>Certification to manage research</b> in sciences of life - University Paris-Est (UPE), Doctoral school agriculture, food, biology, environment, health (ABIES, n°0581), French agency for food, environmental and occupational health and safety (ANSES), Laboratory of food safety (LSAL) - Team genome analysis modelling risk (GAMEr) - Maisons-Alfort, France: Implementation of bacterial genomics - support to public health.
2007-11	<b>PhD</b> in sciences and environmental technologies - Paris-Est university, École des ponts ParisTech (ENPC) (Champs-sur-Marne, France) - UMR MA-102 Laboratory water environment and urban systems (LEESU): Installation of microbiological laboratories, keeping up with bibliography, analytical development and

	application to environmental samples, writing and publication of scientific papers and activity reports, national and inter-national communication in congress, teaching, bacteriology, molecular biology, bioinformatic, parametric and non-parametric tests.
2006-07	<b>Master of Science in Public Health</b> (4 <sup>th</sup> /86), specialized in Quality and Safety of Food and Environment - Health Engineering Institute of Lille - University of Lille (Loos, France) - Health engineering institute of Lille (ILIS): Evaluation of chemical and microbiological risks, Quality, Management, Bibliography.
2004-06	<b>Credential of engineer, bachelor of science</b> (6 <sup>th</sup> /33) and <b>license</b> (9 <sup>th</sup> /34) in biotechnologies and bio-industries - University of littoral in opal cost (ULCO) - University Professional Institute of quality of food and seafood processes (Boulogne-sur-Mer, France): Biosafety level-3 laboratory, microbiological and physico-chemical analyses, molecular biology, fermentation, physical engineering, principal component analyses, predictive models.
2000-02	<b>University diploma</b> (two years' undergraduate study) in biotechnology (10 <sup>th</sup> /28), option food and bio-industries (IAB) - university of Caen - university institute and technology (IUT) in biology (Caen, France): Chemistry, Microbiology, Molecular biology, Physiology, Histology, Basic statistic, Lab work.

## QUALIFICATIONS

2020	<b>Certification to manage research in sciences of life</b> (Paris, France): University Paris-Est (UPE), Doctoral school agriculture, food, biology, environment, health (ABIES, n°0581).
2011-14	<b>Qualified to apply for an assistant professor position in French University</b> (Paris, France): Section 65 Cellular Biology (N°14265227300, February 05, 2014), Section 67 Biology of populations and Ecology (N°12267227300, February 02, 2012), Section 68 Biology of Organisms (N°12268227300, January 26, 2012).
2013	<b>Québec selection certificate</b> (Montreal, Canada): CNP 4122 Assistant of teaching and research at the university (N°C0005780756, April 23, 2013).
2011-15	<b>Certificates care and handling of laboratory animals and biosafety level-3 laboratory</b> (Montreal, Canada): Research institute of McGill university health center (RI MUHC).
2007	<b>Certificate biosafety level-3 laboratory</b> (Maisons-Alfort, France): French agency of food safety (AFSSA).

## OTHER TRAINING

04/12/2025 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training Cybersecurity.
19/11/2025 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training Giornata di studio del Centro di Referenza Nazionale GENPAT.
12-13/11/2025 (2 days)	<b>Seminar</b> (Parma, Italy): EFSA training Workshop on protein safety assessments in food and feed – Alternative methods and approaches.
22-23/10/2025 (2 days)	<b>Seminar</b> (Stockholm, Sweden): ECDC training Genepi-Biotrain, Virtual Training 21: Bacterial strain taxonomy for genomic surveillance.
10/10/2025 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training One Health Award 2025. Nuove Geografie. (not registered)
07/11/2024 (2 days)	<b>Seminar</b> (Teramo, Italy): IZSAM training Giornata di studio del CRN GenPat Genomica e sanità pubblica veterinaria: nuove frontiere e sfide.
12/06/2024 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training La giornata di studio del Laboratorio Nazionale di Riferimento per <i>Listeria monocytogenes</i> .
05/12/2023 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training Giornata di studio sulla Bluetongue.
09-10/11/2023 (2 days)	<b>Seminar</b> (Teramo, Italy): IZSAM training Giornata di studio del Centro di Referenza Nazionale GENPAT.
08/11/2023 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training Il Laboratorio Nazionale di Riferimento per <i>Listeria</i> .
07/11/2023 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training Il Laboratorio Nazionale di Riferimento per <i>Campylobacter</i> .
17/02/2023 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training

	Supporto - la nuova versione del sistema di ticketing online.
01/12/2022 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training La piatta forma del centro di riferimento nazionale GENPAT.
14/11/2022 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training Il Laboratorio Nazionale di Riferimento per <i>Campylobacter</i> .
30/11/2021 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training Giornata di studio del Centro di Referenza Nazionale per Sequenze Genomiche di microrganismi patogeni: banca dati e analisi di bioinformatica (GENPAT).
28/10/2021 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training Il Laboratorio Nazionale di Riferimento per <i>Listeria monocytogenes</i> .
25/10/2021 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training Giornata di studio sulla Brucellosi.
28/09/2021 (1 day)	<b>Seminar</b> (Torino, Italy): IZSTO training Microrganismi patogeni e approccio on health: Il ruolo del laboratorio ufficiale di analisi.
24/06/2021 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training Inquinanti Organici Persistenti Alogenati negli alimenti, nei mangimi e nell'ambiente.
17/06/2021 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training I risultati della ricerca corrente condotta dall'Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise - anno 2020.
27/04/2021 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training Giornata di studio del Centro di Referenza Nazionale per lo studio e l'accertamento delle malattie esotiche degli animali (CESME).
05/04/2021 (7 days)	<b>Seminar</b> (Teramo, Italy): IZSAM training Verso horizon Europe: Scenarion e prospettive del nuovo programma Europeo per la ricerca e l'innovazione - Moduli 2 e 3.
04-12/2021 (9 months)	<b>Seminar</b> (Teramo, Italy): IZSAM training The eLearning course for Food Microbial Bioinformatician - Module 3: Core-competence pathway.
13/04/2021 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training Verso horizon Europe : Scenario e prospettive del nuovo programma Europeo per la ricerca e l'innovazione - Modulo 1.
03-09/2021 (6 months)	<b>Seminar</b> (Teramo, Italy): IZSAM training The eLearning course for Food Microbial Bioinformatician - Module 1: Microbiological pathway.
21/12/2020 (1 day)	<b>Seminar</b> (Teramo, Italy): IZSAM training Il Centro per la Biologia delle Acque si racconta.
14-16/12/2020 (3 days)	<b>Seminar</b> (Teramo, Italy): IZSAM training Workshop Annuale del Laboratorio Nazionale di Riferimento per l'Antibioticoresistenza e del Centro di Referenza Nazionale per l'Antibioticoresistenza 2020.
2018 (4 days)	<b>Python language</b> (Bordeaux, France): CNRS Formation Programing principles, iterative- and object-oriented coding, collaborative coding, BioPython applications.
2018 (3 days)	<b>Database and SQL language for non-informatics professionals</b> (Paris, France): ORSYS Database modelling, SQL principles and functions, SQL developments and queries.
2017-2018 (6 days)	<b>Statistic and R language</b> (Maisons-Alfort, France): École de l'ADN Advanced methods of data management, complex graphical representations.
2015-2019 (6 days)	<b>Molecular phylogeny</b> (Maisons-Alfort, France): BioSciences and Co Evolution models, maximum likelihood, Bayesian models, molecular clock.
2017 (3 days)	<b>PhD student training</b> (Maisons-Alfort, France): Adoc Mètis Risk analysis, management of co-management, PhD comities, science integrity.
2017 (2 days)	<b>Biological risk, flux and warning</b> (Maisons-Alfort, France): ANSES Classification of risks in laboratory, urgency procedures, fire fighting, rescue.
2006-2019	<b>Bioinformatics</b> : data management (Bash, Python), database (SQL, XML), web site (Dreamweaver, Nvu), taxonomy (Bionumerics, BioEdit, MEGA, Best, MrBayes, RAxML, IQ-Tree), statistics (R, JMP,



(14 years) Statgraphics), molecular primer and probe design (AllelID, Beacon designer), genome comparison (SPAdes, MinH, MeDuSa, GapCloser, FastQC, Integrated Genome viewer, Burrows-Wheeler Aligner, Bowtie 2, Genome Analyser Tool Kit, Picard, Samtool, UnifiedGenotyper, HalotypeCaller, MycoHit).

## RISK ASSESSMENT

**2025 EFSA talent pool** (Parma, Italy): Scientific Officer in Molecular Biology - EFSA/X/AD/2024/06 (valid until 31/12/2026).

**2025 EFSA expert contract** (Parma, Italy): Member (since 18/07/2025) of EFSA Pesticides and Micro-organisms Meetings (WG/U/PREV/2011/03) in the Pesticide peer Review (PREV) to study applications for approval of microbial active substances as pesticides (amending Regulation (EU) No 283/2013 as regards the information to be submitted for active substances and the specific data requirements for micro-organisms).

**2024 EFSA expert contract** (Parma, Italy): Chair (since 21/07/2025) and Member (since 02/01/2024) of the EFSA Microbial Pesticides Scientific Panel (WG/U/PREV/2023/03-WG-PREV) in the Pesticide peer Review (PREV) Unit to study applications for approval of microbial active substances as pesticides (amending Regulation (EU) No 283/2013 as regards the information to be submitted for active substances and the specific data requirements for micro-organisms).

**2024 EFSA shortlisted expert** (Parma, Italy): Membership of the Scientific Panels and the Scientific Committee - EFSA/E/2023/01 (valid until 30/06/2029).

**2023 EFSA shortlisted expert** (Parma, Italy): Scientific and Technical Support - Various Scientific and Communication Profiles - EO/EFSA/2022/01 (valid until 23/10/2027).

**2021-2022 EFSA expert contract** (Parma, Italy): European project related to the EFSA call for scientific and technical support in the areas of whole genome sequence analysis (EO/EFSA/SCIENCE/2020/01) aiming at developing an algorithm to define relationship between single linkages thresholds and pairwise distances thresholds in the framework of bacterial outbreak investigation based genomic data (contract # CT06BIOCONTAM).

**2021 EFSA shortlisted expert** (Parma, Italy): Scientific and Technical Support - Various Scientific Profiles - EO/EFSA/2020/01 (valid until 25/03/2024).

## CONCEPTION, REALIZATION AND MANAGEMENT OF RESEARCH PROJECTS

**2025-2027 Research program** (Teramo, Italy): Current research project (GENPAT-IZSAM) related to the project 'machine learning based on genomic data to predict categorical phenotypes by classification and continuous phenotypes by regression' (GEPREDi) aiming at developing analytical workflows to train machine learning models and predict categorical and numerical phenotypes based on genomic data such like genes, alleles, variants, kmers (grant # IZS 06/24 RC) - Conception, submission and realization - Bioinformatics workflows and dashboards about genomics-based analyses of virus and bacteria (1 Article).

**2020-2023 Research program** (Teramo, Italy): National project (GENPAT-IZSAM) related to the project 'Livestock Environment Opendata' (LEO) aiming at bringing together in a single digital database all the information relating to the livestock sector in Italy in order to support and improve the quality of livestock production while respecting animal welfare and the environment through accessible information facilitating exchange, sharing and transparency in the livestock supply and food chain (LEO grant # MAFAATE219) - Conception, submission and realization - Bioinformatics workflows and dashboards about genomics-based analyses of SARS-Cov2, *Salmonella* and *Listeria* (7 Articles).

**2020-2022 Research program** (Maisons-Alfort, France): European collaboration (several countries) related to the project 'assessing determinants of the non-decreasing incidence of *Salmonella*' (ADONIS, one health european joint project (EJP), grant #77380) - Conception, submission and realization - Association study to identify genetic mutations explaining *Salmonella* increasing in Europe since 2014 (1 Article).

**2018-2020 Research program** (Maisons-Alfort, France): European collaboration (several countries) related to the project 'risk and disease burden of antimicrobial resistance' (RaDAR, one health european joint project (EJP), grant #773830) - Participation to conception and realization - Exhaustive database of plasmids completely assembled, description of bacterial plasmid populations (1 Article).

**2016-2019 Research program** (Maisons-Alfort, France): National collaboration (ANSES and INRA) related to the project 'Automatic method of bacterial typing by pangenome and coregenome variants from high throughput sequencing' (grant #Typautobac) - Conception, submission and realization - Association study and gene ontology at the pangenome scale, deciphering of host adaptation of *Salmonella* based on high throughput sequencing data (2 Articles).

**2015-2019 Research program** (Maisons-Alfort, France): European collaboration (several countries) of working package 4 and 7 funded by the project 'collaborative management platform for detection and analyses of re-emerging and foodborne outbreaks in Europe' (COMPARE, Horizon 2020, grant #643476) -

	Participation to conception and realization - Installation of high throughput sequencing and bacterial genomics, tool development for <i>de novo</i> assembly (ARTwork), tool development for variant calling (iVARcall2), installation LINUX network for analysis and data storage, LINUX training for colleagues, application to <i>Salmonella</i> , <i>Listeria</i> , <i>Clostridium</i> , <i>Bacillus</i> and <i>Staphylococcus</i> (9 Articles).
2014-15 (14 months)	<b>Postdoctoral fellowship</b> (Montréal, Canada): Institutional collaboration (several laboratories from the institute) funded by the research institute of McGill university health center (RI MUHC) (9 000 \$ CAN net) and health research funding of Québec (FRQS) (30 000 \$ CAN net) in the framework of the project 'Tuberculosis in Nunavik' (grant #29836) - Participation to conception, submission and realization - Installation et development of analyses in bacterial genomics, evolution deciphering of <i>Mycobacterium tuberculosis</i> causing outbreaks in the Nunavik region of Canada (2 Articles).
2011-13 (29 months)	<b>Postdoctoral fellowship</b> (Montréal, Canada): Institutional collaboration (several laboratories from the institute) funded by the research institute of McGill university health center (RI MUHC) (50 250 \$ CAN net) and health research funding of Québec (FRQS) (60 000 \$ CAN net) in the framework of the project 'Tuberculosis in Nunavik' (grant #26274) - Participation to conception, submission and realization - Installation and development of analyses in bacterial genomics, development of tools for diagnosis of Crohn's disease, deciphering of virulence loss of <i>Mycobacterium tuberculosis</i> (2 Articles).
2007-11 (39 months)	<b>PhD and teaching fellowships</b> (Marne-la-Vallée, France): National collaboration (LEESU, ENPC, Eau de Paris, APHP) funded by 'École des ponts ParisTech' (ENPC) (65 139 € net) and Paris-Est university of Créteil (UPEC) (6 640 € net) in the framework of the project 'Sources of non-tuberculosis mycobacteria in watersheds' supported by the interdisciplinary research program of water and environment of watersheds of Seine river (PIREN-Seine), the observatory of urban pollutants (OPUR) and the city of Paris (grant #CRECEP-STEa) - Conception, submission and realization - Development of bacteriological and molecular methods, identification of sources of <i>Mycobacterium</i> in the environment, comparison of genomes to improve molecular targets (5 Articles).
2007 (6 months)	<b>Master training fellowship</b> (Maisons-Alfort, France): National collaboration (INRA et AFSSA) funded by the 'veterinary network of laboratories researching into improved diagnosis and epidemiology of mycobacterial diseases' (VENoMYC), the INRA and AFSSA (grant #AIP P00297) - Realization - Description of genetic diversity by conventional molecular typing, association of host specificity of <i>Mycobacterium avium</i> (1 Article).

## COLLABORATIONS AND SCIENTIFIC PARTNERSHIPS

Period	Research partnerships	Partner laboratories	Agreement building
2015-2019 (5 years)	Partnership to develop analyses in genomics applied on <i>Salmonella</i> , <i>Listeria</i> , <i>Staphylococcus</i> , <i>Bacillus</i> and <i>Clostridium</i>	INRA-ANSES (M.Y. Mistou) INRA (M. Mariadassou) INRA (H. Chiapello) INRA (P. Velge)	Agreement ANSES-INRA Typautobac (Automatic method of bacterial typing by pangenome and coregenome variants from high throughput sequencing)
2011-2015 (5 years)	Partnership to study human outbreaks of <i>Mycobacterium tuberculosis</i> in Nunavik	RI MUHC (M.A. Behr, M.B. Reed) VirginiaTech (J.O. Falkinham) Paris Sud (C. Sola)	Research institute of McGill university health center (RI MUHC) and health research funding of Québec (FRQS)
2007-2011 (5 years)	Partnership to study sources of non-tuberculous mycobacteria in watersheds	LEESU (F. Lucas, R. Moilleron) Eau de Paris (L. Moulin) CNR Mycobacteria (E. Cambau) AFSSA-UZB (M.L. Boschirolì)	Interdisciplinary research program of water and environment of watersheds of Seine river (PIREN-Seine) and observatory of urban pollutants (OPUR)

## TRAINEE SUPERVISOR

Period	Level	Mos.	Student	CTZ	Subject (School - University)	Rate (%)	Articles
2021-22	PhD	24	Madeleine De Sousa Violante	FR	Phylogeny developments (Doctoral school ABIES)	100	2
2020	Master	6	Lilian Yang Crosson	FR	Association study with <i>Salmonella</i> (Biology informatics - Paris Diderot)	100	0
2017-2019	PhD	36	Méryl Vila Nova	FR	Bacterial genomics (Doctoral school ABIES)	100	1
2019	Master	6	Marie-Noel Mansour	LB	Phylogeny of <i>Salmonella</i> (Food chemistry - St. Joseph of Beirut)	100	0
2018	Master	6	Kévin La	FR	Associations study of genomes (Biology informatics - Paris Diderot)	100	1

2018	PhD	12	Lena Frisch	DE	Bioinformatic and writing (Doctoral school ABIES)	20	1
2017-2018	PhD	48	Abakabir-Mahamat	TD	Bioinformatics applied on <i>Clostridium</i> (Doctoral school ABIES)	40	1
2017-2018	PhD	36	Yann Sévellec	FR	Bioinformatics applied on <i>Salmonella</i> (Doctoral school ABIES)	40	3
2016	Master	6	Méryl Vila Nova	FR	Algorithms of fixed variants detection (Genomics Inform. Math. Health - Paris Saclay)	100	1
2015	UG	1	Audrey Artignan	FR	Literature about evolution rates (Human genetics - Univ. London College)	100	0
2013-14	PhD	24	Robyn S. Lee	CA	Phylogeny and identification of SNPs (Epidemiology - University McGill)	20	2
2014	Master	6	Trevor Tarakjian	CA	High throughput data management (Epidemiology - University McGill)	15	0
2013	Master	6	Andrei Dan	RO	Detection methods of <i>Leifsonia</i> (Epidemiology - University McGill)	40	0
2012	UG	3	Jeremy Dabor	CA	Mycobacterial DNA extraction (Epidemiology - University McGill)	10	0
2011	Medicine	24	Louis Kreitmann	FR	<i>In vitro</i> analyses in laboratory (Medicine - University of Lille)	10	1
2010	Master	6	Yacine Boudali	AG	Quantification of <i>Mycobacterium</i> (Sciences of Env. - University of Créteil)	80	0
2009	Master	6	Laetitia Betelli	FR	Quantification of <i>E. coli</i> and <i>Enterococcus</i> (Sciences of Env. - University of Créteil)	20	1

## RESEARCH LEADING

## Co-organisation of seminar

Period	Laboratory - Institute	Subject	Frequency
2015-19	GAMeR - LSAL - ANSES	Debates around bioinformatics and genomics (DEBUG) open inside and outside the agency	3-4 month
2011-15	Behr Lab - RI MUHC	Laboratory seminars about results of research units from the institute	2-3 months
2007-11	LEESU - UMR MA102	PhD spokesman in charge of PhD seminars and reports for lab conceal	3-4 months

## Membership of learned societies

French society of bioinformatics (SFBI).  
 American chemistry society (ACS).  
 French society of microbiology (SFM).  
 French society of mycobacteriology (Mycoclub).  
 French association of microbial ecology (AFEM).

## Organization of PhD comities

## Members of two PhD comities of the PhD student Méryl Vila Nova (2017 and 2018) :

Pr. Hélène Chiapello (INRA, Unit of applied mathematics and informatics, Toulouse).  
 Arnaud Felten (ANSES, Genome analysis modelling risk, Maisons-Alfort).  
 Valentin Loux (INRA, Platform of bioinformatics MIGALE, Jouy-en-Josas).  
 Pr Philippe Velge (INRA, Infection study and public health, Nouzilly).  
 Pr Daniel Wilson (John Radcliffe Hospital, Microbiology department, Oxford).

## Member of PhD jury

Year	Role	PhD student	University	PhD subject
2019	Examiner	Damien Richard	University of La Réunion	Genomic adaptation of <i>Xanthomonas citri</i> pv. <i>citri</i>
2018	Examiner	Franck Cerutti	University Toulouse III - Paul Sabatier	Evolutionary dynamics of <i>Listeria monocytogenes</i>

## Member of PhD committees

Period	Number	PhD student	University	PhD subject
2017-2018	2	Maëlllys Kevin	Paris-Est (UPE)	Genomic diversity of <i>Francisella tularensis</i> from human and animal origins

## Reviews in peer-reviewed journals

**Microbial Genomics** (1 review since 2019).  
**Frontiers in Microbiology** (2 reviews since 2018).  
**Infection, Genetics and Evolution** (1 review since 2015).  
**Environmental Science and Technology** (1 review since 2014).  
**Diagnostic Microbiology and Infectious Disease** (2 reviews since 2014).  
**PloS One** (5 reviews since 2013).  
**Journal of Clinical Microbiology** (12 reviews since 2012).  
**Applied and Environmental Microbiology** (4 reviews since 2011).  
**Journal of Environmental Science and Health** (2 reviews since 2011).  
**International Journal of Systematic and Evolutionary Microbiology** (2 reviews since 2011).  
**Letters in Applied Microbiology** (5 reviews since 2011).  
**Journal of Applied Microbiology** (2 reviews since 2011).  
**Journal of Medical Microbiology**, section Clinical Microbiology and Virology (2 reviews since 2010).

## SHORT-TERM RESIDENCE IN RESEARCH LABORATORY

**2010 (3 months)** **International Mobility Fellowship** (Marne-la-Vallée, France): International collaboration (École des ponts ParisTech and Virginia polytechnic institute) funded by the university Paris-Est(UPE) Paris-Est (5 000 € net) in the framework of the project 'Sources of non-tuberculous mycobacteria in watersheds' - Conception, submission and realization - Technological transfer of a molecular method to quantify *Mycobacterium* in environment (1 Book chapter).

## PARTICIPATION TO CONGRESSES AS LISTENER

Genome microbial identifier #14 (GMI): September 04 to 06, 2024 in Barcelona (Spain).  
 Printemps des territoires: June 6, 2019 in Paris (France).  
 Genome microbial identifier #11 (GMI): March 18 to 20, 2018 in Geneva (Sutherland).  
 Pathobiome 2018: March 18 to 20, 2018 in Ajaccio (France).  
 Genome microbial identifier #10 (GMI): May 15 to 17, 2017 in Cabo San Lucas (Mexico).  
 Genome microbial identifier #11 (GMI) and Food and Agriculture Organization: April 24 to 27, 2016 in Rome (Italia).  
 Pathobiome 2015: June 24 to 26, 2015 in Maisons-Alfort (France).

## TEACHING

Year	Location (project)	Level	Nature	Discipline	Hour
2024	Tunis (FiraBiot/WOAH)	Professional	practical work	Coding in bioinformatics	35
2020	Teramo (IZSAM/LEGO)	Master	practical work	Coding in bioinformatics	24
2015	Champs (ENPC)	Engineering	tutorial	Bioinformatic workflow	16
2010	Créteil (IUT)	Undergraduate	tutorial	Medical microbiology	64
2009	Champs (ENPC)	Master	lecture	Analytical tools in epidemiology	3
2009	Créteil (IUT)	Undergraduate	practical work	General microbiology	64
2008	Créteil (IUT)	Undergraduate	practical work	General microbiology	30

## VALORIZATION OF RESEARCH

### International publications

Khemiri H., Lorusso A., Ayouni K., **Radomski N.**, Khaled M.B., Mangone I., Di Pasquale A., Cammà C., Ben Fraj I., Mekki N., Meftah K., Souiai O., Ben Mustapha I., Rekaya S., Touzi H., Sadraoui A., Meddeb Z., Hogga N., Smaoui H., Barbouche M.R., Ouederni M., Gdoura M., Triki H. and S. Haddad-Boubaker. Intra-host diversity of SARS-CoV-2 in children with long-term and short-term excretion in nasopharyngeal samples. 2025, BMC Infectious Diseases, 25(1): 1491. doi: 10.1186/s12879-025-11759-9 (IF 2024: 3.0).

de Ruvo A., Castelli P., Bucciacchio A., Mangone I., Mixão V., Borges V., **Radomski N.** and Di Pasquale A. cgDist: An Enhanced Algorithm for Efficient Calculation of pairwise SNP and InDel differences from Core Genome Multilocus Sequence Typing. 2025, bioRxiv, doi: 10.1101/2025.10.16.682749 (preprint server).

de Ruvo A., Castelli P., Bucciacchio A., Mangone I., Mixão V., Borges V., **Radomski N.** and Di Pasquale A. Supplementary Data of "cgDist: An Enhanced Algorithm for Efficient Calculation of pairwise SNP and InDel differences from Core Genome Multilocus Sequence Typing". 2025, Zenodo, doi: 10.5281/zenodo.17285517 (repository server).

Mixão V., Pinto M., Brendebach H., Sobral D., Dourado Santos J., **Radomski N.**, Majgaard Uldall A.S., Bomba A., Pietsch M., Bucciacchio A., de Ruvo A., Castelli P., Iwan E., Simon S., Coipan C.E., Linde J., Petrovska L., Sommer Kaas R., Grimstrup Joensen K., Holtsmark Nielsen S., Kiil K., Lagesen K., Di Pasquale A., Gomes J.P., Deneke C., Tausch S.H. and Borges V. Multi-country and intersectoral assessment of cluster congruence between pipelines for genomics surveillance of foodborne pathogens. 2025, Nature Communications, 16(3961): 1-27, doi: 10.1038/s41467-025-59246-8 (IF 2023: 14.7).



- Puglia I., Caporale M., Mangone I., Petrova T., Castelli P., **Radomski N.**, De Ruvo A., Di Pasquale A. and Lorusso A. Analysis of zoonotic mutations of avian influenza viruses. 2024, Zenodo, doi: 10.5281/zenodo.14024885 (preprint server).
- Mixão V., Pinto M., Brendebach H., Sobral D., Santos J.D., **Radomski N.**, Majgaard Uldall A.S., Bomba A., Pietsch M., Bucciachio A., de Ruvo A., Castelli P., Iwan E., Simon S., Coipan C.E., Linde J., Petrovska L., Sommer Kaas R., Grimstrup Joensen K., Holtsmark Nielsen S., Kiil K., Lagesen K., Di Pasquale A., Gomes J.P., Deneke C., Tausch S.H. and Borges V. Multi-country and intersectoral assessment of cluster congruence between different bioinformatics pipelines for genomics surveillance of foodborne bacterial pathogens. 2024, medRxiv, doi: 10.1101/2024.07.24.24310933 (preprint server).
- De Ruvo A., De Luca A., Bucciachio A., Castelli P., Di Lorenzo A., **Radomski N.** and Di Pasquale A. SPREAD: Spatiotemporal Pathogen Relationships and Epidemiological Analysis Dashboard. 2024, Veterinaria Italiana, 60(4): 1-13, doi 10.12834/VetIt.3476.23846.1 (IF 2021: 1.434).
- Castelli P., De Ruvo A., Bucciachio A., D'Alterio N., Cammà C., Di Pasquale A. and **Radomski N.** Harmonization of supervised machine learning practices for efficient source attribution of *Listeria monocytogenes* based on genomic data. 2023, BMC Genomics, 24(560): 1-19, doi: 10.1186/s12864-023-09667-w (IF 2022: 4.558).
- De Sousa Violante M., Michel V., Romero K., Bonifait L., Baugé L., Perrin-Guyomard A., Feurer C., **Radomski N.**, Mallet L., Mistou M.Y. and Cadel-Six S. Tell me if you prefer bovine or poultry sectors and I'll tell you who you are: Characterization of *Salmonella enterica* subsp. *enterica* serovar Mbandaka in France. 2023, Frontiers in Microbiology, 14(1): 1-9, doi: 10.3389/fmicb.2023.1130891 (IF 2022: 6.064).
- Di Lorenzo A., Mangone I., Colangeli P., Cioci D., Curini V., Vincifori G., Mercante M. T., Di Pasquale A., **Radomski N.** and Iannetti S. One health system supporting surveillance during COVID-19 epidemic in Abruzzo region, southern Italy. 2023, One Health, 16(100471): 1-9, doi: 10.1016/j.onehlt.2022.100471 (IF 2022: 8.280).
- De Sousa Violante M., Podeur G., Michel V., Guillier L., **Radomski N.**, Lailier R., Le Hello S., Weill F.X., Mistou M.Y. and Ludovic M. A retrospective and regional approach assessing the genomic diversity of *Salmonella* Dublin. 2022, NAR Genomics and Bioinformatics, 4(3): 1-10, doi.org/10.1093/nargab/lqac047 (IF 2022: under evaluation).
- Félix B., Sevellec Y., Palma F., Douarre P.E., [...], **Radomski N.** [...], Leblanc J.C., Guillier L. and Roussel S. A European-wide dataset to uncover adaptive traits of *Listeria monocytogenes* to diverse ecological niches. 2022, Scientific Data, 9(1): 1-12, doi: 10.1038/s41597-022-01278-6 (IF 2020: 6.444).
- Palma F., Mangone I., Janowicz A., Moura A., Chiaverini A., Torresi M., Garofolo G., Criscuolo A., Brisse S., Di Pasquale A., Cammà C. and **Radomski N.** *In vitro* and *in silico* parameters for precise cgMLST typing of *Listeria monocytogenes*. 2022, BMC Genomics, 23(235): 1-24, doi: 10.1186/s12864-022-08437-4 (IF 2021: 3.969).
- Di Pasquale A., **Radomski N.**, Mangone I., Calistri P., Lorusso A. and Camma C. SARS-CoV-2 surveillance in Italy through phylogenomic inferences based on Hamming distances derived from pan-SNPs, -MNPs and -InDels. 2021, BMC Genomics, 22(1): 782, doi: 10.1186/s12864-021-08112-0 (IF 2020: 3.969).
- Di Pasquale A., **Radomski N.**, Mangone I., Calistri P., Lorusso A. and Camma C. SARS-CoV-2 surveillance in Italy through phylogenomic inferences based on Hamming distances derived from functional annotations of SNPs, MNPs and InDels. 2021, medRxiv, doi: 10.1101/2021.05.25.21257370 (preprint server).
- Palma F., **Radomski N.**, Guérin A., Sévellec Y., Félix B., Bridier A., Soumet C., Roussel S. and L. Guillier. Genomic elements located in the accessory repertoire drive the adaptation to biocides in *Listeria monocytogenes* strains from different ecological niches. 2021, Food Microbiology, 103757(1): 1-11, doi: 10.1016/j.fm.2021.103757 (IF 2021: 5.516).
- Bonis M., Felten A., Payraud S., Dijoux A., Mallet L., **Radomski N.**, Mistou M.Y., Firmesse O., Hennekinne J.A. and S. Herbin. Comparative phenotypic, genotypic and genomic analyses of *Bacillus thuringiensis* associated with foodborne outbreaks in France. 2021, PLoS ONE, 16(2): e0246885, doi: 10.1371/journal.pone.0246885 (IF 2020: 6.220).
- Mansour M.N., Yaghi J., El Khoury A., Felten A., Mistou M.Y., Atoui A. and **N. Radomski N.** Prediction of *Salmonella* serovars isolated from clinical and food matrices in Lebanon and genomic-based investigation focusing on Enteritidis serovar. 2020, International Journal of Food Microbiology, 333(16): 108831, doi: 10.1016/j.ijfoodmicro.2020.108831 (IF 2019: 4.187).
- Douarre P.E., Mallet L., **Radomski N.**, Felten A. and M.Y. Mistou. Analysis of COMPASS, a new comprehensive plasmid database revealed prevalence of multireplicon and extensive diversity of IncF plasmids. 2020, Frontiers in Microbiology, 11(483): 1-15, doi: 10.3389/fmicb.2020.00483 (IF 2018: 4.193).
- Palma F., Brauge T., **Radomski N.**, Mallet L., Felten A., Mistou M.Y., Brisabois A., Guillier L. and G. Midelet-Bourdin. Dynamics of mobile genetic elements of *Listeria monocytogenes* persisting in ready-to-eat seafood processing plants in France. 2020, BMC Genomics, 21(1): 130, doi: 10.1186/s12864-020-6544-x (IF 2017: 3.730).

Vila Nova M, Durimel K., La K., Felten A., Bessi res P., Mistou M.Y., Mariadassou M. and **N. Radomski**. Genetic and metabolic signatures of *Salmonella enterica* subsp. *enterica* associated with animal sources at the pangenomic scale. 2019, BMC Genomics, 20(1): 814, doi: 10.1186/s12864-019-6188-x (IF 2017: 3.730).

**Radomski N.** †, Cadel-Six S. † († **equal contribution**), Cherchame E., Felten A., Barbet P., Palma F., Mallet L., Le Hello S., Weill F.X., Guillier L. and M.Y. Mistou. A simple and robust statistical method to define genetic relatedness of samples related to outbreaks at the genomic scale - Application to retrospective *Salmonella* foodborne outbreak investigations. 2019, Frontiers in Microbiology, 10(2413): 1-13, doi: 10.3389/fmicb.2019.02413 (IF 2017: 4.019).

Abakabir Mahamat A., **Radomski N.**, Delannoy S., Djellal S., Lenegr te M., Hadjab K., Fach P., Hennekinne J.A., Mistou M.Y. and O. Firmesse. Large-scale genomic analyses and toxinotyping of *Clostridium perfringens* implicated in foodborne outbreaks in France. 2019, Frontiers in Microbiology, 10(777): 1-14, doi: 10.3389/fmicb.2019.00777 (IF 2017: 4.019).

S vellec Y., Felten A., **Radomski N.**, Granier S.A., Le Hello S., Petrovska L., Mistou M.Y. and S. Cadel-Six. Genetic diversity of *Salmonella* Derby from poultry sector in Europe. 2019, Pathogens, 8(2): piiE46, doi: 10.3390/pathogens8020046 (IF 2019: 3.520).

Fritsch L., Felten A., Palma F., Mariet J.F., **Radomski N.**, Mistou M.Y., Augustin J.C. and L. Guillier. Insights from genome-wide approaches to identify variants associated to phenotypes at pan-genome scale: Application to *L. monocytogenes* ability to grow in cold conditions. 2018, International Journal of Food Microbiology, 291(16): 181-188, doi.org/10.1016/j.ijfoodmicro.2018.11.028 (IF 2017: 3.451).

S vellec Y., M.L. Vignaud, S.A. Granier, R. Lailler, C. Feurer, S.L. Hello, M.Y. Mistou and S. Cadel-Six (acknowledgment L. Guillier and **N. Radomski**). Polyphyletic nature of *Salmonella enterica* serotype derby and lineage-specific host-association revealed by genome-wide analysis. 2018, Frontiers in Microbiology, 9(891): 1-13, doi.org/10.3389/fmicb.2018.00891 (IF 2017: 4.019).

S vellec Y., Granier S.A., **Radomski N.**, Felten A., Le Hello S., Feurer C., Mistou M.Y. and S. Cadel-Six. Complete genome sequence of *Salmonella enterica* subsp. *enterica* serotype Derby, associated with the pork sector in France. 2018, Microbiology Resource Announcements, 7(12): e01027-18, doi: 10.1128/MRA.01027-18 (IF 2017: 1.180).

Felten A., M. Vila Nova, K. Durimel, L. Guillier, M.Y. Mistou and **N. Radomski**. First gene-ontology enrichment analysis based on bacterial coregenome variants: insights into adaptations of *Salmonella* serovars to mammalian- and avian-hosts. 2017, BMC Microbiology, 17(222): 1-20, doi.org/10.1186/s12866-017-1132-1 (IF 2015: 2.960).

Henri C., Leekitcharoenphon P., Carleton H.A., **Radomski N.**, Kaas R.S., Mariet J.F., Felten A., Aarestrup F.M., Smidt P.G., Roussel S., Guillier L., Mistou M.Y. and R.S. Hendriksen. An assessment of different genomic approaches for inferring phylogeny of *Listeria monocytogenes*. 2017, Frontiers Microbiology, 8(2351): 1-13, doi.org/10.3389/fmicb.2017.02351 (IF 2016: 4.076).

Felten A., Guillier L., **Radomski N.**, Lailler R., Mistou M.Y. and S. Cadel-Six. Genome Target Evaluator (GTEvaluator): a workflow exploiting genome dataset to measure the sensitivity and specificity of genetic markers. 2017, PLoS ONE, 12(7): e0182082, doi: 10.1371/journal.pone.0182082 (IF 2015: 4.411).

Lee R.S. †, **Radomski N.** † († **equal contribution**), Proulx J.F., Levade I., Shapiro, B.J., McIntosh F., Soualhia H., Menzies D. and M.A. Behr. Population genomics of *Mycobacterium tuberculosis* in the Inuit. 2015, Proceedings of the National Academy of Sciences of the United States of America, PNAS, 112(44): 13609-13614, doi: 10.1073/pnas.1507071112 (IF 2014: 9.674).

Wang J., McIntosh F., **Radomski N.**, Dewar K., Simeone R., Enninga J., Brosch R., Rocha E.P., Veyrier F.J. and M.A. Behr. Insights on the emergence of *Mycobacterium tuberculosis* from the analysis of *Mycobacterium kansasii*. 2015, Genome Biology and Evolution, 7(3): 856-870, doi: 10.1093/gbe/evv035 (IF 2013: 4.532).

Lee R.S. †, **Radomski N.** † († **equal contribution**), Proulx J.F., Manry J., McIntosh F., Desjardins F., Soualhia H., Domenech P., Reed M.B., Menzies D. and M.A. Behr. Re-emergence and amplification of tuberculosis in the Canadian Arctic. 2015, Journal of Infectious Diseases, pii(jiv011): 1-10, doi: 10.1093/infdis/jiv011 (IF 2013: 5.778).

Domenech P., Rog A., Moolji J., **Radomski N.**, Fallow A., Leon-Solis L., Bowes J., Behr M.A. and M.B. Reed. The origins of a 350-kilobase genomic duplication in *Mycobacterium tuberculosis* and its impact on virulence. 2014, Infection and Immunity, 82(7): 2902-2912, doi 10.1128/IAI.01791-14 (IF 2012: 4.074).

**Radomski N.**, Roguet A., Lucas F.S., Veyrier F.J., Cambau E., Accrombessi H., Moilleron R., Behr M.A. and L. Moulin. *atpE* gene as a new useful specific molecular target to quantify *Mycobacterium* in environmental samples. 2013, BMC Microbiology, 13(277): 1-12, doi: 10.1186/1471-2180-13-277 (IF 2012 : 3.104).

**Radomski N.**, Kreitmann L., McIntosh F. and M.A. Behr. The critical role of DNA extraction for detection of mycobacteria in tissues. 2013, PLoS ONE, 8(10): e78749, doi: 10.1371/journal.pone.0078749 (IF 2012: 3.703).

**Radomski N.**, Betelli L., Moilleron R., Haenn S., Moulin L., Cambau E., [...] and F.S. Lucas. *Mycobacterium* behavior in wastewater treatment plant, a bacterial model distinct from *Escherichia coli* and enterococci. 2011, Environmental Science & Technology, 45(12), 5380-5386, doi: 10.1021/es104084c (IF 2009: 4.630).

**Radomski N.**, Lucas F.S., Moilleron R., Cambau E., Haenn S. and L. Moulin. Development of a real-time qPCR method for detection and enumeration of *Mycobacterium* spp. in surface water. 2010, Applied and Environmental Microbiology, 76(21), 7348-7351, doi: 10.1128/AEM.00942-10 (IF 2009: 3.686).

**Radomski N.**, Cambau E., Moulin L., Haenn S., Moilleron R. and F.S. Lucas. Comparison of culture methods for isolation of nontuberculous mycobacteria from surface waters. 2010, Applied and Environmental Microbiology, 76(11), 3514-3520, doi: 10.1128/AEM.02659-09 (IF 2009: 3.686).

**Radomski N.**, Thibault V.C., Karoui C., de Cruz K., Cochard T., Gutiérrez C., Supply P., Biet F. and M.L. Boschirolì. Genotypic diversity of *Mycobacterium avium* subspecies from human and animal origins, studied by MIRU-VNTR and IS1311 RFLP typing methods. 2010, Journal of Clinical Microbiology, 48(4), 1026-1034, doi: 10.1128/JCM.01869-09 (IF 2009: 4.162).

Midelet-Bourdin G., Copin S., Leleu G. and P. Malle (acknowledgment Céline Sart, Mylène Gobert, **Nicolas Radomski** and Rémi Cappelaere). Determination of *Listeria monocytogenes* growth potential on new fresh salmon preparations. 2010, Food Control, 21(10), 1415-1418, <https://doi.org/10.1016/j.foodcont.2010.03.009> (IF 2010: 2.812).

### National publications

**Radomski N.** The bacterial genomics in support of public health. Certification to manage research (HDR) in sciences of life. Defence : Mars 13, 2020 under supervision of Anne Brisabois and Michel-Yves Mistou - University Paris-Est (UPE), doi: 10.13140/RG.2.2.10547.99362.

(<http://www.nicolas-radomski.net/pdf/HDR-2020-Nicolas-Radomski.pdf>).

**Radomski N.** Sources of non-tuberculous mycobacteria in watersheds. PhD thesis in sciences and techniques in environment. Defence: February 28, 2011 under supervision of Régis Moilleron - University Paris-Est (UPE), doi: 10.13140/2.1.3436.6401.

(<http://www.nicolas-radomski.net/pdf/PhD-2011-Nicolas-Radomski.pdf>).

### Oral communications

‡**Radomski N.** Genomic data-based machine learning for source attribution of foodborne pathogens (EN): Online webinar of Whole-Genome Sequencing for Food Safety (WGSFS 2025): November 20, 2025 through pre-recorded video lectures (Estonia).

‡**Radomski N.** The use of bioinformatics from basic to advanced methods (EN): Consultancy Meeting to Design Linux and Galaxy Workflows for AMR Gene Characterization (Joint FAO/IAEA Center): August 5-7, 2025 through online lectures in Vienna (Austria).

‡**Radomski N.** The GENPAT microbial genomics platform for monitoring and investigating outbreaks (FR): 4<sup>ème</sup> Congrès International, 14<sup>ème</sup> Journée de la Société Algérienne de Microbiologie Clinique (SAMiC): May 31 – June 01, 2025 in Alger (Algeria).

\*‡**Radomski N.**, De Ruvo A., Bucciachio A., De Luca A., Barbasch C.N., Mangone I., Ferrilli M. and Di Pasquale A. How to use large language models and machine learning for improving One Health (EN): 35<sup>th</sup> Congress of the European Society of Clinical Microbiology and Infectious Diseases (ESCMID Global 2025, ME061 - Hall 3): April 11-15, 2025 in Vienna (Austria).

‡de Ruvo A., De Luca A., Bucciachio A., Castelli C., **Radomski N.** and Di Pasquale A. Integrating quasi real-time data analytics in public health: The dual application of SPREAD for surveillance of viruses and bacteria (EN): 9<sup>th</sup> International Conference on Emerging Zoonoses: June 9-12, 2024 in Palermo (Italy).

‡Castelli P., De Ruvo A., Bucciachio A., D'Alterio N., Cammà C., Di Pasquale A., **Radomski N.** Harmonization of supervised machine learning practices for efficient source attribution of *Listeria monocytogenes* based on genomic data (EN): Annual congress of the National Reference Laboratory for *Listeria monocytogenes*: November 08, 2023 in Teramo (Italy).

\*##**Radomski N.** (Chairman) Highly precise cgMLST typing of *Listeria monocytogenes*. 2023: 8<sup>th</sup> Conference on Innovations in Nutrition and Food Science: September 07-08, 2023 in Rome (Italy).

‡**Radomski N.** Microbial genomics analyses at the Italian National Reference Centre. 2022: 23<sup>th</sup> Iran's International Congress of Microbiology: August 30 - September 01, 2022 in Tehran (Iran).

‡**Radomski N.** *In vitro* and *in silico* parameters for precise cgMLST typing of *Listeria monocytogenes*. 2022: Workshop about microbial genome sequencing and genomics analyses in the RAZI Vaccine and Serum Research Institute: September 03 - 04, 2022 in Tehran (Iran).

‡**Radomski N.** SARS-CoV-2 surveillance in Italy through phylogenomic inferences based on Hamming distances derived from pan-SNPs, -MNP and -InDels. 2022: Workshop about microbial genome sequencing and genomics analyses in the RAZI Vaccine and Serum Research Institute: September 03 - 04, 2022 in Tehran (Iran).

- ‡Palma F., Mangone I., Janowicz A., Moura A., Chiaverini A., Torresi M., Garofolo G., Criscuolo A., Brisse S., Di Pasquale A., Cammà C. and **Radomski N.** *In vitro* and *in silico* parameters for precise cgMLST typing of *Listeria monocytogenes*. 2022: Seminar on Whole Genomic Sequencing of microbial pathogens: June 24, 2022 in Teramo (Italy).
- \*Palma F., Mangone I., Janowicz A., Moura A., Chiaverini A., Torresi M., Garofolo G., Criscuolo A., Brisse S., Di Pasquale A., Cammà C. and **Radomski N.** Core genome MLST precision of *Listeria monocytogenes* typing through wet- and dry-lab parameters. 2022: One Health EJP Annual Scientific Meeting: April 11-13, 2022 in Orvieto (Italy).
- \***Radomski N.**, Di Pasquale A. and Cammà C. One Health Structure In Europe For Omics-based Surveillance: ASM Microbe 2022: June 9-13, 2022 in Washington (USA).
- ‡Palma F., Mangone I., Janowicz A., Moura A., Chiaverini A., Torresi M., Garofolo G., Criscuolo A., Brisse S., Pasquale A.D., Cammà C. and **Radomski N.** *In vitro* and *in silico* parameters influencing cgMLST precision for *Listeria monocytogenes* typing (EN): Centro di Referenza Nazionale per Sequenze Genomiche di microrganismi patogeni: banca dati e analisi Bioinformatica: November 30, 2021 in Teramo (Italy).
- \*Palma F., Mangone I., Janowicz A., Moura A., Chiaverini A., Torresi M., Garofolo G., Criscuolo A., Brisse S., Pasquale A.D., Cammà C. and **Radomski N.** *In vitro* and *in silico* parameters for precise cgMLST typing: a guide towards global surveillance of *Listeria monocytogenes* (EN): Annual congress of the National Reference Laboratory for *Listeria monocytogenes*: October 28, 2021 in Teramo (Italy).
- \*Mangone I., **Radomski N.**, Pasquale A.D., Santurbano A., Calistri P., Cammà C. and Maassen K. Refinement of the COHESIVE Information System towards a unified ontology of food terms for the public health organizations (EN): 2<sup>nd</sup> Integrated Food Ontology Workshop, held at JOWO 2021: Episode VII The Bolzano Summer of Knowledge: September 11 to 18, 2021 in Bolzano (Italy).
- \***Radomski N.** Congruence of genomics contents between *Salmonella* Enterica from Lebanon and other countries (EN): Centro di Referenza Nazionale per Sequenze Genomiche di microrganismi patogeni: banca dati e analisi Bioinformatica: November 25, 2020 online.
- ‡**Radomski N.**, Cadel-Six S., Cherchame E., Felten A., Barbet P., Vignaud M.L., Mallet L., Le Hello S., L. Guillier and M.Y. Mistou. A simple and robust statistical method to define genetic relatedness of samples related to outbreaks at the genomic scale - Application to retrospective *Salmonella* foodborne outbreak investigations (EN): One Health European Joint Programme (OHEJP) Webinar on practical use of NGS: April 29, 2020 online.
- Douarre P.E., Mallet L., **Radomski N.**, Felten A. and M.Y. Mistou. Global analysis of beta-lactams resistant plasmids (EN): 15<sup>e</sup> national congress of the French society of microbiology (SFM): September 30 to October 2, 2019 in Paris (France).
- ‡\*Vila Nova M., Durimel K., La K., Felten A., Bessières F., Mistou M.Y., Mariadassou M. and **N. Radomski.** Adaptation to animal sources of *Salmonella enterica* subsp. *enterica* at the pangenomic scale (EN): Food Safety WGS: March 26 to 28, 2019 in Paris (France) and IWBBIO: May 9 to 10, 2019 in Granada (Spain) and JOBIM: July 2 to 5, 2019 in Nantes (France).
- ‡**Radomski N.**, Cadel-Six S., Cherchame E., Felten A., Barbet P., Vignaud M.L., Mallet L., Le Hello S., L. Guillier and M.Y. Mistou. A simple and robust statistical method to define genetic relatedness of samples related to outbreaks at the genomic scale - Application to retrospective *Salmonella* foodborne outbreak investigations (EN): COMPARE General Meeting (Work packages WP4 et WP7): February 27 to March 1, 2019 in Lyngby (Denmark).
- ‡Felten A., Vila Nova M., Durimel K., Guillier L., Mistou M.Y. and **N. Radomski.** Metabolic processes mainly impacted by fixed coregenome variants during adaptations of *Salmonella* serovars to mammalian- and avian-hosts (EN): COMPARE Meeting (Work packages WP4 et WP7): May 22 to 23, 2018 in the Robert Koch institute in Wernigerode (Germany).
- Radomski N.**, Cadel-Six S., Cherchame E., Hello S.L., Guillier L. and M.Y. Mistou. Foodborne outbreak (FBO) investigations: Is there a faster method than growing a tree? (EN): COMPARE General Meeting (Work packages WP4 et WP7): February 28 to March 2, 2018 in Lyngby (Denmark).
- ‡**Radomski N.** Bioinformatics developments: Bacterial genomics in ANSES and first results in COMPARE about *Salmonella* Typhimurium in France (EN): General COMPARE meeting (Work packages WP4 et WP7): March 1 to 2, 2017 in Rotterdam (Netherlands).
- \***Radomski N.** Lee R.S. and M.A. Behr. Evolution inference *in natura* of *Mycobacterium tuberculosis* during a century of transmissions (EN) : Integrative phylogeny of the first congress "Réseau de Systématique / Muséum national d'Histoire naturelle" (R-Syst / MNHN): September 12 to 14, 2015 in Versailles-Grignon (France).
- Radomski N.**, Lee R.S. and M.A. Behr. Evolution of *Mycobacterium tuberculosis* during a century of evolution (EN): DEBUG-5 of the French agency for food, environmental and occupational health and safety: September 10, 2015 in Maisons-Alfort (France).



‡**Radomski N.**, Lee R.S., Proulx J.X., McIntosh F., Soualhine H., Domenech P., Reed M., Menzies D., and M. A. Behr. Diversity and evolution of *Mycobacterium tuberculosis* in Nunavik (EN): International center about tuberculosis in McGill: June 18, 2014 in Montreal (Canada).

‡**Radomski N.** and M.A. Behr. Blinded identification of SNPs by high throughput sequencing of genomes: Description of outbreaks(s) of tuberculosis in Inuit community (EN): International center about tuberculosis in McGill: January 15, 2014 in Montreal (Canada).

‡**Radomski N.** and M.A. Behr. The critical role of DNA extraction for detection of mycobacteria in tissues (EN): First annual day of young researchers from the international center about tuberculosis in McGill: June 19, 2013 in Montreal (Canada).

**Radomski N.** Ecology, Physiology, Evolution, Epidemiology, and interactions host-bacteria of major Actinobacteria pathogens: The mycobacteria (FR): Lab seminar in UMR 7267 Ecology and biology of interactions, Team microbiology of water of Poitiers university: May 14, 2013 in Poitiers (France).

‡**Radomski N.** and M.A. Behr. Quantification of *Mycobacterium avium* subsp. *paratuberculosis* (MAP) in tissues: DNA extraction, real-time PCR versus culture methods (EN) : Fifth annual Canadian meeting on MAP: October 11 to 13, 2012 in Banff (Canada).

**Radomski N.** Ecology, Physiology, Evolution, Epidemiology, and interactions host-bacteria of major Actinobacteria pathogens: The mycobacteria (FR): Lab seminar in UMR 5557 Microbial ecology of Claude Bernard university (FR): May 22, 2012 in Lyon (France).

\***Radomski N.**, Betelli L., Moilleron R., Haenn S., Moulin L., Cambau E., Pruden A., Falkinham III J.O., Rocher V., Gonçalves A. and F.S. Lucas. Sources and behaviours of non-tuberculous mycobacteria in watershed (FR): Congress of the international research program about water of Seine river: February 7 to 9, 2011 in Paris (France).

\*Mouchel J.M., Passerat J., Ouattara K., Servais P., Ayrault S., Priadi-Rianti C., Gourlay C., Uher E., [...], Eurin J., Alliot F., Desportes A., Bourges C., Chevreuil M., Varrault G., Louis Y., Lorgeoux C. and **N. Radomski**. The river across the city: rain weather in Paris (FR): Congress of the international research program about water of Seine river: February 7 to 9, 2011 in Paris (France).

\***Radomski N.**, Haenn S., Moilleron R., Lucas F.L., Cambau E. and L. Moulin. Development of methods to quantify non-tuberculous mycobacteria in water of Seine river by bacteriology and molecular biology (FR): Congress of the international research program about water of Seine river: January 27 to 28, 2010 in Paris (France).

\***Radomski N.**, Thibault V., Karoui C., De Cruz K., Cochard T., Gutiérrez C., Supply P., Biet F. and M.L. Boschirolì. Genetic diversity of *Mycobacterium avium* subsp. from human and animal by MIRU-VNTR et IS1311 RFLP (EN, FR): 30<sup>th</sup> annual congress of the european society of mycobacteriology: July 5 to 8, 2009 in Porto (Portugal) and 11<sup>th</sup> French day of mycobacteriology: October 15 to 16, 2009 in Bandol (France).

**Radomski N.**, Lucas F.S., Cambau E., Moulin L., Haenn S. and R. Moilleron. Study of sources of atypical mycobacteria in watershed of the Seine river in Paris (FR): Congress of the French association of microbial ecology: Methods of culture of uncultivable bacteria: June 16 au 17, 2008 in Banyuls (France).

\*Gourlay-Francé C., Ayrault S., Chevreuil M., Da Silva A., Eurin J., Labadie P., Lucas F., [...], **Radomski N.**, Rocher V., Servais P., Uher E., Varrault G. and J.M. Mouchel. Microbiological and chemical contaminations in the Seine river following an urban water discharge during rain weather (FR): Congress of the international research program about water of Seine river: February 5 to 6, 2009 in Paris (France).

\* Acts of Congress (n = 15). ‡ Invited lectures for international congress (n = 28). # Congress' award (n = 2).

#### Poster communications

de Ruvo A., Castelli P., Bucciacchio A., Mangone I., **Radomski N.** and Di Pasquale A. cgDIST: SNP-like resolution with cgMLST-like computational efficiency (EN): Rapid Applied Microbial Next-Generation Sequencing and Bioinformatic Pipelines in the American Society for Microbiology (ASM): October 13 to 16, 2024 in Washington, D.C. (USA).

De Sousa Violante M., Feurer C., Michel V., Radomski N., Mistou M.Y. and Mallet L. Characterization of the genomic diversity of *S. Typhimurium* and its monophasic variant in France in pig herds (EN): Journées Ouvertes en Biologie, Informatique et Mathématiques (JOBIM): July 5 to 8, 2022 in Rennes (France) and International Symposium *Salmonella* and Salmonellosis (JOBIM): June 20 to 22, 2022 in Saint-Malo (France).

Palma F., Brauge T., **Radomski N.**, M.Y. Mistou, A. Brisabois, L. Guillier and Midelet-Bourdin G. Mobile genetic elements through *Listeria monocytogenes* clonal complexes contaminating seafood-processing plants of ready-to-eat food products in France (EN): COMPARE General Meeting (Work packages WP4 et WP7): February 27 to March 1, 2019 in Lyngby (Denmark).

Vila Nova M., La K., Felten A., Durimel K., Bessieres P., Mistou M.Y., Mariadassou M. and **N. Radomski**. Host adaptations of *Salmonella enterica* subsp. *enterica* serovars deciphered by the first genome wide association study implementing accessory genes and coregenome variants (EN): May 16 to 18, 2018 in Geneva (Switzerland).

\*Felten A., Vila Nova M., Durimel K., Guillier L., Mistou M.Y. and **N. Radomski**. First gene ontology enrichment analysis based on coregenome variants of bacteria: Throughout adaptation of mammalian and avian to *Salmonella*

serovars (EN): Open day in biology, informatics and mathematics (JOBIM) : June 3 to 6, 2017 in Lille (France) and Bioinformatics of algorithms and applications (BiATA): August 1 to 5, 2017 in St. Petersburg (Russia).

\*#**Radomski N.**, Lee R.S., McIntosh F., Domenech P., Reed M., Menzies D. and M.A. Behr. Evolution of *Mycobacterium tuberculosis* in *natura*: Unique case of Nunavik, Québec (EN) : Initiative for global health, University club of McGill: November 3, 2014 in Montreal (Canada).

Felten A., Guillier L., **Radomski N.**, Mistou M.Y., Lailler R. and S. Cadel-Six. Genome Target Selector: Estimation of specificity and sensitivity of molecular markers based on sequences of bacterial genomes (EN): 11<sup>th</sup> International meeting about microbial epidemiological markers (IMMEM XI). Navigation of microbial genomes. Conference ESCMID - ESGEM: March 9 to 12, 2016 in Estoril (Portugal).

\*#Lee R.S., **Radomski N.**, Proulx J.F., Manry J., McIntosh F., Desjardins F., Soualhine H., Domenech P., Reed M., Menzies D. and M.A. Behr. Re-emergence and amplification of tuberculosis in Canadian arctic (EN): Initiative for global health, University club of McGill: November 3, 2014 in Montreal (Canada).

‡Lee R.S., **Radomski N.**, McIntosh F., Desjardins F., Soualhine H., Proulx J.F., Menzies D. and M.B. Behr. The whole genome sequencing reveals multiple TB outbreaks in a Canadian village (EN): The 18<sup>th</sup> conference of union of north America regions "Stronger together to stop TB" from laboratory to clinic: February 27 to March 1, 2014 in Boston (USA).

\*‡Lucas F.S., **Radomski N.**, Roguet A., Cambau E., Moilleron R., Behr M.A. and L. Moulin. The methods of detection to study non-tuberculous mycobacteria in aquatic systems under pressure of global change (EN): Congress EMBO SAME13: September 8 to 13, 2013 in Stresa (Italia).

Moulin L., Haenn S., Dubrou S., Gaillard J.L., **Radomski N.**, Cambau E., Welté B. and M. Joyeux. Study of diversity of atypical mycobacteria from water distribution system (FR): 27<sup>th</sup> annual congress about water in Eau de Paris: February 24 to 28, 2012 in Paris (France).

\***Radomski N.**, Cambau E., Moulin L., Haenn S., Moilleron R. and F.S. Lucas. Detection of non-tuberculous mycobacteria in surface water: Comparison of culture methods (EN, FR): 30<sup>th</sup> annual congress of the european society of mycobacteriology: July 5 to 8, 2009 in Porto (Portugal) and 11<sup>th</sup> French day of mycobacteriology: October 15 to 16, 2009 in Bandol (France).

\*‡Lucas F.S., **Radomski N.**, Cambau E., Moulin L., Haenn S. and R. Moilleron. Quantification of non-tuberculous mycobacteria in surface water (FR): Development of molecular markers: Annual congress of the european society of mycobacteriology: July 5 to 8, 2009 in Porto (Portugal).

\***Radomski N.**, Haenn S., Moilleron R., Lucas F.S., Cambau E. and L. Moulin. Development of molecular biology method for quantification of non-tuberculous mycobacteria in surface water (FR): Congress of the international research program about water of Seine river: February 5 to 6, 2009 in Paris (France).

\* Acts of Congress (n = 8). ‡ Invited lectures for international congress (n = 7). # Congress' award (n = 2).

### Book chapter

van Meer F., van der Velden B. and M. Takeuchi (acknowledgment **Nicolas Radomski**). Artificial Intelligence for food safety – A literature synthesis, real-world applications and regulatory frameworks (2025) Food and Agriculture Organization of the United Nations (FAO), Rome, Italy (Ed.), 88, ISBN 978-92-5-140196-5, doi. 10.4060/cd7242en

**Radomski N.**, Moilleron R., Lucas F.S. and J.O. Falkinham III. Challenges in environmental monitoring of pathogens: Case study in *Mycobacterium avium* (2011) Current Research, Technology and Education Topics in Applied Microbiology and Microbial Biotechnology (In.), A. Méndez-Vilas (Ed.), (2), 1551-1561.

### Patents

Cadel-Six S., Felten A., Fach P., Guillier L., **Radomski N.**, Mistou M.Y. and R. Lailler. ANSES - Food safety laboratory (Unit SEL / Team GAMeR / Platform IdentityPath). Algorithms of specific and sensitive kmer selection at the genomic scale and *in vitro* check of molecular targets by real-time PCR for identification of Salmonella serovars. 2018 (under review).

### Awards

**2014** **Congress price** (Montreal, Canada): International center of tuberculosis in McGill: (Oral, 18/06/2014) and initiative for global health (Poster, 03/11/2014).

**2012** **PhD thesis classified among the 48 best thesis in 2011** (Paris, France): Paris Institute of Technology (ParisTech), University Paris-Est (UPE).

## CONTACTS AND REFERENCES

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Dr Mahendra Mariadassou	INRAE	Dr Emmanuelle Cambau	AP-HP
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