

Curriculum Vitae



PERSONAL INFORMATION

Family name, First name: Ferrando, Maria Laura
Researcher unique identifier(s): 0000-0002-1398-8244 (ORCID)
Date of birth: 10 September 1972
Nationality: Italian
Google Scholar Profile: <https://scholar.google.com/citations?user=9aAb8BkAAAAJ&hl=en>
Institutional web page: <https://irgb.cnr.it/people/laura-ferrando/>

EDUCATION

- 2012 **PhD**, Title thesis: '*Interactions of Streptococcus suis with host mucosa*'
Department of Host-Microbe Interactomics, Wageningen University & Research (WUR).
The Netherlands. Name of PhD Supervisors: Prof. Jerry Wells, Dr Hilde E Smith
- 2007 **Postgraduate Specialization** in "Microbiology and Virology", University of Cagliari (IT),
awarded *cum laude*. Title thesis: '*Role of the Two-Component Systems (TCS) of Streptococcus pneumoniae in virulence*'
- 1998 **Master's in Biological Science** ("Laurea Magistrale", corresponding to 5 years of
university-level studies), awarded *cum laude*. Faculty of Mathematics, Science and Physics,
University of Cagliari, Italy

CURRENT POSITIONS

- Feb 2024-now **Researcher, Level III**, on a fixed-term contract within the research project "*Ageing Well in an Ageing Society – Age-It*," funded by the European Union – Next Generation EU, National Recovery and Resilience Plan (PNRR).
IRGB-CNR, Monserrato (IT)
- I investigate the impact of intestinal and vaginal microbiota on the onset of cardiometabolic diseases in women.

PREVIOUS POSITIONS

- JUL 2022 - JEN 2024 **Researcher**, on a fixed-term contract, 'Joint Programming Initiative on Antimicrobial Resistance (JPIAMR)' project ICONIC '*Ionophore coccidiostats: risk of CO-selection of Antimicrobial Resistance - Clinical impact and intervention strategies*.' – IRCCS San Raffaele Scientific Institute, Emerging Bacterial Pathogens Unit. Milan (IT)
- I investigated the ionophore resistance in enterococci from a One Health perspective. Responsible for the surveillance of nosocomial infections caused by Multidrug-Resistant Micro-Organisms (MDRO) and diagnosed by Next Generation Sequencing (NGS)
- Nov 2017 - Oct 2021 **Postdoctoral Researcher** employed on a fixed-term EU Horizon2020 research project PIGSs '*Program for Innovative Global Prevention of Zoonotic Bacterial Disease*' – Department of Host-Microbe Interactomics, Wageningen University & Research (NL).
- Responsible for investigating the influence of host (animal and human) microbiota on the onset of infectious diseases and studying bacterial virulence mechanisms.
- Mar 2012 - Feb 2016 **Postdoctoral Researcher** employed on a fixed-term EU-FP7 program ANTIGONE '*ANTicipating the Global Onset of Novel Epidemics*' – Academic Medical Center. Dept. Medical Microbiology - Amsterdam (NL)
- I investigated the transmission of zoonotic pathogens from pig to human using *in vivo* and *in vitro* models of host-microbe interactions.
- Jan 2008 - Jun 2012 **PhD candidate** employed on a fixed-term 'Programma binnen KB-thema 8 Diergezondheid' I.POP and CVI kennisbasis' project '*Role of cell envelope proteins in virulence and pathogenicity of Streptococcus suis infections in pigs*' – Department of Host-Microbe Interactomics, Wageningen University & Research (NL).
- I study the progression of infectious diseases in the host, having acquired strong knowledge in microbial genomics, molecular microbiology, and host-microbe interactions.
- Jun 2006 - Dic 2007 **Research Fellowship winner** (2 years), founded by 'Programma Operativo del Fondo Sociale Europeo (PO FSE) Master and Back European Post-Graduated Program' Swammerdam Institute (SILS) at the University of Amsterdam (NL)

- Development of novel antimicrobial agents against bacterial pathogens. Researcher in protein engineering and antimicrobial mechanisms.
- May 2004 - May 2006 **Clinical Research Associate** at the University of Cagliari. Istituto di Sanità Pubblica. Cagliari (IT)
 - Microbiological environmental monitoring
- May 2002 - Apr 2004 **Junior Research Fellow** at Experimental Zootechnical Institute Lombardia-Emilia Romagna. Brescia (IT)
 - Development of molecular methods for the detection of zoonotic viruses in animals and food
- 2000 **Junior Research Fellow winner** (3 months), funded by Italian National Grant, CIB. National Institute of Agriculture & Botany (NIAB). Cambridge (The UK)
 - Development of molecular markers (i.e., microsatellites) in plants
- Jan 1999 - Dec 2001 **Junior Research Fellow** at the University of Parma. Parma (IT)
 - Detection of Genetically Modified Organisms (GMOs) in food

RESEARCH ACTIVITY

My current position was obtained through a competitive public selection process (**BANDO N. 400.2 IRGB PNRR Progetto “AGE.IT” CUP B83C22004880006**). In this role, I have been involved in analyzing vaginal and intestinal microbiota in the context of women’s health and during ageing process. Previously, I researched both animal and human microbiota, primarily focusing on elucidating the biological mechanisms underlying microbiota alterations, using metagenomic approaches and host–microbe interaction studies. The knowledge and experience I have gained align well with the research activities and novel research proposals of the IRGB-CNR group and have enabled me to play a significant role in metagenomic analyses, omics data interpretation, and the study of the functional mechanisms of the microbiota.

SKILLS AND PROFESSIONAL KNOWLEDGE

Metagenomics and microbial genomics

- **Metagenomics 16S rRNA analysis pipeline:** knowledge of Illumina NGS and Nanopore platforms, CLC Microbial Genomics Module for CLC Genomics Workbench, Qiagen (software for analyzing microbial data); Ridom™ SeqSphere⁺ (software for automatic processing and analyzing of NGS (e.g., Illumina, Ion Torrent) for microbial analysis); *open-source* Galaxy platform bioinformatics; MicrobiomeAnalyst (Bioinformatics pipelines, statistics, and data visuals); Canoco 5 for visualization of multivariate data and visualization
- **Transcriptomics:** qRT-PCR, microarrays, RNA-seq
- **Other bioinformatics skills for microbial analysis:** Artemis Comparison Tool, eBURST V3-MLST, MicrobesOnLine, RegPrecise DB, MEME, GenBank, BLAST; DNA/Protein manipulation: Benchling, VectorNTI, PROSITE, ExPASy, Oligo6, Primer Express; multiplex qPCR design Beacons designer; DNA sequence Analysis: Bioedit, Chromas, CodonCode Aligner, ClustalΩ; Omics data: Blast2Go, TMEV (Multiple Array Viewer), KEGG, Statistical analysis of data (e.g., GraphPad Prism)

Host-microbe interactions

- **Clinical Microbiology:** handling Category 2 and 3 bacterial pathogens, microbial culture, biochemical tests, genotyping, Multidrug-Resistant Micro-Organisms (MDRO) molecular typing and surveillance service for the Hospital, Epidemiological cut-off values (ECOFFs) according to EUCAST, determination of Minimum Inhibitory Concentration (MIC) for antibiotics by broth microdilution, E-test
- **Molecular Biology:** Plasmid purification, DNA and RNA extraction including Bead-Beads technique, quantification of DNA/RNA/proteins by Qubit Fluorometers, electrophoresis, PCR, simplex and multiplex qPCR, complex probes design (TaqMan, Beacons), Northern and Western blotting, cloning, high-throughput LIC cloning and expression test, mutagenesis by gene replacement with antibiotic cassette marker and CRISPR/Cas9 system, complemented mutants, DNA-protein interaction (EMSA)
- **Biochemistry:** in vitro protein production and recombinant protein purification by affinity chromatography and size exclusion with HPLC AKTA chromatography system, enzyme assays, SDS-PAGE; Cell Biology: cell culture, organoid systems from porcine ileum, cytotoxicity assay, transepithelial electrical resistance (TEER), Permeability Assays (FITC)-dextran, IF confocal microscopy, immunohistochemistry
- **Bacteria-host interactions:** cell culture systems using primary and secondary cells grown in filter systems; analysis of bacterial adhesion, invasion, and translocation across host epithelium. *In vivo* infection studies: experimental infections using animal models (piglets)
- **Cell biology:** Dendritic Cells culture, phagocytosis assay, immunoassay (flow cytometry), Toll-like receptor signaling assay, ELISA; Cell-based biological assays, SpectraMax M5 Multimode microplate reader for fluorescence (Molecular Devices), luminescence assays
- **Languages:** Italian (Mother Language), English (Proficient, C1 level), Dutch (Beginners, A1-A2 level)

MOST RELEVANT PROFESSIONAL TRAINING:

2018	'Metagenomics applied to Surveillance of Pathogens & Antimicrobial Resistance' (workshop, e-learning), Tallinn (EE)
2012	'International Course Laboratory Animal Science' (Article 9), Utrecht University (NL)
2011	'Advanced visualization, integration and biological interpretation of -omics data'. Wageningen University (NL)
2011	'Techniques for writing and presenting a scientific paper'. Wageningen University
2011	'Statistics for Life Sciences'. Wageningen University (NL)
2011	'Statistics course Animal Design of Experiments'. Wageningen University (NL)

PUBLICATIONS AND CONGRESSES

- **Coautrice di 24 pubblicazioni scientifiche** (14 pubblicazioni in prima e seconda posizione, 1 in co-ultima posizione) su riviste internazionali (più 4 in fase di revisione)
- **Relatrice in 14 conferenze internazionali** (8 presentazioni orali* – 6 presentazioni poster) * 3 volte *INVITED SPEAKER*

1. Mugabi R, Silva APSP, Haden C, Wells J, Murray GGR, Gussak A, Rotolo R, Williams T, Gottschalk M, Schmidt C **Ferrando ML**, Baarken P, Brown J, Weinert L, Rademacher C, Li G, Robbins R, Cano JP, Karricher L, Harms P, Tucker AW, Clavijo MJ. Disease-associated *Streptococcus suis* (DASS) in lactation: Detection patterns and implications for control, PREPRINT (Version 1) (2025) available at Research Square: [HTTPS://DOI.ORG/10.21203/RS.3.RS-6804475/V1](https://doi.org/10.21203/rs.3.rs-6804475/v1) Accepted in *Porcine Health Management*
2. Vinerbi E, Chillotti F, Maschio A, Lenarduzzi S, Camarda S, Crobu F, Zhernakova DV, Lo Faro V, Beltrame GV, Incollu S, Spreckels J, Kuzub N, Kadric A, Gacesa R, Zhernakova A, De Seta F, Mazzà D, Busonero F, **Ferrando ML**, Girotto G, Sanna S. Vaginal microbiota changes during a natural menstrual cycle in the Women4Health cohort highlights specific features of the Italian population [Internet]. bioRxiv; (2025) Available from: <https://www.biorxiv.org/content/10.1101/2025.03.12.642767v1> Accepted in *mSystem*
3. **Ferrando ML**, Saluzzo F, Frederiksen RF, Slettebakk JS, Urdahl AM, Simm R, Skarżyńska M, Zajac M, Lalak A, Niczyporuk J, Wasyl D, Duval L, Tardy F, Schapendonk C, Rapallini M, Tosi G, Perulli S, Cirasella L, Cirillo DM, Pikkemaat MG. Determination of epidemiological cut-off values for Narasin, Salinomycin, Lasalocid, and Monensin in *Enterococcus faecium*. (2025) *J Antimicrob Chemother.* Sep 3;80(9):2361-2368. doi: 10.1093/jac/dkaf113. PMID: 40740068; PMCID: PMC12404726.
4. Fredriksen S, Neila-Ibáñez C, Hennig-Pauka I, Guan X, Dunkelberger J, de Oliveira IF, **Ferrando ML**, et al. *Streptococcus suis* infection on European farms is associated with an altered tonsil microbiome and resistome. *Microb Genomics.* (2024);10(12).
5. Sterzi L, Nodari R, Di Marco F, **Ferrando ML**, Saluzzo F, Spitaleri A, et al. Genetic barriers more than environmental associations, explain *Serratia marcescens* population structure. *Commun Biol.* 2024;7(1).
6. Alvaro A, Piazza A, Papaleo S, Perini M, Pasala AR, Panelli S, Nardi T, Nodari R, Sterzi L, Pagani C, Merla C, Castelli D, Olivieri E, Bracco S, **Ferrando ML**, Saluzzo F, Rimoldi SG, Corbella M, Cavallero A, Prati P, Farina C, Cirillo DM, Zuccotti G, Comandatore F (2024). Cultivation and sequencing-free protocol for *Serratia marcescens* detection and typing. *iScience* 27: 109402.
7. Sterzi L, Nodari R, Di Marco F, **Ferrando ML**, Saluzzo F, Spitaleri A, et al. (2024) Genetic barriers more than environmental associations explain *Serratia marcescens* population structure. *Commun Biol* 7: 468.
8. Murray GGR, Hossain ASMM, Miller EL, Bruchmann S, Balmer AJ, Matuszewska M, Herbert J, Hadjirin NF, Mugabi R, Li G, **Ferrando ML**, Fernandes de Oliveira IM, Nguyen T, Yen PLK, Phuc HD, Zaw Moe A, Su Wai T, Gottschalk M, Aragon V, Valentin-Weigand P, Heegaard PMH, Vrieling M, Thein Maw M, Thidar Myint H, Tun Win Y, Thi Hoa N, Bentley SD, Clavijo MJ, Wells JM, Tucker AW, Weinert LA. (2023) The emergence and diversification of a zoonotic pathogen from within the microbiota of intensively farmed pigs. *Proc Natl Acad Sci U S A* 120: e2307773120.
9. Gussak A, **Ferrando ML**, Schrama M, van Baarlen P, Wells JM. Precision Genome Engineering in *Streptococcus suis* Based on a Broad-Host-Range Vector and CRISPR-Cas9 Technology. *ACS Synth Biol.* (2023) Aug 21. doi: 10.1021/acssynbio.3c00110. Epub ahead of print. PMID: 37602730.
10. Casula E, Contu MP, Demontis C, Coghe F, Steri GC, Scano A, **Ferrando ML** & Orrù G. (2022) "Changes in the oral status and periodontal pathogens in a Sardinian rural community from pre-industrial to modern time." *Sci Rep.* Sep 23;12(1):15895. doi: 10.1038/s41598-022-20193-9.
11. **Ferrando ML**, Gussak A, Mentink S, Gutierrez MF, van Baarlen P, Wells JM. (2021). Active Human and Porcine Serum Induce Competence for Genetic Transformation in the Emerging Zoonotic Pathogen *Streptococcus suis*. *Pathogens* 10.
12. Orrù G, Scano A, Fais S, Loddo M, Carta MG, Steri GC, Santus S, Cappai R, **Ferrando ML**, Coghe F. (2021). Evaluation of "Caterina assay": An Alternative Tool to the Commercialized Kits Used for Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Identification. *Pathogens* 10:325.

13. **Ferrando ML**, Coghe F, Scano A, Carta MG, Orrù G. (2021). Co-infection of *Streptococcus pneumoniae* in Respiratory Infections Caused by SARS-CoV-2. *Biointerface Res Appl Chem* 11:12170–12177.
14. Vacca C, Contu MP, Rossi C, **Ferrando ML**, Blus C, Szmukler-Moncler S, Scano A, Orrù G. (2020). In vitro interactions between *Streptococcus intermedius* and *Streptococcus salivarius* K12 on a titanium cylindrical surface. *Pathogens* 9:1–15.
15. van Dijk IA, **Ferrando ML**, van der Wijk AE, Hoebe RA, Nazmi K, *et al.* (2017) Human salivary peptide histatin-1 stimulates epithelial and endothelial cell adhesion and barrier function. *FASEB J*.
16. **Ferrando ML**, Willemse N, Zaccaria E, Pannekoek Y, van der Ende A, *et al.* (2017) Streptococcal Adhesin P (SadP) contributes to *Streptococcus suis* adhesion to the human intestinal epithelium. *PLoS One* 12: e0175639.
17. **Ferrando ML**, Schultsz C (2016) A hypothetical model of host-pathogen interaction of *Streptococcus suis* in the gastrointestinal tract. *Gut Microbes*: 0.
18. **Ferrando ML**, de Greeff A, van Rooijen WJ, Stockhofe-Zurwieden N, Nielsen J, *et al.* (2015) Host-pathogen Interaction at the Intestinal Mucosa Correlates With Zoonotic Potential of *Streptococcus suis*. *J Infect Dis* 212: 95-105.
19. **Ferrando ML**, van Baarlen P, Orru G, Piga R, Bongers RS, *et al.* (2014) Carbohydrate availability regulates virulence gene expression in *Streptococcus suis*. *PLoS One* 9: e89334.
20. Meijerink M, **Ferrando ML**, Lammers G, Taverne N, Smith HE, *et al.* (2012) Immunomodulatory effects of *Streptococcus suis* capsule type on human dendritic cell responses, phagocytosis and intracellular survival. *PLoS One* 7: e35849.
21. **Ferrando ML**, Fuentes S, de Greeff A, Smith H, Wells JM (2010) ApuA, a multifunctional alpha-glucan-degrading enzyme of *Streptococcus suis*, mediates adhesion to porcine epithelium and mucus. *Microbiology* 156: 2818-2828.
22. Orru G, **Ferrando ML**, Meloni M, Liciardi M, Savini G, *et al.* (2006) Rapid detection and quantitation of *Bluetongue virus* (BTV) using a Molecular Beacon fluorescent probe assay. *J Virol Methods* 137: 34-42.
23. Losio MN, **Ferrando ML**, Daminelli P, Chegdani F (2004) Setting up a PCR-based method to trace animal species in processed meat products. *Vet Res Commun* 28 Suppl 1: 253-255.
24. Bertasi B, Bignotti E, **Ferrando ML**, D'Abrosca F, Scaratti L, *et al.* (2003) The Standardization of a Molecular Biology Method to Verify the Presence of *Microcystis aeruginosa*. *Vet Res Commun* 27: 277-279.

PUBLICATIONS (ONLINE OR UNDER REVIEW)

1. KlebNET-GSP AMR Geno-Pheno Group. Ciprofloxacin resistance in *Klebsiella pneumoniae*: phenotype prediction from genotype and global distribution of resistance determinants. Available (2025) (<https://www.biorxiv.org/content/10.1101/2025.09.24.678318v1>) Under revision in *Genome medicine*
2. Peters Y, **Ferrando ML** (first co-shared author), Zhou C, te Morsche C R van der Leeden B; Cremers R; Dat Le P; van Dijk L; WM Schrauwen R; Tan AC, van der Post R.S.; van Baarlen P; Siersema P.D.; Boleij A., *Lactobacillus casei* Shirota intervention modulates the esophageal microbiome composition in Barrett's esophagus. (2025) Under revision *iScience*
3. **Ferrando ML**, Busonero F, Crobu F, Sanna S. Ageing in Women – the Microbiome Perspective. (2025) Under revision in *Ageing Research Reviews*
4. Gaiser R, **Ferrando ML**, Oddo A, Pereira M, Guan X, Molist F, Fernandez-Gutierrez M, Fredriksen S, Bryant C, Petras D, Dorrestein P, Boeren S, Medema M, Hill C, Kleerebezem M, van Baarlen P, Wells JM. A mammalian commensal of the oropharyngeal cavity produces antibiotic and antiviral valinomycin *in vivo*. (2022). <https://www.researchsquare.com/article/rs-126949/v1> under revision in *Nature Communications*

Oral presentations - Invited speaker*

1. Vinerbi E, Maschio A, Busonero F, Crobu F, **Ferrando ML**, Lenarduzzi S, Mazzà D, Spreckels JE, Stracquadini M, Elena Stefani, De Seta F, Girotto G, Sanna S. Vaginal microbiome compositional changes during a menstrual cycle: results from the women4health cohort. *10th International Human Microbiome Consortium Congress (IHMC) 2024*. Rome (IT)
2. Badalucco Ciotta F, Saluzzo F, Pescò A, Mori G, Carletti S, Rizzi P, Chiurlo M, Ripa M, Tassan Din C, Tonelli M, Di Marco F, **Ferrando ML**, Batignani V, Moro M, Scarpellini P, Mancini N, Castagna A, Cirillo D M, Oltolini C. Ceftazidime/avibactam resistance in KPC-*Klebsiella pneumoniae*: genomic characterization and clinical features. *European Congress of Clinical Microbiology and Infectious Diseases (ECCMID) 2023* Copenhagen (DK)
3. Fredriksen S, Neila C, Hennig-Pauka I, Guan X, Dunkelberger J de Oliveira IF, **Ferrando ML**, Correa-Fiz F, Aragon V, Boekhorst J, van Baarlen P, Wells JM. *Streptococcus suis* isolate genomes from tonsil microbiome study on European farms. *WIAS meeting 2022* Wageningen (NL)
4. Gussak A, **Ferrando ML**, Murray G, Hossain M, Weinert L, van Baarlen P, Wells JM.. Identification and characterization of genes contributing to the virulence of the major swine pathogen *Streptococcus suis*, p. 52. *In Wias Annual Conference: Frontiers in Animal Sciences. WIAS meeting 2020* Wageningen (NL)

5. Fredriksen S, Neila C, de Oliveira IF, Murray G, Guan X, **Ferrando ML**, Correa-Fiz F, van Baarlen P, Aragon V, Wells JM. The tonsillar microbiome of *Streptococcus suis* diseased piglets, p. 22. In *WIAS Annual Conference: Frontiers in Animal Sciences. WIAS meeting 2020* Wageningen (NL)
6. **Ferrando ML** Growth of *Streptococcus suis* in normal porcine serum induces natural competence and increased expression of virulence factors and metabolic pathways predicted to promote survival in the blood and organs. 4th *International Workshop on Streptococcus suis* **2019** Montreal (Canada)
7. **Ferrando ML*** “*Streptococcus suis* an intestinal pathogen for pigs and humans.” *Annual Meeting of the Japanese Society for Bacteriology*. **2016** Osaka (Japan)
8. **Ferrando ML**,* *et al.* “Host-pathogen interaction at the intestinal mucosa correlates with zoonotic potential of *S. suis*” *Medische Microbiologie en de Nederlandse Vereniging voor Microbiologie (NVvM)*. **2015** Papendal (NL)
9. **Ferrando ML**, “Host-pathogen interaction at the intestinal mucosa correlates with zoonotic potential of *Streptococcus suis*.” 3rd *International One Health Congress*. **2015** Amsterdam (NL)
10. **Ferrando ML** *et al.* “Host-pathogen interaction at the intestinal mucosa correlates with zoonotic potential of *Streptococcus suis*.” XIX *Lancefield International Symposium on Streptococci and Streptococcal Diseases*. **2014** Buenos Aires - Argentina
11. **Ferrando ML**,* “Interaction of *Streptococcus suis* with intestinal epithelial cells” 1st *International workshop on Streptococcus suis Canada-China collaboration*. **2013** Beijing (China)
12. **Ferrando ML**, *et al.* “*Streptococcus suis* interaction with human intestinal epithelial cells.” *Medische Microbiologie en de Nederlandse Vereniging voor Microbiologie (NVvM)* **2013** Papendal (NL)
13. **Ferrando ML**, *et al.* “Metabolic pathways targets for anti-infective” 2nd *Stars network and Marie Curie training event*. **2011** Siena (IT)
14. **Ferrando ML**, *et al.* “Transcriptional control mechanisms linking carbohydrate metabolism, colonization and virulence in *Streptococcus suis*.” XVIII *Lancefield International Symposium*. **2011** Palermo (IT)
15. Ferrari M, Soncini M, Losio MN, **Ferrando ML**, Gilberti F, Corradi A, Petroniani P. Xenotrapianti e rischi correlati alla trasmissione dei retrovirus endogeni del suino. **2003** *Large Animals Review* 4:39-43.
16. Ferrari M, Tosini A, Corradi A, Borghetti P, Scalvini A, Cantoni AM, **Ferrando ML**, Alborali L. Experimental infection with a Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) strain with relevant genomic mutations in the ORF5 region. **2003** Congress paper – 4th *International Symposium on Emerging and Re-emerging Pig Diseases*

Poster presentations

1. **Chair-person poster session*** **Ferrando M.L., et al.** “Host-pathogen interaction at the intestinal mucosa correlates with zoonotic potential of *Streptococcus suis*.” XIX *Lancefield International Symposium*. **2014** Buenos Aires (AR)
2. **Ferrando ML**, *et al.* “*Streptococcus suis* virulence determinants associated with zoonotic potential” *Young Antigone meeting 2014*, Scheveningen (NL)
3. **Ferrando ML**, *et al.* “Intestinal translocation contributes to *Streptococcus suis* infection in piglets.” *Medische Microbiologie en de Nederlandse Vereniging voor Microbiologie (NVvM)* **2014** Papendal (NL)
4. **Ferrando ML**, *et al.* “ApuA, a multifunctional α -glucan-degrading enzyme of *Streptococcus suis* mediates adhesion to porcine epithelium and mucus” *Medische Microbiologie en de Nederlandse Vereniging voor Microbiologie (NVvM)* **2010** Papendal (NL)
5. **Ferrando ML**, *et al.* “Role of a multifunctional carbohydrate utilization gene *apuA*, in the virulence of *Streptococcus suis*”. *Microbial Pathogenesis & Host Response*. **2009** *Cold Spring Harbor Laboratory meetings*, New York (USA)
6. **Ferrando ML**, *et al.* “Surface virulence determinants of *Streptococcus suis*.” *WIAS Science Day* **2008**. Wageningen (NL)

SEMINAR AND MEETINGS:

Invited speaker*

1. **Ferrando ML*** “Microbiome development in piglets and colonization resistance against zoonotic pathogens” **2018** Seminar at Cagliari University (IT)
2. **Ferrando ML**, *et al.* “Microbiome development in piglets and colonization resistance against *Streptococcus suis*” 1^o meeting PIGSs **2018** Cambridge (UK)
3. **Ferrando ML** *et al.* “Microbiota-mediated colonization resistance against pathogens” NCOH Science Café **2018** Wageningen
4. **Ferrando ML**, *et al.* “Role of Streptococcal adhesin protein P in the interaction at the host intestinal mucosa of *Streptococcus suis*.” *Young Antigone meeting*, **2015**, Rotterdam
5. **Ferrando ML**, *et al.*, “A transcriptional control mechanism linking carbohydrate metabolism and virulence in *S. suis*” *WIAS Science Day* **2011** Wageningen