

CURRICULUM VITAE

CLAIRE ROGEL-GAILLARD

Date of birth: April 7th, 1964

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IN BRIEF

Claire Rogel-Gaillard is a senior scientist working at the French National Research Institute for Agriculture, Food and Environment (INRAE). Her current research activities focus on the characterization and prediction of individual variability of immune capacity and vaccine response mainly in pigs. She leads projects that combine large-scale phenotyping of immune and production traits, genetics, functional genomics and metagenomics, in a perspective of data integration and systems immunology. She also promotes multidisciplinary projects on global health concerns by fostering initiatives that connect scientific communities working on animals, humans, plants and the environment.

Claire Rogel-Gaillard heads the INRAE-AgroParisTech joint Laboratory of Animal Genetics and Integrative Biology (GABI, www.gabi.fr) and coordinates Sciences Animales Paris-Saclay (SAPS, <http://SAPS.paris>), a multidisciplinary alliance for research, training and innovation in the animal sciences that is anchored in the Paris-Saclay University (UPSaclay, <https://www.universite-paris-saclay.fr/en>).

ACADEMIC BACKGROUND

- 1987 Engineer of the National Institute for Agronomic Research (AgroParisTech)
Master degree in animal productions, Laboratory of Ichtyopathology, INRA
- 1992 PhD (AgroParisTech), Laboratory of Papillomaviruses, INSERM-Pasteur Institute
- 2008 Habilitation to conduct research (HDR, Univ. of Versailles Saint Quentin en Yvelines)

SCIENTIFIC INTERESTS

- Genetic determinism of individual variability of immune capacity and vaccine response
- Immunogenetics and MHC
- Genome mapping and sequencing, structural and functional genomics
- Gut microbiome and host-microbiome interactions
- Systems immunology
- Main species of interest: pig as a biomedical model and as a farm animal

HONORS AND DISTINCTIONS

- Vermeil Medal of the French Academy of Agriculture
- Chevalier de l'Ordre National du Mérite (National Order of Merit)
- Chevalier de l'Ordre du Mérite Agricole (Order of Agricultural Merit)
- Since 2019 : corresponding member of the National Academy of Agriculture (Animal Productions)

SUCCESSIVE POSITIONS

- 1987 INRA, Laboratory of Ichtyopathology (Master degree)
- 1988-92 INSERM, Laboratory of Papillomaviruses, Pasteur Institute, Paris (PhD)
- 1992 Permanent researcher at INRA, Laboratory of Fish Genetics
- 1994 INRA-CEA, Laboratory of Radiobiology and Genome Studies (LREG)
- 2007-2008 Head of the LREG
- 2009-2011 Vice head of the GABI unit, leader of the team Genetics Immunity and Health
- 2011-2012 Scientific adviser to the President of INRA
- Since 2013 Head of the GABI unit

CAREER-RELATED ACTIVITIES

National

- Since 2014 Member of the scientific council of the Veterinary School of Maisons Alfort (ENVA)
- Since 2015 Head of Sciences Animales Paris-Saclay (<http://saps.paris>)
- Since 2014 Elected member of the scientific council of INRA
- Since 2015 Member of the scientific council of the Doctoral School SDSV of UPSaclay
- 2015-2019 Member of the academic council of the UPSaclay and of its board
- 2016-2019 Vice-head of the Life Sciences division of the UPSaclay
- Since 2017 Member of the scientific council of the DIM 1HEALTH

International

- Member of the SLA Nomenclature Committee of the VIC and International Society for Animal Genetics (ISAG)
- 2014-2016: Chair of the standing committee of the ISAG on “Genetics of immune response and disease resistance”
- 2019-2021; Chair of the new ISAG committee on Animal Microbiomes
- 2020-2022: Chair of the VIC of IUIS

STAYS IN FOREIGN LABORATORIES FOR COLLABORATIVE PROJECTS

- 1999 University of Minnesota, USA
- 2000-02-05 State Key Laboratory, Agricultural University of Beijing, China (bilateral programs)
- 2008 University of Debrecen, Hungary (bilateral programs)
- 2013-14 BGI-Shenzhen, China

PUBLICATIONS

- 81 peer-reviewed publications indexed in PubMed (on January 2020) (<https://www.ncbi.nlm.nih.gov/pubmed/?term=rogel-gaillard>)
- H-index = 27 (WOS categories)

Publications during the last five years and a selection of few others:

Moroldo M, Munyaka PM, Lecardonnel J, Lemonnier G, Venturi E, Chevaleyre C, Oswald IP, Estellé J, Rogel-Gaillard C. 2020. Integrative analysis of blood and gut microbiota data suggests a non-alcoholic fatty liver disease (NAFLD)-related disorder in French SLA(dd) minipigs. *Sci Rep*, 10(1):234

Hammer SE, Ho CS, Ando A, Rogel-Gaillard C, Charles M, Tector M, Tector AJ, Lunney JK. 2020. Importance of the Major Histocompatibility Complex (Swine Leukocyte Antigen) in Swine Health and Biomedical Research. *Annu Rev Anim Biosci*, 2019 Dec 17. [Epub ahead of print]

Massacci FR, Tofani S, Forte C, Bertocchi M, Lovito C, Orsini S, Tentellini M, Marchi L, Lemonnier G, Luise D, Blanc F, Castinel A, Bevilacqua C, Rogel-Gaillard C, Pezzotti G, Estellé J, Trevisi P, Magistrali CF. 2020. Host genotype and amoxicillin administration affect the incidence of diarrhoea and faecal microbiota of weaned piglets during a natural multiresistant ETEC infection. *J Anim Breed Genet*, 137(1):60-72.

Revilla M, Friggens NC, Broudiscou LP, Lemonnier G, Blanc F, Ravon L, Mercat MJ, Billon Y, Rogel-Gaillard C, Le Floch N, Estellé J, Muñoz-Tamayo R. 2019. Towards the quantitative characterisation of piglets' robustness to weaning: a modelling approach. *Animal*, 13(11):2536-2546

Munyaka PM, Kommadath A, Fohse J, Wilkinson J, Diether N, Stothard P, Estellé J, Rogel-Gaillard C, Plastow G, Willing BP. 2019. Characterization of whole blood transcriptome and early-life fecal microbiota in high and low responder pigs before, and after vaccination for *Mycoplasma hyopneumoniae*. *Vaccine*, 37(13):1743-175

Maroille T, Berri M, Lemonnier G, Esquerré D, Chevaleyre C, Mélo S, Meurens F, Coville JL, Leplat JJ, Rau A, Bed'hom B, Vincent-Naulleau S, Mercat MJ, Billon Y, Lepage P, Rogel-Gaillard C, Estellé J. 2018. Immunome differences between porcine ileal and jejunal Peyer's patches revealed by global transcriptome

sequencing of gut-associated lymphoid tissues. *Sci Rep*, 8:9077

Lee C, Moroldo M, Perdomo-Sabogal A, Mach N, Marthey S, Lecardonnel J, Wahlberg P, Chong AY, Estellé J, Ho SYW, Rogel-Gaillard C, Gongora J. 2018. Inferring the evolution of the major histocompatibility complex of wild pigs and peccaries using hybridisation DNA capture-based sequencing. *Immunogenetics*, 70:401-417

Maroille T, Lemonnier G, Lecardonnel J, Esquerré D, Ramayo-Caldas Y, Mercat MJ, Rogel-Gaillard C, Estellé J. 2017 Deciphering the genetic regulation of peripheral blood transcriptome in pigs through expression genome-wide association study and allele-specific expression analysis. *BMC Genomics*, 18:967

Xiao L, Estellé J, Kiilerich P, Ramayo-Caldas Y, Xia Z, Feng Q, Liang S, Pedersen AØ, Kjeldsen NJ, Liu C, Maguin E, Doré J, Pons N, Le Chatelier E, Prifti E, Li J, Jia H, Liu X, Xu X, Ehrlich SD, Madsen L, Kristiansen K, Rogel-Gaillard C, Wang J. 2016. A reference gene catalogue of the pig gut microbiome. *Nature Microbiology*, 1:16161

Ramayo-Caldas Y, Mach N, Lepage P, Levenez F, Denis C, Lemonnier G, Leplat JJ, Billon Y, Berri M, Doré J, Rogel-Gaillard C, Estellé J. 2016. A phylogenetic network inference analysis applied to porcine gut microbiota composition identifies a consistent ecosystem structure linked with host growth traits. *ISME J*, 10:2973-2977

Gourbeyre P, Berri M, Lippi Y, Meurens F, Vincent-Naulleau S, Laffitte J, Rogel-Gaillard C, Pinton P, Oswald IP. 2015. Pattern recognition receptors in the gut: analysis of their expression along the intestinal tract and the crypt/villus axis. *Physiol Rep*, 3(2): e12225

Jacquier V, Estellé J, Schmaltz-Panneau B, Lecardonnel J, Moroldo M, Lemonnier G, Turner-Maier J, Duranthon V, Oswald IP, Gidenne T, Rogel-Gaillard C. 2015. Genome-wide immunity studies in the rabbit: transcriptome variations in peripheral blood mononuclear cells after in vitro stimulation by LPS or PMA-Ionomycin. *BMC Genomics*, 16:26

Gourbeyre P, Berri M, Lippi Y, Meurens F, Vincent-Naulleau S, Laffitte J, Rogel-Gaillard C, Pinton P, Oswald IP. 2015. Pattern recognition receptors in the gut: analysis of their expression along the intestinal tract and the crypt/villus axis. *Physiol Rep*, 3(2): e12225

Mach N, Berri M, Esquerré D, Chevalere C, Lemonnier G, Billon Y, Lepage P, Oswald IP, Doré J, Rogel-Gaillard C, Estellé J. 2014. Extensive expression differences along porcine small intestine evidenced by transcriptome sequencing. *PLoS One*, 9(2):e88515

Carneiro M, Rubin CJ, Di Palma F, Albert FW, Alföldi J, Martinez Barrio A, Pielberg G, Rafati N, Sayyab S, Turner-Maier J, Younis S, Afonso S, Aken B, Alves JM, Barrell D, Bolet G, Boucher S, Burbano HA, Campos R, Chang JL, Duranthon V, Fontanesi L, Garreau H, Heiman D, Johnson J, Mage RG, Peng Z, Queney G, Rogel-Gaillard C, Ruffier M, Searle S, Villafuerte R, Xiong A, Young S, Forsberg-Nilsson K, Good JM, Lander ES, Ferrand N, Lindblad-Toh K, Andersson L. 2014. Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. *Science*, 345(6200):1074-1079

Mach N, Gao Y, Lemonnier G, Lecardonnel J, Oswald I, Estellé-Fabrellas J, Rogel-Gaillard C. 2013. The peripheral blood transcriptome reflects variations in immunity traits in swine: towards the identification of biomarkers. *BMC Genomics*, 14:1-17

Dawson HD, Loveland JE, Pascal G, Gilbert JG, Uenishi H, Mann KM, Sang Y, Zhang J, Carvalho-Silva D, Hunt T, Hardy M, Hu Z, Zhao SH, Anselmo A, Shinkai H, Chen C, Badaoui B, Berman D, Amid C, Kay M, Lloyd D, Snow C, Morozumi T, Cheng RP, Bystrom M, Kapetanovic R, Schwartz JC, Kataria R, Astley M, Fritz E, Steward C, Thomas M, Wilming L, Toki D, Archibald AL, Bed'Hom B, Beraldi D, Huang TH, Ait-Ali T, Blecha F, Botti S, Freeman TC, Giuffra E, Hume DA, Lunney JK, Murtaugh MP, Reecy JM, Harrow JL, Rogel-Gaillard C, Tuggle CK. 2013. Structural and functional annotation of the porcine immunome. *BMC Genomics*, 14:332

Groenen MA, Archibald AL, Uenishi H, Tuggle CK, Takeuchi Y, Rothschild MF, Rogel-Gaillard C, Park C, Milan D, Megens HJ, Li S, Larkin DM, Kim H, Frantz LA, Caccamo M, Ahn H, Aken BL, Anselmo A, Anthon C, Auvil L, Badaoui B, Beattie CW, Bendixen C, Berman D, Blecha F, Blomberg J, Bolund L, Bosse M, Botti S, Bujie Z, Bystrom M, Capitanu B, Carvalho-Silva D, Chardon P, Chen C, Cheng R, Choi SH, Chow W, Clark RC, Clee C, Crooijmans RP, Dawson HD, Dehais P, De Sapio F, Dibbits B, Drou N, Du ZQ,

Eversole K, Fadista J, Fairley S, Faraut T, Faulkner GJ, Fowler KE, Fredholm M, Fritz E, Gilbert JG, Giuffra E, Gorodkin J, Griffin DK, Harrow JL, Hayward A, Howe K, Hu ZL, Humphray SJ, Hunt T, Hornshøj H, Jeon JT, Jern P, Jones M, Jurka J, Kanamori H, Kapetanovic R, Kim J, Kim JH, Kim KW, Kim TH, Larson G, Lee K, Lee KT, Leggett R, Lewin HA, Li Y, Liu W, Loveland JE, Lu Y, Lunney JK, Ma J, Madsen O, Mann K, Matthews L, McLaren S, Morozumi T, Murtaugh MP, Narayan J, Nguyen DT, Ni P, Oh SJ, Onteru S, Panitz F, Park EW, Park HS, Pascal G, Paudel Y, Perez-Enciso M, Ramirez-Gonzalez R, Reecy JM, Rodriguez-Zas S, Rohrer GA, Rund L, Sang Y, Schachtschneider K, Schraiber JG, Schwartz J, Scobie L, Scott C, Searle S, Servin B, Southey BR, Sperber G, Stadler P, Sweedler JV, Tafer H, Thomsen B, Wali R, Wang J, Wang J, White S, Xu X, Yerle M, Zhang G, Zhang J, Zhang J, Zhao S, Rogers J, Churcher C, Schook LB. 2012. Analyses of pig genomes provide insight into porcine demography and evolution. *Nature*, 491:393-398

Gao Y, Wahlberg P, Marthey S, Esquerré D, Jaffrézic F, Lecardonnell J, Hugot K, Rogel-Gaillard C. 2012. Analysis of porcine MHC using microarrays. *Vet Immunol Immunopathol*, 148:78-84

Flori L, Gao Y, Laloë D, Lemonnier G, Leplat JJ, Teillaud A, Cossalter A. M, Laffitte J, Pinton P, De Vaureix C, Bouffaud M, Mercat MJ, Lefèvre F, Oswald I, Bidanel J. P, Rogel-Gaillard C. 2011. Immunity traits in pigs: substantial genetic variation and limited covariation. *Plos One*, 6:e22717

Kusza S, Flori L, Gao Y, Teillaud A, Hu R, Lemonnier G, Bosze Z, Bourneuf E, Vincent-Naulleau S, Rogel-Gaillard C. 2011. Transcription specificity of the class Ib genes SLA-6, SLA-7 and SLA-8 of the swine major histocompatibility complex and comparison with class Ia genes. *Anim Genet*, 42(5):510-20

Hu R, Lemonnier G, Bourneuf E, Vincent-Naulleau S, Rogel-Gaillard C. 2011. Transcription variants of SLA-7, a swine non classical MHC class I gene. *BMC Proc*, 5 Suppl 4:S10

Anselmo A, Flori L, Jaffrezic F, Rutigliano T, Cecere M, Cortes-Perez N, Lefèvre F, Rogel-Gaillard C, Giuffra E. 2011. Co-expression of host and viral microRNAs in porcine dendritic cells infected by the pseudorabies virus. *PLoS One*, 6(3):e17374

Gao Y, Flori L, Lecardonnell J, Esquerré D, Hu ZL, Teillaud A, Lemonnier G, Lefèvre F, Oswald IP, Rogel-Gaillard C. 2010. Transcriptome analysis of porcine PBMCs after in vitro stimulation by LPS or PMA/ionomycin using an expression array targeting the pig immune response. *BMC Genomics*, 11:292

Ho CS, Lunney JK, Ando A, Rogel-Gaillard C, Lee JH, Schook LB, Smith DM. 2009. Nomenclature for factors of the SLA system, update 2008. *Tissue Antigens*, 73(4):307-15

Tanaka-Matsuda M, Ando A, Rogel-Gaillard C, Chardon P, Uenishi H. 2009. Difference in number of loci of swine leukocyte antigen classical class I genes among haplotypes. *Genomics*, 93(3):261-73

Flori L, Rogel-Gaillard C, Cochet M, Lemonnier G, Hugot K, Chardon P, Robin S, Lefèvre F. 2008. Transcriptomic analysis of the dialogue between Pseudorabies virus and porcine epithelial cells during infection. *BMC Genomics*, 9:123.

Chantry-Darmon C, Urien C, Hayes H, Bertaud M, Chadi-Taourit S, Chardon P, Vaiman D, Rogel-Gaillard C. 2005. Construction of a cytogenetically anchored microsatellite map in rabbit. *Mamm Genome*, 16(6):442-59

Rogel-Gaillard C, Piumi F, Billault A, Bourgeaux N, Save JC, Urien C, Salmon J, Chardon P. 2001. Construction of a rabbit bacterial artificial chromosome (BAC) library: application to the mapping of the major histocompatibility complex to position 12q.1.1. *Mamm Genome*, 12(3):253-5

Rogel-Gaillard C, Bourgeaux N, Billault A, Vaiman M, Chardon P. 1999. Construction of a swine BAC library: application to the characterization and mapping of porcine type C endoviral elements. *Cytogenet Cell Genet*, 85(3-4):205-11

Velten F, Rogel-Gaillard C, Renard C, Pontarotti P, Tazi-Ahnini R, Vaiman M, Chardon P. 1998. A first map of the porcine major histocompatibility complex class I region. *Tissue Antigens*, 51(2):183-94

Rogel-Gaillard C, Vaiman M, Renard C, Chardon P, Yerle M. 1997. Localization of the beta 2-microglobulin gene to pig chromosome 1q17. *Mamm Genome*, 8(12):948

Rogel-Gaillard C, Bourgeaux N, Save JC, Renard C, Coullin P, Pinton P, Yerle M, Vaiman M, Chardon P.

1997. Construction of a swine YAC library allowing an efficient recovery of unique and centromeric repeated sequences. *Mamm Genome*, 8(3):186-92

Rogel-Gaillard C, Hayes H, Coullin P, Chardon P, Vaiman M. 1997. Swine centromeric DNA repeats revealed by primed in situ (PRINS) labeling. *Cytogenet Cell Genet*, 9(1-2):79-84

Rogel-Gaillard C, Pehau-Arnaudet G, Breitburd F, Orth G. 1993. Cytopathic effect in human papillomavirus type 1-induced inclusion warts: in vitro analysis of the contribution of two forms of the viral E4 protein. *J Invest Dermatol*, 101(6):843-51

Rogel-Gaillard C, Breitburd F, Orth G. 1992. Human papillomavirus type 1 E4 proteins differing by their N-terminal ends have distinct cellular localizations when transiently expressed in vitro. *J Virol*, 66(2):816-23