

**DAMIEN F. MEYER**

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**Molecular microbiology and Genomics – Infectious strategies of Anaplasmataceae**

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Phone : +590 (0)590 25 59 47, e-mail : [damien.meyer@cirad.fr](mailto:damien.meyer@cirad.fr)**PROFESSIONAL PREPARATION**

Postdoc Pr. Adam J. Bogdanove, supervisor ; 2007-2008  
 Postdoc Dr. Charles Manceau, supervisor ; 2006-2007  
 Ph.D. Microbiology and Plant Pathology, Paul Sabatier Univ., Toulouse, France, Pr. Matthieu Arlat, advisor ; 2005  
 M.Sc. Biology, Paul Sabatier Univ., Toulouse, France ; 2000  
 Certificate Animal Experimentation, Level 1, Blaise Pascal Univ., Clermont-Fd, France ; 2000  
 B. Sc Cellular biology and Physiology, Blaise Pascal Univ., Clermont-Fd , France ; 1999

**ACADEMIC POSITIONS**

2008-present *Research Scientist* (Tenure), CIRAD, Joint Research Unit 117 CIRAD/INRA ASTRE "Animal, Santé, Territoires, Risques et Ecosystèmes", Guadeloupe, France  
 2006-2008 *Postdoctoral Research Associate*, Iowa State University, Dept. of Plant Pathology, USA, 2007-2008 ; INRA Angers, Joint Research Unit of Plant Pathology, France, 2006-2007  
 2001-2005 *Ph.D Student*, Paul Sabatier Univ., Toulouse, France  
 2000 *Research Assistant*, Kansas State University, KS, USA  
 1995-2000 *Undergraduate Student*, Blaise Pascal Univ., Clermont-Fd, France

**PROFESSIONAL SOCIETY MEMBERSHIPS**

Public Library of Science (PLOS, since 2005)  
 American Society for Microbiology (ASM, since 2010)  
 Société Française de Microbiologie (SFM, since 2010)

**GRANTS AND AWARDS**

2019 Winner of the 2019 PLOS Computational Biology T-Shirt design  
 2018 Competitive grant from Région Guadeloupe (fellowship for PhD student)  
 2017 Competitive grant from SATT-AXLR (for innovation transfer)  
 2012 Nominated as ASM Ambassador to Guadeloupe (2012-2014)  
 Grant for Franco-Portuguese Project PAUILF 2012 (*Proteomics*)  
 2006 Post-doctoral fellowship of the Conseil Régional Pays de la Loire  
 2003 Fellowship awarded by Asedis-SO Association (to attend to the 11<sup>th</sup> International MPMI Congress, St-Petersburg, Russia)  
 2001 Competitive Research training award (to support Ph.D's research) from the Ministère de la Recherche et de l'Enseignement Supérieur  
 2000 Grant from the Graduate School of Biology, Health and Biotechnology, University Paul Sabatier (fellowship to support Master's thesis)

**PUBLICATIONS**

(\*), *contributed equally to the work*

- **Peer-reviewed articles (refereed ; h-index = 18)**

1. Noroy C, Lefrançois T, and **Meyer DF** (2019) Searching Algorithm for Type IV Effector proteins (S4TE) 2.0 : improved tools for type IV effector prediction, analysis and comparison in proteobacteria. *PLOS Computational Biology*, in press
2. Pruneau L, Lebrigand K, Mari B, Lefrançois T, **Meyer DF** and Vachiery N (2018) Comparative transcriptome profiling of virulent and attenuated *Ehrlichia ruminantium* strains highlighted strong regulation of map1- and metabolism-related genes. *Frontiers in Cellular and Infection Microbiology*, 301150 ; doi : <https://doi.org/10.3389/fcimb.2018.00153>
3. Noroy C, Lefrançois T, and **Meyer DF** (2018) Searching Algorithm for Type IV Effector proteins (S4TE) 2.0 : improved tools for type IV effector prediction, analysis and comparison. *bioRxiv*, 301150 ; doi : <https://doi.org/10.1101/301150>
4. Moumène A, Gonzalez-Rizzo S, Lefrançois T, Vachiéry N and **Meyer DF** (2018) Iron starvation Conditions Upregulate *Ehrlichia ruminantium* Type IV Secretion System, tr1 Transcription Factor and map1 Genes Family through the Master Regulatory Protein ErxR. *Frontiers in Cellular and Infection Microbiology*, 7:535. doi : [10.3389/fcimb.2017.00535](https://doi.org/10.3389/fcimb.2017.00535)
5. Noroy C, and **Meyer DF**. (2017) Comparative genomics of the zoonotic pathogen *Ehrlichia chaffeensis* reveals candidate type IV effectors and putative host cell targets. *Frontiers in Cellular and Infection Microbiology*, 6:204. doi : [10.3389/fcimb.2016.00204](https://doi.org/10.3389/fcimb.2016.00204). Featured on *Frontiers in Cellular and Infection Microbiology* website.
6. Cangi N, Gordon J, Bournez L, Pinarello V, Aprelon R, Huber K, Lefrançois T, Neves L, and **Meyer DF**, and Vachiéry N. (2016). Recombination is a major driving force of genetic diversity in the *Anaplasmataceae Ehrlichia ruminantium*. *Frontiers in Cellular and Infection Microbiology*, 6:111, <http://dx.doi.org/10.3389/fcimb.2016.00111>.
7. Tago D, and **Meyer DF**. (2016). Economic Game Theory to Model the Attenuation of Virulence of an Obligate Intracellular Bacterium. *Frontiers in Cellular and Infection Microbiology*, 6:86, <http://dx.doi.org/10.3389/fcimb.2016.00086>.
8. Yao J, Saenkham P, Levy J, Ibanez F, Noroy C, Mendoza A, Huot O, **Meyer DF**, and Tamborindeguy C. (2016). Interactions ‘*Candidatus Liberibacter solanacearum*’ – *Bactericera cockerelli* : haplotype effect on vector fitness and gene expression analyses. *Frontiers in Cellular and Infection Microbiology*, 6:62, <http://dx.doi.org/10.3389/fcimb.2016.00062>.
9. Moumène A, and **Meyer DF**. (2016). *Ehrlichia*'s molecular tricks to manipulate their host cells. *Microbes and Infection*, Volume 18, Issue 3, March 2016, Pages 172-179, ISSN 1286-4579, <http://dx.doi.org/10.1016/j.micinf.2015.11.001>.
10. Villar M, Ayllón N, Kocan KM, Bonzón-Kulichenko E, Alberdi P, Blouin EF, Weisheit S, Mateos-Hernández L, Cabezas-Cruz A, Bell-Sakyi L, Vancová M, Bílý T, **Meyer DF**, Sterba J, Contreras M, Rudenko N, Grubhoffer L, Vázquez J, de la Fuente J. (2015). Identification and Characterization of *Anaplasma phagocytophilum* Proteins Involved in Infection of the Tick Vector, *Ixodes scapularis*. *PLOS ONE*, 10.1371/journal.pone.0137237.
11. Moumène A, Marcelino I, Ventosa M, Gros O, Lefrançois T, Vachiery N, **Meyer DF\*** and Coehlo AV\*. (2015) Proteomic Profiling of the Outer Membrane Fraction of the Obligate Intracellular Bacterial Pathogen *Ehrlichia ruminantium*. *PLOS ONE* 10: e0116758
12. Pruneau L, Moumène A, **Meyer DF**, Marcelino I, Lefrançois T, Vachiéry N. (2014). Understanding Anaplasmataceae pathogenesis using ‘Omics’ approaches. *Frontiers in Cellular*

*and Infection Microbiology*, doi : 10.3389/fcimb.2014.00086

13. **Meyer DF**, Noroy C, Moumène A, Raffaele S, Albina E, Vachiéry N. (2013). Searching algorithm for type IV secretion system effectors 1.0 : a tool for predicting type IV effectors and exploring their genomic context. *Nucleic Acids Research*, 41 (20) : 9218-9229, first published online August 13, 2013, doi:10.1093/nar/gkt718 (website <http://sate.cirad.fr>).
14. Marcelino I, de Almeida AM, Ventosa M, Pruneau L, **Meyer DF**, Martinez D, Lefrançois T, Vachiery N and Coelho AV. (2012). Tick-borne diseases in cattle: applications of Proteomics to develop new generation vaccines. *Journal of Proteomics*, 75 : 4232-4250.
15. Marcelino I, de Almeida AM, Brito C, **Meyer DF**, Barreto M, Sheikboudou C, Franco CF, Martinez D, Lefrançois T, Vachiery N, Carrondo MJT, Coelho AV and Alves PM. (2012). Proteomic analyses of *Ehrlichia ruminantium* highlight differential expression of MAP1-family proteins. *Veterinary Microbiology*, 156 (2012) 305–314.
16. Pruneau L\*, Emboule L\*, Gely P, Marcelino I, Mari B, Pinarello V, Sheikboudou C, Martinez D, Daigle F, Lefrançois T, **Meyer DF\*** and Vachiery N\*. (2011). Global gene expression profiling of *Ehrlichia ruminantium* at different stages of development. *FEMS Immunology and Medical Microbiology*, 64(1):66-73.
17. Pilet H, Vachiery N, Berrich M, Bouchouicha R, Durand B, Pruneau L, Pinarello V, Saldana A, Carasco-Lacombe C, Lefrançois T, **Meyer DF**, Martinez D, Boulouis H-J and Haddad N. (2011). A new discriminatory typing technique for the Rickettsiales *Ehrlichia ruminantium*: Multiple-Locus Variable Number Tandem Repeat Analysis. *Journal of Microbiological Methods*, 88 (2012) 205–211.
18. Bogdanove AJ, Koebnik R, Lu H, Furutani A, Angiuoli SV, Patil PB, Van Sluys MA, Ryan RP, **Meyer DF**, Han SW, Aparna G, Rajaram M, Delcher AL, Phillippy AM, Puiu D, Schatz MC, Shumway M, Sommer DD, Trapnell C, Benahmed F, Dimitrov G, Madupu R, Radune D, Sullivan S, Jha G, Ishihara H, Lee SW, Pandey A, Sharma V, Sriariyanun M, Szurek B, Vera-Cruz CM, Dorman KS, Ronald PC, Verdier V, Dow JM, Sonti RV, Tsuge S, Brendel VP, Rabinowicz PD, Leach JE, White FF, Salzberg SL. (2011). Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic *Xanthomonas* spp. *Journal of Bacteriology*, 193 (19) : 5450-64.
19. Lefrançois T, Vachiéry N, **Meyer DF**, Pardel J and Martinez D. (2011). Stratégies innovantes de lutte contre les maladies émergentes animales. *Innovations Agronomiques*, 16, 105-116.
20. Hajri A, **Meyer D**, Delort F, Guillaumès J, Brin C and Manceau C. (2010). Identification of a genetic lineage within *Xanthomonas arboricola* pv. *juglandis* as the causal agent of vertical oozing canker of Persian (English) walnut in France. *Plant Pathology*, 59: 1014–1022.
21. Adakal H, Stachurski F, Konkobo M, Zoungrana S, **Meyer DF**, Pinarello V, Aprelon R, Marcelino I, Alves PM, Martinez D, Lefrançois T, Vachiéry N. (2010). Efficiency of inactivated vaccines against heartwater in Burkina Faso: impact of *Ehrlichia ruminantium* genetic diversity. *Vaccine*, 23;28(29):4573-80.
22. Ahoussou S, Lancelot R, Sanford B, Porphyre T, Bartlette-Powell P, Compton E, Henry L, Maitland R, Lloyd R, Mattioli R, Chavernac D, Stachurski F, Martinez D, **Meyer DF**, Vachiery N, Pegram R, Lefrançois T. (2010). Analysis of *Amblyomma* surveillance data in the Caribbean: lessons for future control programmes. *Veterinary Parasitology*, 10;167(2-4):327-35.
23. Raliniaina M\*, **Meyer DF\***, Pinarello V, Sheikboudou C, Emboulé L, Kandassamy Y, Adakal H, Stachurski F, Martinez D, Lefrançois T, Vachiéry N. (2010). Mining the genetic diversity of *Ehrlichia ruminantium* using *map* genes family. *Veterinary Parasitology*, 10;167(2-4):187-95.
24. Emboulé L, Daigle F, **Meyer DF**, Mari B, Pinarello V, Sheikboudou C, Magnone V, Frutos R, Viari A, Barbry P, Martinez D, Lefrançois T, Vachiéry N. (2009). Innovative approach for

transcriptomic analysis of obligate intracellular pathogen: selective capture of transcribed sequences of *Ehrlichia ruminantium*. *BMC Molecular Biology*, 24;10:111.

25. Adakal H, **Meyer DF**, Carasco-Lacombe C, Pinarello V, Allègre F, Huber K, Stachurski F, Morand S, Martinez D, Lefrançois T, Vachierey N, Frutos R. (2009.) MLST scheme of *Ehrlichia ruminantium*: genomic stasis and recombination in strains from Burkina-Faso. *Infection, Genetics and Evolution*, 9(6):1320-8.
26. Salzberg SL, Sommer DD, Schatz MC, Phillippy AM, Rabinowicz PD, Tsuge S, Furutani A, Ochiai H, Delcher AL, Kelley D, Madupu R, Puiu D, Radune D, Shumway M, Trapnell C, Aparna G, Jha G, Pandey A, Patil PB, Ishihara H, **Meyer DF**, Szurek B, Verdier V, Koebnik R, Dow JM, Ryan RP, Hirata H, Tsuyumu S, Won Lee S, Seo YS, Sriariyanum M, Ronald PC, Sonti RV, Van Sluys MA, Leach JE, White FF, Bogdanove AJ. (2008). Genome sequence and rapid evolution of the rice pathogen *Xanthomonas oryzae* pv. *oryzae* PXO99A. *BMC Genomics*, 1;9:204.
27. Darsonval A, Darrasse A, **Meyer D**, Demarty M, Durand K, Bureau C, Manceau C, Jacques MA. (2008). The Type III secretion system of *Xanthomonas fuscans* subsp. *fuscans* is involved in the phyllosphere colonization process and in transmission to seeds of susceptible beans. *Applied and Environmental Microbiology*, 74(9):2669-78.
28. Blanvillain S\*, **Meyer D\***, Boulanger A, Lautier M, Guynet C, Denancé N, Vasse J, Lauber E\*, Arlat M\*. (2007). Plant carbohydrate scavenging through tonB-dependent receptors: a feature shared by phytopathogenic and aquatic bacteria. *PLOS ONE*, 2007 21;2(2):e224.
29. **Meyer D**, Cunnac S, Guéneron M, Declercq C, Van Gijsegem F, Lauber E, Boucher C, Arlat M. (2006). PopF1 and PopF2, two proteins secreted by the type III protein secretion system of *Ralstonia solanacearum*, are translocators belonging to the HrpF/NopX family. *Journal of Bacteriology*, 88(13):4903-17.
30. **Meyer D**, Lauber E, Roby D, Arlat M, Kroj T. (2005). Optimization of pathogenicity assays to study the *Arabidopsis thaliana*-*Xanthomonas campestris* pv. *campestris* pathosystem. *Molecular Plant Pathology*, 1;6(3):327-33. (cover of the issue)
31. Poussier S\*, Thoquet P\*, Trigalet-Demery D, Barthet S, **Meyer D**, Arlat M, Trigalet A. (2003). Host plant-dependent phenotypic reversion of *Ralstonia solanacearum* from non-pathogenic to pathogenic forms via alterations in the *phcA* gene. *Molecular Microbiology*, 49(4):991-1003.

#### • Book Chapters

Oura C, Mahase-Gibson A, Stephen C eds. ; contributors **Meyer DF et al.** (2017) Caribbean Resilience and Prosperity Through One Health. UWI Press. (Trinidad and Tobago). 112pp. ISBN : 978-976-620-293-4. *Invited contribution*

**Meyer DF** and Bogdanove AJ. (2009). Genomics-driven advances in *Xanthomonas* biology. *In* Plant Pathogenic Bacteria: Genomics and Molecular Biology, R.W. Jackson, ed.(Norwich, UK: Horizon Scientific Press), pp. 147-161.

Blanvillain S\*, **Meyer D\***, Déjean G, Boulanger A, Lautier M, Guynet C, Denancé N, Vasse J, Lauber E\* and Arlat M\*. (2008). Plant carbohydrate scavenging through TonB-dependent receptors by the phytopathogenic bacterium *Xanthomonas campestris* pv. *campestris*. *In* Biology of Plant-Microbe Interactions, Volume 6, Proceedings of the 13<sup>th</sup> International Congress on Molecular Plant-Microbe Interactions, Sorrento (Naples), Italy, July 21–27, 2007.

#### • Softwares

1. Noroy C and **Meyer DF**. (2016) Searching Algorithm for Type IV secretion system Effector proteins (SATE) version 1.4. This software has been registered with the "Agence pour la Protection des Programmes (APP)" for version 1.4 under registration number IDDN.FR.001.310023.001.S.P.2012.000.31230, filled March 2016.

2. Noroy C and **Meyer DF**. (2012) Searching Algorithm for Type IV secretion system Effector proteins (SATE) version 1.0. This software has been registered with the "Agence pour la Protection des Programmes (APP)" for version 1.0 under registration number IDDN.FR.001.310023.000.S.P.2012.000.31230, filled June 2012.