



**Damien F. MEYER**

[damien.meyer@cirad.fr](mailto:damien.meyer@cirad.fr) (pro) / [damien.meyer@gmail.com](mailto:damien.meyer@gmail.com) (perso)

<http://www.damienmeyer.fr>

**Research scientist in Microbiology and Genomics  
UX Researcher**

*Infectious strategies of Anaplasmataceae*

Centre for Research and surveillance on Vector-borne diseases in the Caribbean  
UMR ASTRE CIRAD-INRAE | Domaine de Duclos, Prise d'eau, 97170 Petit-Bourg |  
Guadeloupe, FRANCE

**Education**

2001-2005 Ph.D. (Microbiology), Toulouse, France  
1999-2000 M.Sc. (Molecular & Cellular biology), Toulouse, France  
Level 1 Certificate in Animal Experimentation, Clermont-Ferrand, France  
1995-1998 B.Sc. (Cellular biology & Physiology), Clermont-Ferrand, France

**Employment**

2008– Research Scientist (tenure), group leader  
CIRAD, Joint Research Unit CIRAD/INRAE ASTRE, Guadeloupe, France  
2007–2008 Post-doctoral research associate  
Iowa State University, USA  
2006–2007 Post-doctoral research associate  
INRAe Angers, France  
2000 Graduate research assistant  
Kansas State University, USA

**Research experience**

systems biology of bacterial infections; functional and comparative genomics; genome and data visualization; virulence attenuation modelling; predictive softwares development; bioinformatics infrastructure design and management

**Impact**

	<u>all</u>	<u>since 2018</u>
Citations	1985	788
<i>h</i> -index	20	15
i10-index	28	21

*updated Jan 2023*

• **Publications — Refereed papers (h-index = 20; \* contributed equally to the work)**

1. Dereeper A., Summo M., and **Meyer D.F.** (2022) PanExplorer : a web-based tool for exploratory analysis and visualization of bacterial pan-genomes, *Bioinformatics*, btac504 ; <https://doi.org/10.1093/bioinformatics/btac504>
2. Pinarello V., Bencurova E., Marcelino I., Gros O., Puech C., Bhide M., Vachiery N., and **Meyer D.F.** (2022) *Ehrlichia ruminantium* uses its transmembrane protein Ape to adhere to host bovine aortic endothelial cells. *Peer Community Journal*, Volume 2 (2022), article no. e70. doi : 10.24072/pcjournal.189. <https://peercommunityjournal.org/articles/10.24072/pcjournal.189/>
3. Conjard S., **Meyer D. F.**, Aprelon R., Pages-Martinez N., and Gros O. (2022) Evidence of new strains of *Wolbachia* symbiont colonising water-striders (Hemiptera : Gerroidea) in the mangrove of the Lesser Antilles. *PLOS ONE*, Aug 30 ;17(8):e0273668 ; <https://doi.org/10.1371/journal.pone.0273668>
4. Gordon J.L., Chavez A.S.O., Martinez D., Vachiery N., and **Meyer D.F.** (2022) Possible biased virulence attenuation in the Senegal strain of *Ehrlichia ruminantium* by *ntrX* gene conversion from an inverted segmental duplication. *PLOS ONE*, in press
5. Couvin D., Dereeper A., **Meyer D.F.**, Noroy C., Gaete S., Bhakkan B., Pouillet N., Gaspard S., Bezault E., Marcelino I., Pruneau L., Segretier W., Stattner E., Cazenave D., Garnier M., Pot M., Tressières B., Deloumeaux J., Breurec S., Ferdinand S., Gonzalez-Rizzo S., and Reynaud Y. for the KaruBioNet Team. (2021) KaruBioNet : a network and discussion group for a better collaboration and structuring of bioinformatics in Guadeloupe (French West Indies) *Bioinformatics Advances*, Volume 2, Issue 1, 2022, vbac010 ; <https://doi.org/10.1093/bioadv/vbac010>
6. Noroy C., and **Meyer D.F.** (2021) The super repertoire of type IV effectors in the pangenome of *Ehrlichia* spp. provides insights into host-specificity and pathogenesis. *PLOS Computational Biology*. doi : 10.1371/journal.pcbi.1008788
7. Gruel G., Diouf M-B., Abadie C.\*, Chilin-Charles Y.\*, Etter E.M.C.\*, Geffroy M.\*, Herrmann Storck C\*, **Meyer D.F.\***, Pagès N.\*, Pressat G.\*, Teycheney P-Y.\*, Umber M.\*, Vega-Rúa A.\* and Pradel J. (2021) Critical evaluation of cross-sectoral collaborations to inform the implementation of the “One Health” approach in Guadeloupe. *Frontiers in Public Health*. doi : 10.3389/fpubh.2021.652079
8. 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*, 15(3):e1006847. <http://dx.doi.org/10.1371/journal.pcbi.1006847>
9. 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>
10. 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
11. 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. Featured on *Frontiers in Cellular and Infection Microbiology* website.
12. Cangi N, Gordon J, Bournez L, Pinarello V, Aprelon R, Huber K, Lefrancois 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>.
13. 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>.
14. 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>.

15. 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>.

16. 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.

17. Moumène A, Marcelino I, Ventosa M, Gros O, Lefrançois T, Vachiery N, Meyer DF\* and Coelho AV\*. (2015) Proteomic Profiling of the Outer Membrane Fraction of the Obligate Intracellular Bacterial Pathogen *Ehrlichia ruminantium*. *PLOS ONE*, 10: e0116758

18. 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

19. 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>).

20. 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.

21. 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.

22. 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.

23. 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.

24. 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.

25. 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.

26. 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.

27. 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.

28. 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**, Vachieri 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.

29. 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.

30. 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.

31. Adakal H, **Meyer DF**, Carasco-Lacombe C, Pinarello V, Allègre F, Huber K, Stachurski F, Morand S, Martinez D, Lefrançois T, Vachieri 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.

32. 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.

33. 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.

34. 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.

35. **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.

36. **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)

37. 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.

#### • Publications — Patents/Softwares

**Meyer D**, Gordon J, Vachiéry N, Martinez D. Live attenuated bacterial strain and its use as a vaccine. 2019. Genève : OMPI, 44 p. N° de dépôt international : PCT/EP2018/075634, N° de brevet international : WO2019057909A1, N° de dépôt européen : 17306235.7, N° de brevet européen : EP3459561

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.

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.

#### • Publications — 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.

• **Publications — preprints**

Pinarello V., Bencurova E., Marcelino I., Gros O., Puech C., Bhide M., Vachierey V., and **Meyer D.F.** (2021) *Ehrlichia ruminantium* uses its transmembrane protein Ape to adhere to host bovine aortic endothelial cells. **bioRxiv**,06.15.447525 ; doi : <https://doi.org/10.1101/2021.06.15.447525>

Gordon J.L., Chavez A.S.O., Martinez D., Vachierey N., and **Meyer D.F.** (2020) Possible biased virulence attenuation in the Senegal strain of *Ehrlichia ruminantium* by *ntrX* gene conversion from an inverted segmental duplication. **bioRxiv**, 11.26.400648 ; doi : <https://doi.org/10.1101/2020.11.26.400648>