

DAMIEN F. MEYER

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Molecular microbiology and Genomics – Systems biology of *Ehrlichia* infection

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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 CIRAD/INRA Control of Exotic and Emerging Animal Diseases, 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

2012 Nominated as ASM Ambassador to Guadeloupe
 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 11th 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 = 11)**

1. Moumene, A., Marcelino, I., Ventosa, M., Gros, O., Lefrancois, T., Vachieri, 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
2. Pruneau L, Moumène A, **Meyer DF**, Marcelino I, Lefrançois T, Vachiéry N. (2014). Understanding Anaplasmatataceae pathogenesis using 'Omics' approaches. *Frontiers in Cellular and Infection Microbiology*, doi : 10.3389/fcimb.2014.00086
3. **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>).
4. Marcelino I, de Almeida AM, Ventosa M, Pruneau L, **Meyer DF**, Martinez D, Lefrançois T, Vachieri N and Coelho AV. (2012). Tick-borne diseases in cattle: applications of Proteomics to develop new generation vaccines. *Journal of Proteomics*, 75 : 4232-4250.
5. Marcelino I, de Almeida AM, Brito C, **Meyer DF**, Barreto M, Sheikboudou C, Franco CF, Martinez D, Lefrançois T, Vachieri 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.
6. Pruneau L*, Emboule L*, Gely P, Marcelino I, Mari B, Pinarello V, Sheikboudou C, Martinez D, Daigle F, Lefrançois T, **Meyer DF*** and Vachieri N*. (2011). Global gene expression profiling of *Ehrlichia ruminantium* at different stages of development. *FEMS Immunology and Medical Microbiology*, 64(1):66-73.
7. Pilet H, Vachieri 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.
8. 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.
9. 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.
10. 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.
11. Adakal H, Stachurski F, Konkobo M, Zoungrana S, **Meyer DF**, Pinarello V, Aprelon R, Marcelino I, Alves PM, Martinez D, Lefrancois 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.
12. 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.
13. 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.

14. 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.
15. Adakal H, **Meyer DF**, Carasco-Lacombe C, Pinarello V, Allègre F, Huber K, Stachurski F, Morand S, Martinez D, Lefrançois T, Vachiery 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.
16. 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. Erratum in: *BMC Genomics*. 2008;9:534. Seo, Young-Su [added]; Sriariyanum, Malinee [added]
17. 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.
18. 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.
19. **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.
20. **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)
21. 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**

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 13th International Congress on Molecular Plant-Microbe Interactions, Sorrento (Naples), Italy, July 21–27, 2007.

- **Software**

Noroy C and **Meyer DF**. (2012) Searching Algorithm for Type IV secretion system Effector proteins (SATE). 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.