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PERSONAL INFORMATION

- born 1967 in Dessau (Germany)
- married, one child
- nationality: German

PROFILE

I am a researcher and teacher in the field of epigenetics with international working experience in industry, university and research institutes. My current research interest is to understand the relative importance of the genome and the epigenome as a source of heritable phenotypic variation in evolution. My responsibilities included - besides research - teaching of undergraduate and graduate students, supervision of technical staff and postdoctoral fellows, and grant writing. I have been working as reviewer for the journals NAR, BioTechniques BMC Bioinformatics, Mol. Carcinogenesis, JBB, PloS One and others since 2003. I am member of the DNA methylation society, the French Society for Bioinformatics and permanent Member of the German Scholarship Foundation (Studienstiftung des Deutschen Volkes).

RESEARCH EXPERIENCE

Professeur des Universités (Full Professor) University of Perpignan (2013 - present)
Research: We see epigenetics and genetics as a whole and attempt to decipher the relative importance of both inheritance systems in the co-evolution of symbionts and hosts in parasitic and non-parasitic interactions (e.g. *Schistosma mansoni*, *Biomphalaria spp.* and *Pocillopora damicornis*)
Teaching: Epigenetics (Master), Cell Biology, Microbiology, Animal Physiology. (Licence)

Maître de Conférence (Associate Professor) University of Perpignan (2007 - 2013)
Research: My group is interested in the role of epigenetics in evolution and the impact of environmental changes on the epigenotype. Our study model are systems in which selective pressure is strong and evolution is fast (e.g. the human blood fluke *Schistosma mansoni* and the coral *Pocillopora damicornis*)
Teaching: Epigenetics, Applied Bioinformatics, (Master), Cell Biology, Microbiology, Animal Physiology. (Licence)

ATER (Attaché temporaire d'enseignement et de recherche) with Prof. G. Mitta, University of Perpignan (2006 2007)
Research: The impact of induced epimutations on the phenotypic variability of the blood fluke *Schistosoma mansoni* was studied. Phenotypic variability is the basis of infection success of this human parasite. *Teaching*: Lectures in Epigenetics (Master 1 and 2), Practical classes in Animal Physiology.(Licence)

PostDoc with Prof. A. Hüttenhofer, University of Innsbruck (Austria) 2006
Alexander Hüttenhofer is an expert in the field of generation of libraries of non-coding RNA. I learned the technique of RNA immunoprecipitation using antibodies against fibrillarin and MeCP2, and cloned the immunoprecipitated RNA into cDNA libraries.

PostDoc with Dr. A. De Sario, IGH Montpellier (head: Dr. M. Mechali) (France) 2002 - 2005
Bisulfite genomic sequencing, chromatin immunoprecipitation experiments and chromatin modifying drugs were used to investigate DNA methylation and chromatin structure in the pericentromeric region

of human chromosome 21. I identified a characteristic chromatin substructure and proposed this structure as the boundary between pericentromeric heterochromatin and euchromatin. DNA hypomethylation at a specific locus in this region was found to be cancer-specific, and was patented as a new early tumor marker.

PostDoc with Dr. G. Roizes, IGH Montpellier (**head: Dr. J. Demaille**) (**France**) **2000 - 2002**
Transformation-associated-recombination (TAR) cloning in yeast was used to clone the centromere of a truncated human chromosome 21 in order to generate a human artificial chromosome. The project was abandoned after an American group published the successful TAR cloning of a human centromere.

researcher with Prof. A. Rosenthal, IMB Jena (**Germany**) **1999**
Creation of the DNA methylation database MethDB (www.methdb.net).

PhD student with Prof. A. Rosenthal, Friedrich-Schiller-University Jena (**Germany**) **1995 - 1998**
During my PhD thesis I investigated tissue-specific DNA methylation patterns in human DNA by a large-scale approach. Part of my PhD thesis I did in the laboratory of Dr. Susan Clark (CSIRO Sydney, Australia). I improved the original bisulfite conversion method for the detection of methylated cytosine residues, developed bioinformatics tools for the data analysis, and could show that DNA methylation patterns are locus and tissue specific, but do not depend on transcription level. Defense of the thesis took place 15/12/1999.

PreDoc with Dr. T. Kudo, RIKEN Tokyo (**Japan**) **1994 - 1995**
In order to investigate non-cultivable micro-organisms in the hind-gut of termites, phylogenetically conserved loci were amplified by PCR, sequenced and analyzed by family-tree-building algorithms. Based on the sequence analysis, species were proposed and matched to the corresponding sequence by *in-situ* hybridization.

PreDoc with Dr. H-J. Schönfeld, Hoffmann-LaRoche, Basel (**Switzerland**) **1994**
Identification of the molecular ratio of members of the hsp70 chaperone system for protein folding.

FUND RAISING EXPERIENCE

year	source	project	sum
2010 2014	ANR EPIGEVOL	Epigenetic and genetic mechanisms of adaptive evolution	270 000 €
2004	BioSTIC	DNA methylation database MethDB	5 000 €
2002	Génopole LR		8 000 €
1999 2002	Klaus-Tschira-Foundation		34 000 €

TEACHING EXPERIENCE

public	field	type	location
high-school students	genetics, biotechnology	summer course	Marburg (Germany)
Master students	molecular genetics, epigenetics, bioinformatics	lecture	Jena (Germany), Perpignan (France)
Licence	Cell Biology, Animal Physiology, Microbiology	Lecture, Practical classes	Perpignan (France)

SUPERVISING EXPERIENCE

year	name	level	project
2012-present	David Roquis	PhD	The molecular basis of *Dauermodifikation* in invertebrates
2011-present	Sara Fneich	PhD	Nature and heritability of epiallels in the Schistosoma Biomphalaria interaction
2010	Cécile Perrin	PostDoc	Cloning and sequencing of promotor regions of the polymorphic *Sm*PoMuc gene family
2009-2012	Julie Lepesant	PhD	The role of epigenetics in the generation of phenotypic variability in *Schistosoma mansoni* and its impact on infection success
2008-2009	Virginie Thuillier	Master 1 & 2	Analysis of epigenetic variability in the steelhead trout, Generation of a genomic library of *S.mansoni*
2008	Laura Cluzel	Master 1	Measuring DNA methylation by MS-AFLP
2007-2008	Céline Cosseau	PostDoc	Epigenetic control of phenotypic variability in *Schistosoma mansoni*
2007-2008	Azzi Abdelhalim	Master 1 & 2	Epigenetic control of phenotypic variability in *Schistosoma mansoni*
2001 2004	several students	PhD students	bisulfite treatment of genomic DNA

2003	Vincent Negre	ingénieur d'étude	LDAS server for MethDB
2003	Guillaume Granier	DEA	DNA methylation analysis in colon cancer
2003	Magalie Colomines	Maîtrise	antibody-based DNA methylation detection
2002	Matthieu Cubells	DEA	generation of artificial human chromosomes by TAR cloning
2002	Céline Amoreira	DESS	on-line submission system for MethDB
2000 2002	Dr. Eric Renault	PostDoc	data annotation in MethDB

EDUCATION

- Friedrich-Schiller-University Jena & Max-Delbrück-Centre Berlin (Germany) Diploma, 1993 - 1994
- Friedrich-Schiller-University Jena (Germany) 1992 - 1993
- Kings College London (UK) 1992
- Friedrich-Schiller-University Jena (Germany) 1988 - 1991

SKILLS

biology
Bisulfite sequencing, chromatin immunoprecipitation (ChIP), RNA immunoprecipitation, cloning, protein purification, Fluorescence in-situ hybridisation (FISH), RT-PCR, quantitative PCR, mammalian cell culture, *S.mansoni* culture

bioinformatics
Galaxy, Massive sequencing analysis, Gbrowse, FileMakerPro, Perl, HTML, PHP as administrator; sequence analysis software as user

languages
German, English, French (fluent); Russian, Japanese (basic)

PUBLICATIONS

1. Perrin, C., Roger, E., Lepesant, J.M., Duval, D.F., Fneich, S., Thuillier, V., Allienne, J.F., Mita, K., **Grunau**, C. and Cosseau, C.: Schistosoma mansoni mucin genes expression (SmPoMuc): an epigenetic control to shape the adaptation to new host. PloS Path (2013)

2. Vidal-Dupiol, J., Zoccola, D., Tambutte, E., **Grunau**, C., Cosseau, C., Smith, K.M., Freitag, M., Dheilly, N.M., Allemand, D. and Tambutte, S.: Genes Related to Ion-Transport and Energy Production Are Upregulated in Response to CO2-Driven pH Decrease in Corals: New Insights from Transcriptome Analysis. PLoS ONE 8 (2013) e58652.

3. Lepesant, J.M., Boissier, J., Climent, D., Cosseau, C. and **Grunau**, C.: Female biased sex-ratio in Schistosoma mansoni after exposure to an allopatric intermediate host strain of Biomphalaria glabrata. Exp Parasitol (2013)

4. Fneich, S., Dheilly, N., Adema, C., Rognon, A., Reichelt, M., Bulla, J., **Grunau**, C. and Cosseau, C.: 5-methyl-cytosine and 5-hydroxy-methyl-cytosine in the genome of Biomphalaria glabrata, a snail intermediate host of Schistosoma mansoni. Parasit Vectors 6 (2013) 167.

5. Mourao, M.M., **Grunau**, C., Loverde, P.T., Jones, M.K. and Oliveira, G.: Recent advances in Schistosoma genomics. Parasite Immunol. 34 (2012) 151-162.

6. Lepesant, J.M., Roquis, D., Emans, R., Cosseau, C., Arancibia, N., Mitta, G. and **Grunau**, C.: Combination of de novo assembly of massive sequencing reads with classical repeat prediction improves identification of repetitive sequences in Schistosoma mansoni. Exp Parasitol 130 (2012) 470 474.

7. Lepesant, J.M., Cosseau, C., Boissier, J., Freitag, M., Portela, J., Climent, D., Perrin, C., Zerlotini, A. and **Grunau**, C.: Chromatin structure changes around satellite repeats on the Schistosoma mansoni female sex chromosome suggest a possible mechanism for sex chromosome emergence. Genome Biol 13 (2012) R14.

8. Thomas, F., Fisher, D., Fort, P., Marie, J.P., Daous, S., Roche, B., **Grunau**, C., Cosseau, C., Mitta, G., Baghdiguian, S., Rousset, F., Lassus, P., Assenat, E., Grégoire, D., Missé, D., Lorz, A., Billy, F., Vainchecker, W., Delhommeau, F., Koscielny, S., Itzykson, R., Tang, R., Fava, F., Ballesta, A., Lepoutre, T., Krasinska, L., Dulic, V., Raynaud, P., Blanche, P., Quittau-Prevostel, C., Vignal, E., Trauchessec, H., Perthame, B., Clairambault, J., Volpert, V., Solary, E., Uibner, U. and Hochberg, M.E.: Applying ecological and evolutionary theory to cancer: a long and winding road. Evolutionary Applications (2012)

9. Beltran, S., Gourbal, B., Boissier, J., Duval, D., Kieffer-Jaquinod, S., Pierce, R.J., **Grunau**, C., Theron, A. and Mitta, G.: Vertebrate host protective immunity drives genetic diversity and antigenic polymorphism in Schistosoma mansoni. J Evol Biol 24 (2011) 554-572.

10. Lepesant, M.J., J, **Grunau**, C. and Cosseau, C.: Towards an understanding of the epigenetics of schistosomes: a comparative epigenomic study. Mem Inst Oswaldo Cruz 106 (2011) 823-830.

11. Cosseau, C. and **Grunau**, C.: Native chromatin immunoprecipitation. Methods Mol. Biol. 791 (2011) 195-212.

12. **Grunau**, C.: Methylation mapping in humans. In: Hallgrimsson, B. and Hall, B.K. (Eds.), Epigenetics: Linking Genotype and Phenotype in Development and Evolution. 2011, pp.

13. Chantepie, S.P., Vaur, D., **Grunau**, C., Salaun, V., Briand, M., Parienti, J.J., Heutte, N., Cheze, S., Roussel, M., Gauduchon, P., Leporrier, M. and Krieger, S.: ZAP-70 intron1 DNA methylation status: determination by pyrosequencing in B chronic lymphocytic leukemia. Leuk. Res. 34 (2010) 800-808.

14. Portela, J., **Grunau**, C., Cosseau, C., Beltran, S., Dantec, C., Parrinello, H. and Boissier, J.: Whole-genome in-silico subtractive hybridization (WISH) - using massive sequencing for the identification of unique and repetitive sex-specific sequences: the example of Schistosoma mansoni. BMC Genomics 11 (2010) 387.

15. **Grunau**, C. and Boissier, J.: No evidence for lateral gene transfer between salmonids and schistosomes. Nat. Genet. 42 (2010) 918-919.

16. Blouin, M.S., Thuillier, V., Cooper, B., Amarasinghe, V., Cluzel, L., Araki, H. and **Grunau**, C.: No evidence for large differences in genomic methylation between wild and hatchery steelhead (Oncorhynchus mykiss). Canadian Journal of Fisheries and Aquatic Sciences 67 (2010) 217-224.

17. Cosseau, C., Azzi, A., Rognon, A., Boissier, J., Gourbière, S., Roger, E., Mitta, G. and **Grunau**, C.: Epigenetic and phenotypic variability in populations of Schistosoma mansoni a possible kick-off for adaptive host/parasite evolution. Oikos 119 (2010) 669-678.

18. Azzi, A., Cosseau, C. and **Grunau**, C.: Schistosoma mansoni: developmental arrest of miracidia treated with histone deacetylase inhibitors. Exp Parasitol 121 (2009) 288-291.

19. Cosseau, C., Azzi, A., Smith, K., Freitag, M., Mitta, G. and **Grunau**, C.: Native chromatin immunoprecipitation (N-ChIP) and ChIP-Seq of Schistosoma mansoni: Critical experimental pa-

rameters. Molecular & Biochemical Parasitology 166 (2009) 70-76.

20. Dubois, F., Caby, S., Oger, F., Cosseau, C., Capron, M., **Grunau**, C., Dissous, C. and Pierce, R.J.: Histone deacetylase inhibitors induce apoptosis, histone hyperacetylation and up-regulation of gene transcription in Schistosoma mansoni. Mol Biochem Parasitol 168 (2009) 7-15.

21. Chantepie, S., Vaur, D., **Grunau**, C., Salaun, V., Briand, M., Cheze, S., Gauduchon, P., Leporrier, M. and Krieger, S.: ZAP-70 Intron-1 DNA Methylation Status: A Simplified Method of Determination by Pyrosequencing in B Chronic Lymphocytic Leukemia. Blood 112 (2008) 385.

22. Bouchut, A., Roger, E., Gourbal, B., **Grunau**, C., Coustau, C. and Mitta, G.: The compatibiuty polymorphism in invertebrate host/trematodes interactions: research of molecular determinants. Parasite 15 (2008) 304-309.

23. Roger, E., Mitta, G., Mone, Y., Bouchut, A., Rognon, A., **Grunau**, C., Boissier, J., Theron, A. and Gourbal, B.E.: Molecular determinants of compatibility polymorphism in the Biomphalaria glabrata/Schistosoma mansoni model: new candidates identified by a global comparative proteomics approach. Mol Biochem Parasitol 157 (2008) 205-216.

24. Roger, E., Gourbal, B., **Grunau**, C., Pierce, R.J., Galinier, R. and Mitta, G.: Expression analysis of highly polymorphic mucin proteins (Sm PoMuc) from the parasite Schistosoma mansoni. Mol Biochem Parasitol 157 (2008) 217-227.

25. Roger, E., **Grunau**, C., Pierce, R.J., Hirai, H., Gourbal, B., Galinier, R., Emans, R., Cesari, I.M., Cosseau, C. and Mitta, G.: Controlled Chaos of Polymorphic Mucins in a Metazoan Parasite (Schistosoma mansoni) Interacting with Its Invertebrate Host (Biomphalaria glabrata). PLoS Negl. Trop. Dis. 2 (2008) e330.

26. **Grunau**, C., Brun, M.E., Rivals, I., Selves, J., Hindermann, W., Favre-Mercuret, M., Granier, G. and De Sario, A.: BAGE hypomethylation, a new epigenetic biomarker for colon cancer detection. Cancer Epidemiol Biomarkers Prev 17 (2008) 1374-1379.

27. Guillou, F., Roger, E., Mone, Y., Rognon, A., **Grunau**, C., Theron, A., Mitta, G., Coustau, C. and Gourbal, B.E.: Excretory-secretory proteome of larval Schistosoma mansoni and Echinostoma caproni, two parasites of Biomphalaria glabrata. Mol Biochem Parasitol 155 (2007) 45-56.

28. Negre, V. and **Grunau**, C.: The MethDB DAS server: adding an epigenetic information layer to the human genome. Epigenetics 1 (2006) 101-105.

29. **Grunau**, C., Buard, J., Brun, M.E. and De Sario, A.: Mapping of the juxtacentromeric heterochromatin-euchromatin frontier of human chromosome 21. Genome Res. 16 (2006) 1198-1207.

30. **Grunau**, C., Sanchez, C., Ehrlich, M., van der Bruggen, P., Hindermann, W., Rodriguez, C., Krieger, S., Dubeau, L., Fiala, E. and De Sario, A.: Frequent DNA hypomethylation of human juxtacentromeric BAGE loci in cancer. Genes Chromosomes Cancer 43 (2005) 11-24.

31. Krieger, S., **Grunau**, C., Sabbah, M. and Sola, B.: Cyclin D1 gene activation in human myeloma cells is independent of DNA hypomethylation or histone hyperacetylation. Exp Hematol 33 (2005) 652-659.

32. de Meeus, T., Humair, P.F., **Grunau**, C., Delaye, C. and Renaud, F.: Non-Mendelian transmission of alleles at microsatellite loci: an example in Ixodes ricinus, the vector of Lyme disease. Int. J. Parasitol. 34 (2004) 943-950.

33. Negre, V. and **Grunau**, C.: eL-DASionator: an LDAS upload file generator. BMC Bioinformatics 5 (2004) 55.

34. Roizes, G., **Grunau**, C., Buard, J., De Sario, A. and Puechberty, J.: Centromeres and neocentromeres. Methods Mol. Biol. 240 (2004) 77-104.

35. **Grunau**, C.: MethDB - The DNA methylation database. In: Lorkowski, S. and Cullen, P.M. (Eds.), Analysing Gene Expression, A Handbook of Methods: Possibilities and Pitfalls. Wiley-VCH, 2003, pp.

36. Amoreira, C., Hindermann, W. and **Grunau**, C.: An improved version of the DNA Methylation database (MethDB). Nucleic Acids Res. 31 (2003) 75-77.

37. **Grunau**, C.: The DNA methylation database MethDB. In: (Ed.), 2002, pp.

38. Warnecke, P.M., Stirzaker, C., Song, J., **Grunau**, C., Melki, J.R. and Clark, S.J.: Identification and resolution of artifacts in bisulfite sequencing. Methods 27 (2002) 101-107.

39. **Grunau**, C., Renault, E. and Roizes, G.: DNA Methylation Database "MethDB": a user guide. J. Nutr. 132 (2002) 2435S-2439S.

40. **Grunau**, C., Renault, E., Rosenthal, A. and Roizes, G.: MethDB--a public database for DNA methylation data. Nucleic Acids Res. 29 (2001) 270-274.

41. **Grunau**, C., Clark, S.J. and Rosenthal, A.: Bisulfite genomic sequencing: systematic investigation of critical experimental parameters. Nucleic Acids Res. 29 (2001) E65-5.

42. **Grunau**, C., Schattevoy, R., Mache, N. and Rosenthal, A.: MethTools--a toolbox to visualize and analyze DNA methylation data. Nucleic Acids Res. 28 (2000) 1053-1058.

43. **Grunau**, C., Hindermann, W. and Rosenthal, A.: Large-scale methylation analysis of human genomic DNA reveals tissue-specific differences between the methylation profiles of genes and pseudogenes. Hum. Mol. Genet. 9 (2000) 2651-2663.

44. Rohde, A., **Grunau**, C., De Beck, L., Van Montagu, M., Rosenthal, A. and Boerjan, W.: Carpel, a new Arabidopsis epi-mutant of the SUPERMAN gene: phenotypic analysis and DNA methylation status. Plant Cell Physiol 40 (1999) 961-972.

45. **Grunau**, C.: Transient demethylation during spermatogenesis is possibly the cause for ectopic expression of pseudogenes and transgenes in the testis. Methylation Society (1998)

46. Ohkuma, M., Ohtoko, K., **Grunau**, C., Moriya, S. and Kudo, T.: Phylogenetic identification of the symbiotic hypermastigote Trichonympha agilis in the hindgut of the termite Reticulitermes speratus based on small-subunit rRNA sequence. J Eukaryot Microbiol 45 (1998) 439-444.

47. **Grunau**, C., Dettmer, R., Behlke, J. and Bernhardt, R.: Bovine adrenodoxin--a mitochondrial iron-sulphur protein--binds to chaperonin GroEL. Biochem. Biophys. Res. Commun. 210 (1995) 1001-1008.

48. Erdmann, B., Henning, M., Uhlmann, H., Beckert, V., **Grunau**, C. and Bernhardt, R.: Immunocytochemical localization of heterologously expressed adrenodoxin and its electron acceptor cytochrome P45011B1 in Escherichia coli. Eur. J. Cell Biol. 65 (1994) 220-228.

BOOK CHAPTERS

Grunau C. *Methylation mapping in humans.* In: Hallgrimsson B, Hall BK, editors. Epigenetics: Linking Genotype and Phenotype in Development and Evolution. (2011)

Grunau, C. *MethDB - The DNA methylation database* in Analysing Gene Expression - A handbook of methods: Possibilities and Pitfalls (2002)

PATENTS

Grunau, C. and A. De Sario "Utilisation des loci BAGE comme marqueurs tumoraux" French patent for the CNRS (2003), international extension PCT/FR04/01170 (2004)