Christoph Grunau

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PERSONAL INFORMATION

- born 9/3/1967 in Dessau (Germany)
- married, no children
- nationality: German

PROFILE

I am a confirmed researcher in the field of epigenetics with international working experience in industry, university and research institutes. My current research interest is to understand the role of epigenetics 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, and PloS One 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

Maître de Conférence (Associate Professor) University of Perpignan (2007 - present)
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 humanblood fluke Schistosma mansoni) *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	350 000 €
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
2010	Cécile Perrin	PostDoc	Cloning and sequencing of promotor regions of the polymorphic *Sm*PoMuc gene family
2009-present	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

MILITARY SERVICE

- Hagenow (former East Germany) 1985 - 1988

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
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. Portela,J., **Grunau,C.**, Cosseau,C., Beltran,S., Dantec,C., Parrinello,H. and Boissier,J. (2010) *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, 387.
2. 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. (2010) *ZAP-70 intron1 DNA methylation status: determination by pyrosequencing in B chronic lymphocytic leukemia.* Leuk. Res. 34, 800-808.
3. Cosseau,C., Azzi,A., Rognon,A., Boissier,J., Gourbière,S., Roger,E., Mitta,G. and **Grunau,C.** (2010) *Epigenetic and phenotypic variability in populations of Schistosoma mansoni–a possible kick-off for adaptive host/parasite evolution* Oikos 119, 669-678.
4. Blouin,M.S., Thuillier,V., Cooper,B., Amarasinghe,V., Cluzel,L., Araki,H. and **Grunau,C.** (2010) *No evidence for large differences in genomic methylation between wild and hatchery steelhead (Oncorhynchus mykiss)* Canadian Journal of Fisheries and Aquatic Sciences 67, 217-224.
5. Dubois, F., Caby, S., Oger, F., Cosseau, C., Capron, M., **Grunau, C.**, Dissous, C., Pierce, R.J. (2009) *Histone deacetylase inhibitors induce apoptosis, histone hyperacetylation and up-regulation of gene transcription in Schistosoma mansoni* Molecular and Biochemical Parasitology 168 (1), 7-15
6. Cosseau, C., Azzi, A., Smith, K., Freitag, M., Mitta, G., **Grunau, C.** (2009) *Native chromatin immunoprecipitation (N-ChIP) and ChIP-Seq of Schistosoma mansoni: Critical experimental parameters* Molecular and Biochemical Parasitology 166 (1), 70-6
7. Azzi, A., Cosseau, C., **Grunau, C.** (2009) *Schistosoma mansoni: Developmental arrest of miracidia treated with histone deacetylase inhibitors* Experimental Parasitology 121 (3), 288-91
8. Chantepie, S, Vaur, D, **Grunau, C,** Salaun, V, Briand, M, Cheze, S, Gauduchon, P, Leporrier, M and Krieger, S. (2008) *ZAP-70 Intron-1 DNA Methylation Status: A Simplified Method of Determination by Pyrosequencing in B Chronic Lymphocytic Leukemia.* Blood 112, 385.
9. Roger, E, **Grunau, C,** Pierce, RJ, Hirai, H, Gourbal, B, Galinier, R, Emans, R, Cesari, IM, Cosseau, C,Mitta, G (2008) *Controlled Chaos of Polymorphic Mucins in a Metazoan Parasite (Schistosoma mansoni) Interacting with Its Invertebrate Host (Biomphalaria glabrata)*. PLoS Negl Trop Dis 2, e330.
10. Bouchut, A, Roger, E, Gourbal, B, **Grunau, C**, Coustau, C,Mitta, G, (2008) *The compatibility polymorphism in invertebrate host/trematodes interactions: research of molecular determinants.* Parasite 15, 304-09.
11. Roger,E., Gourbal,B., **Grunau,C.**, Pierce,R.J., Galinier,R. and Mitta,G. (2008) *Expression analysis of highly polymorphic mucin proteins (Sm PoMuc) from the parasite Schistosoma mansoni.* Mol Biochem Parasitol 157, 217-227.
12. Roger,E., Mitta,G., Mone,Y., Bouchut,A., Rognon,A., **Grunau,C.**, Boissier,J., Theron,A. and Gourbal,B.E. (2008) *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, 205-216.

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

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

15. **Grunau C**, Buard J, Brun ME, De Sario A. *Mapping of the juxtacentromeric heterochromatin-euchromatin frontier of human chromosome 21.* Genome Res. 2006. 16(10):p. 1198-207.

16. Negre, V and **C. Grunau** *The MethDB DAS Server: Adding an Epigenetic Information Layer to the Human Genome* Epigenetics 2006. 1(2): p 101-5

17. Krieger, S., **C. Grunau**, M. Sabbah, and B. Sola, *Cyclin D1 gene activation in human myeloma cells is independent of DNA hypomethylation or histone hyperacetylation.* Exp Hematol, 2005. **33**(6): p. 652-9.

18. **Grunau, C.**, C. Sanchez, M. Ehrlich, P. van der Bruggen, W. Hindermann, C. Rodriguez, S. Krieger, L. Dubeau, E. Fiala, and A. De Sario, *Frequent DNA hypomethylation of human juxtacentromeric BAGE loci in cancer.* Genes Chromosomes Cancer, 2005. **43**(1): p. 11-24.

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

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

21. de Meeus, T., P.F. Humair, **C. Grunau**, C. Delaye, and F. Renaud, *Non-Mendelian transmission of alleles at microsatellite loci: an example in Ixodes ricinus, the vector of Lyme disease.* Int J Parasitol, 2004. **34**(8): p. 943-50.

22. Amoreira, C., W. Hindermann, and **C. Grunau**, *An improved version of the DNA Methylation database (MethDB).* Nucleic Acids Res, 2003. **31**(1): p. 75-7.

23. Warnecke, P.M., C. Stirzaker, J. Song, **C. Grunau**, J.R. Melki, and S.J. Clark, *Identification and resolution of artifacts in bisulfite sequencing.* Methods, 2002. 27(2): p. 101-7.

24. **Grunau, C.**, E. Renault, and G. Roizes, *DNA Methylation Database "MethDB": a user guide.* J Nutr, 2002. 132(8 Suppl): p. 2435S-2439S.

25. **Grunau, C.**, E. Renault, A. Rosenthal, and G. Roizes, *MethDB--a public database for DNA methylation data.* Nucleic Acids Res, 2001. 29(1): p. 270-4.

26. **Grunau, C.**, S.J. Clark, and A. Rosenthal, *Bisulfite genomic sequencing: systematic investigation of critical experimental parameters.* Nucleic Acids Res, 2001. 29(13): p. E65-5.

27. **Grunau, C.**, R. Schattevoy, N. Mache, and A. Rosenthal, *MethTools--a toolbox to visualize and analyze DNA methylation data.* Nucleic Acids Res, 2000. 28(5): p. 1053-8.

28. **Grunau, C.**, W. Hindermann, and A. Rosenthal, *Large-scale methylation analysis of human genomic DNA reveals tissue-specific differences between the methylation profiles of genes and pseudogenes.* Hum Mol Genet, 2000. **9**(18): p. 2651-63.

29. Rohde, A., **C. Grunau**, L. De Beck, M. Van Montagu, A. Rosenthal, and W. Boerjan, *Carpel, a new Arabidopsis epi-mutant of the SUPERMAN gene: phenotypic analysis and DNA methylation status.* Plant Cell Physiol, 1999. **40**(9): p. 961-72. (joint first authorship)

30. Ohkuma, M., K. Ohtoko, **C. Grunau**, S. Moriya, and T. Kudo, *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, 1998. **45**(4): p. 439-44.

31. **Grunau, C.**, R. Dettmer, J. Behlke, and R. Bernhardt, *Bovine adrenodoxin--a mitochondrial iron-sulphur protein--binds to chaperonin GroEL.* Biochem Biophys Res Commun, 1995. **210**(3): p. 1001-8.

32. Erdmann, B., M. Henning, H. Uhlmann, V. Beckert, **C. Grunau**, and R. Bernhardt, *Immunocytochemical localization of heterologously expressed adrenodoxin and its electron acceptor cytochrome P45011B1 in Escherichia coli.* Eur J Cell Biol, 1994. **65**(1): p. 220-8.

BOOK CHAPTERS

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)

ORAL PRESENTATIONS

International conferences

- " Evolutionary Epigenetics: environmentally induction of phenotypic variability in blood-fluke populations a possible kick-off for adaptive evolution " Epigenetics World Conference Berlin (Germany) 17-18/9/2009
- " The Compatibility Polymorphism In Invertebrate Host/Trematodes Interactions: Research of Molecular Determinants " (Keynote speaker) European Multicolloquium of Parasitology Paris (France) 24-28/8/2008
- " The DNA methylation database MethDB " INSERM workshop " Epigenetic aspects of reproduction " La Londe Les Maures (France) 9-11/9/2004
- " Making better MAC - final meeting " Trieste (Italy) 19/11/2003
- " Making better MAC - mid-term meeting " Montpellier (France) 18-20/4/2002 (organizer)
- " Making better MAC - kick-off meeting " Edinburgh (G.B.) 15/2/2001
- " The DNA methylation database MethDB " Trans-HHS Workshop "Diet, DNA methylation Processes and Health" Bethesda (USA) - 6-8/8/2001 (invited speaker)

Seminars

- "Epigenetics of human juxtacentromeric regions" University of Perpignan (France) - 4/11/2005 (invited)
- " The role of epigenetics in the control of chromosome architecture " IMB Jena (Germany), 22/3/2005 (invited)
- " Epigenetic control of chromosome architecture " University of Perpignan (France), 14/1/2005 (invited)
- " Breaking the silence : how juxtacentromeric genes escape from inactivation " ENS Lyon, 17/5/2004 (invited)
- " DNA methylation who cares ? " CRLC Val d'Aurelle Montpellier, 11/2/2003
- " C.cohnii as a new model for eukaryotic DNA methylation ? " Laboratoire Arago Banyuls, 9/12/2002

POSTERS

- " Schistosoma mansoni: what makes a girl a girl? " **Grunau C,** Boissier J, Cosseau C, Beltran S, Duval D, Portela J, Gourbal B, Theron A, Mitta G, ASTMH Meeting Washington (EU) 18-22/11/2009
- " ZAP-70 Intron-1 DNA Methylation Status : A Simplified Method of Determination by Pyrosequencing in B Chronic Lymphocytic Leukemia " S.Chantepie, D.Vaur, **C.Grunau,** V. Salaun, M.Briand, S.Cheze, P.Gauduchon, M.Leporrier, S.Krieger, American Society of Hematology Meeting, San Francisco (EU) 3-7/12/2008

- " Heterochromatin-euchromatin transition in the juxtacentromeric region of human chromosome 21 " **C.Grunau**, J.Buard, M-E.Brun, A-M.Laurent, A.Desario, EMBO conference, EMBO/FEBS Conference on Nuclear Structure and Dynamics, La Grande Motte (France) 24-28/9/2005

- " Human juxtacentromeric loci BAGE are activated by DNA demethylation and histone acetylation during neoplastic transformation " **C. Grunau**, A. De Sario, Second Weissenburg Symposium, Weissenburg (Germany) 12-15/5/2004

- " A role for DNA de-methylation in the activation of the cancer-testis antigens BAGE? " **C.Grunau**, M.Ruault, P. van der Brueggen, G.Roizes and A.Desario, CNIO Cancer Conference, Madrid (Spain) 29-31/5/2002

- " MethDB - a Relational DNA-Methylation Database " M.Schilling, **C.Grunau**, A. Rosenthal German conference on Bioinformatics, Cologne (Germany) 7-10/10/1998

- " Systematic Determination and Semi-automated Analysis of Methylation Patterns in Human DNA " **C.Grunau**, D.Stötzer, M.Schilling, R.Schattevoy, A.Rosenthal, Curie Workshop on Epigenetics and DNA Methylation, Paris (France) 23 -27/9/1998

- " Systematic determination of methylation patterns in Xq28 " **C.Grunau**, V.Brenner, A.Rosenthal, Cold Spring Harbour Meeting "Genome Mapping, Sequencing and Biology", Cold Spring Harbour (USA) 13 - 17/5/1998

DATABASES

- " The database of DNA methylation and environmental epigenetic effects" http://www.methdb.net