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Personal data sheet

Current situation:

- Chair of the Department “Fundamental Microbiology and Pathogenicity” (Microbiologie fondamentale et pathogénicité, MFP, UMR 5234) of the CNRS and the University of Bordeaux. http://www.mfp.cnrs.fr/mfp/index_en.php. In France, this position is an elected one allowing two 5-year mandates. I was recently re-elected for the second period.

The Department has c. 80 staff members and trainees working in Parasitology, Bacteriology, Mycology and in particular Virology. The academic staff of the Diagnostic Virology Service of the University Hospitals of Bordeaux (CHU de Bordeaux) and also the WHO reference center for HIV resistance is part of the Department. MDs in Infectious Diseases are associated. In contrast to the nationwide funding reduction, I could increase the subventions. I could was further able to attract in 2015 and for 2016 two new research teams, which are excellent in cryo electron microscopy (Rémi Fronzes) and in Trypanosome metabolism (Frédéric Bringaud).

- Full Professor of Medicine in the Diagnostic Virology Service of the University Hospitals of Bordeaux with a specialization in “Biologie Médicale”, which comprises Microbiology but also related domains as Immunology and Laboratory Medicine. The Service in which I am working is the largest in South-Western France, performing c. 250.000 serological and c. 80.000 PCR analyses per year.
- Responsible for a research team “Intracellular dynamics of subviral structures”, which focuses on hepatitis B virus (HBV), parvoviruses and adenoviruses.
- Teaching of Virology for students in Medicine and Life Sciences (c. 80 h/year). Training of MDs in virology of hepatitis viruses. Responsible for Virology-Parasitology-Immunology training for Master students in Life Sciences.
- Invited Professor at the University of Tsukuba, Japan.
- Director of Aquitaine Microbiologie. This start-up is focused on test development in Microbiology for industry in particular in human and veterinary medicine.
http://www.mfp.cnrs.fr/mfp/team_am.php

since 2012	Full professor in Medicine at the University of Bordeaux, France.
since 2011	Invited professor at the University of Tsukuba, Japan. Accreditation as specialist for "Medical Biologist" in France, which comprises Microbiology and Immunology but also Hematology and Biochemistry. Chair of the Department "Fundamental Microbiology and Pathogenicity".
since 2010	Director of "Aquitaine Microbiologie".
since 2009	Physician at the Virological Diagnostic Department at the University Hospitals of Bordeaux, France.
2006 - 2012	Full professor in Life Science at the University Victor Ségalen Bordeaux, France.
2006 - 2010	Member of the Faculty Board in Life Sciences, University of Bordeaux, France.
2005 - 2006	Associated Professor at the University Victor Ségalen Bordeaux, France.
2005	Habilitation in Life Sciences at the University of Bordeaux Ségalen.
2003 - 2005	Deputy Director of the Institute of Medical Virology at Giessen University.
2003	Löffler-Frosch research award for "The fundamental Research on the Life cycle of the Hepatitis B Virus" by the Society of Virology (Germany-Austria-Switzerland).
2002 – 2004	Head of the study group "Cell biology of viral infections" at the Society of Virology (Germany-Austria-Switzerland).
since 2000	Member of the International Committee for the Taxonomy of Viruses (ICTV).
2000 - 2005	Assistant Professor for Clinical Virology at the Justus Liebig University Giessen. Expert for Hepatitis B nominated by the Germany Ministry of Health.
1998 – 2000	Lecturer at Justus Liebig University Giessen, Germany.
1997 – 2005	Principle investigator of a research group at Justus Liebig University Giessen, Germany. Deputy Director of the virological diagnostic department at the University Hospital, Giessen, Germany.
1997	Habilitation in Medicine at the Justus Liebig University Giessen, Germany.
1995 - 1996	Scholarship of the Deutsche Forschungsgemeinschaft to acquire qualification as a university lecturer.
1995	Postdoc at the Department of Cell Biology, Yale University, New Haven, CT, U.S.A.
1992 – 1995	Postdoc at the Institute of Virology, Justus Liebig University Giessen, Germany (National Reference Centre for Hepatitis B). Vocational training in Virology and in Internal Medicine.
1990	Defense of thesis "Characterization of hepatitis B virus polymerase by prokaryotic expression", University of Göttingen, Germany.
1988 – 1992	Physician at the Institute of Hygiene, Göttingen University, Germany. Vocational training to get the degree as specialist for Microbiology.
1988	End of medical studies and certificate to practice.
1982 - 1988	Studies of human medicine at Georg August University, Göttingen, Germany, including training at Green College, Oxford University, UK.

Research

Summary

Aim of my research team is the identification of cellular and viral factors linked to efficiency of infection. This research is performed on three viruses: HBV, parvoviruses including adeno-associated virus (AAV) vectors and adenoviruses. Given that the experimental systems have virus-dependent limits not all steps can be addressed with all viruses. This is exemplified by HBV for which no culture system exists, which allow virus propagation. On the other hand, HBV allows the assembly of clinical data, which are difficult to obtain for AAV.

- Hepatitis B: the aim of our studies is the understanding of the impact of fundamental processes of hepatitis B virus trafficking and variability on disease development. This includes the development of model systems allowing the verification of future treatment options.
- Parvoviruses: we analyze the biology of different parvoviruses for their capacity of DNA delivery into the nucleus. These investigations are driven by the successful use of parvoviruses in gene therapy.

The activities on HBV and parvoviruses are currently executed by one senior scientist, one postdoc, two PhD students and one technician. Research on adenoviruses is supervised by my co principle investigator.

Research projects

HBV (capsids) and parvoviruses (PV) have in common that they replicate in the nucleus. In analogy to other viruses, it was thought that their genome is liberated from the surrounding capsid in the cytoplasm or at the cytoplasmic face of the nuclear pore complex (NPC). Our electron microscopy-based finding in collaboration with Nelly Panté, Vancouver, Canada, showed that the functional diameter of the NPC is 40 nm instead of 26 nm, which was furthermore thought to be restricted by an additional central transport complex (Panté and Kann, *Mol Biol Cell*, 2002; 353 – 900 x cited, dependent upon source). This observation changed the perspective in that both capsids – HBV 36 nm; PV 18 to 25 nm - could pass the NPC followed by genome release inside the nucleus.

Hepatitis B. Analyzing the nuclear transport of HBV capsids we observed however that the capsids passed the NPC intact mediated by the cellular transport receptors importin α and β (Kann et al., *J Cell Biol*, 1999). Unlike classical karyophilic cargos, the capsids became however arrested on the nuclear side of the NPC by interaction with a specific NPC protein called Nup153 (Schmitz et al., *PLoS Pathog*, 2010). This strategy was a unique new finding and raised our interest in cell biology of the nuclear pore. Exclusively at the NPC (Rabe et al., *J Vir*, 2006) the capsids dissociate to capsid (core) protein dimers, followed by re-association to genome-devoid capsids (Rabe et al., *PLoS Pathog*, 2009). The dissociation was strictly correlated to genome maturation (Rabe et al., *PNAS*, 2003; recommended by the faculty of 1000), which transforms the viral RNA pregenome into a partially double stranded DNA, and which linked to structural changes of the capsid. These changes also occur upon capsid protein phosphorylation (Kann et al., *J Cell Biol*, 1999; Rabe et al., *PNAS* 2003) and in capsids devoid of nucleic acids (Chen et al., *PLoS Pathog*, 2016). Despite of this detailed knowledge there are, however, significant lacks, which are important for developing experimental systems, also needed for verification of therapeutical concepts.

The recently discovered receptor for HBV – hNTCP – allow after expression in non-permissive cultured cells infection although no virus propagation was achieved in culture. Expressing hNTCP in transgenic mice however failed to generate HBV susceptible animals although another virus, which uses the same receptor and import pathway, multiplies. Our recent findings showed that the intracytoplasmic

transport of the capsid is facilitated via the dynein light chain Dyn LL1 (Osseman et al., PLoS Pathog, in review), which is conserved in man and mice without exhibiting any polymorphism. We thus hypothesize that the block occurs after arrival of the capsid at the NPC and after entering the nuclear phase of the pore. The HBV replication cycle demands a repair of the genome to a chromatinized covalently closed form needing several enzymatic activities, which are poorly known. Having identified some candidates which are different in man and mice we focus on the understanding of genome repair also assuming that these protein(s) are involved in genome liberation. This project is strongly enhanced by an agreement with the company Neovirtech, which gives me the exclusive right to use their patented system allowing the real time follow-up of single HBV genomes.

In patients, the HBV viral load is largely controlled by the immune system, namely CD8⁺ T cells but establishment of infection is likely also controlled by the intrinsic immune response of the cell. In a collaborative project with Percy Knolle, Munich, Germany, we investigate the phenomenon that the TNF α sensitizing activity of some adenoviral proteins is counterbalanced by HBV (upon transduction). This finding is in agreement with the proposed longer life span of HBV infected hepatocytes. Further remarkable is that it also occurs in TNF2 negative mice, showing that the CD8⁺ response is not required indicating a new pathway of innate immune response.

Yet another factor influencing the viral load is the variability of HBV genomes. This assumption is supported by early findings of others showing that the viral load is genotype-dependent. For better understanding the underlying molecular background we performed full genome sequencing of >400 samples from untreated, chronically infected patients. This work was based on a pilot study in which we sequenced the core protein ORF in 50 patients and which revealed a cluster of four amino acids statistically correlated with a 2 logs higher viral load (Wittkop et al., Antivir Ther, 2009). Consistently, transfection also resulted in a higher virus concentration in cell culture supernatants. In collaboration with Maura Dandri, Hamburg, we are currently investigating the replication capacity in liver-humanized mice.

The full genome Sanger sequencing showed a remarkable variability but also exhibited that the majority of sera contained just one sequence. Of note, deep sequencing of 28 sera showed only polymorphisms, which were also represented in the panel of Sanger sequences. We thus conclude that the spectrum of polymorphisms obtained by Sanger sequencing represents a very large percentage – if not all - of theoretically existing HBV sequences. This allowed us to determine the impact of intracellular mutations on virus release, which are known to be strictly controlled in HBV. Having clinical data of most patients we conclude that e.g. APOBECG modifications do not have a significant impact, arguing against a recent hypothesis published in Science. However, the statistical analyses in particular with regard to the correlation of the viral load with specific genome sequences is ongoing in collaboration with the local centre of biostatistics and epidemiology in Bordeaux (Linda Wittkop, ISPED).

Parvoviruses. In analogy to the HBV research, we investigated the nuclear interactions of different PV. We investigated intact PV capsids for analyzing the infection process but also the transport of partially preassembled capsid proteins. The latter step is required for assembling progeny virus, which occurs intranuclear. While the import of preassembled capsid proteins occurred “normally” through the NPCs although by an unknown transport receptor pathway (collaboration with Jose-Maria Almendral, Madrid, Spain; Rioloobos et al., J Vir 2010; Gil-Renando et al., PLoS Pathog 2015), we observed that different PV did not only bind to the NPC but made holes in the nuclear envelope (Porval et al., PLoS Pathog 2013). This finding was exciting, as such an effect of viruses on the nucleus was never observed. Collaborating with Mario Schelhaas, Muenster, Germany, we observed that these hole were large enough to allow diffusion of even larger structures as e.g. papillomavirus capsids (50 – 60 nm) after PV infection (Aydin et al., PLoS Pathog, 2014). Using different approaches, we could unravel a part of the underlying mechanisms, which is similar in different cell types. We could show that interaction with the NPC changes PV structure, which than makes holes in the nuclear envelope, leading to Ca⁺⁺ efflux from the space between inner and outer leaflet of the nuclear membrane. According to the current models of

how nuclear envelope breakdown (NEBD) is initiated upon mitosis, we found that several enzymes involved in mitosis were also required for PV-mediated NEBD. Of note, this NEBD was independent upon soluble cytosolic proteins allowing to investigate mitotic processes in the absence of shuttling proteins. There are however significant differences between mitotic and parvoviral NEBD namely that the latter was temporary and local. Microinjection experiments revealed that although being a stable phenomenon PV NEBD varied between cells in terms of time after injection.

Collaborative transduction experiments with Giovanni Di Pasquale, NIH, U.S.A., using a GFP-expressing adeno-associated virus (AAV) vector also showed a huge variability between individual cells despite of the fact that all cells were permissive. Combining transduction with microinjection showed a correlation between the entry on NEBD and the permissiveness of the cells (unpublished). We thus conclude that NEBD and infection correlates. This is in agreement with earlier finding of us, showing that PV H-1 mutants deficient in infection also failed to cause NEBD in permeabilized cells (Popa-Wagner, J Vir, 2012). Given the importance of efficient infection/transduction in gene therapy, we currently investigate the restricting factors in collaboration with Martin Mueller and Oliver Mueller, Heidelberg, Germany, aiming to increase transduction efficiency in epithelial cells.

Variability of nuclear import. The well-known phenomenon that the efficiency of nuclear localization of karyophilic structures is variable between individual cells let us investigate potential mechanisms existing aside of established modifications of the target proteins. These analyses were largely driven by our observations using HBV and PV considering that nuclear import receptors mediating transport are homogenously expressed amongst different cells and organs. We thus focused systematically on proteins of the NPC and in particular on their posttranslational modifications. Using thousands of permeabilized cells, exposed to artificial substrates and identical cytosol, we observed fulminant differences for two different import pathways (via transportins and importins), which could be modulated by changing cell growth conditions. This in turn allowed the analysis if the different transport capacity was correlated with posttranslational Nup modifications. Statistical analysis revealed that only one modification of one Nup (Nup62 glycosylation) explained import modifications via the nuclear transport receptor transportin, while the importin-mediated pathway was dependent upon modification/quantity of seven Nups (manuscript submitted). Aside of showing a new regulation mechanism of how cells can respond to external triggers, we assume that this principle can also play an essential role in infection efficiency of viruses when individual cells serve as super spreader as it is established in epidemiology. Considering the correlation of nuclear import capacity – also of housekeeping proteins - with the cell environment of the cells we hypothesize that the Nup modifications could also be important in cancer development or metastasis.

Future aspects. The overall aim is the understanding the determinants for virus spread and, for HBV, the mechanisms linked to disease development. This requires translational approaches as limiting factors can be on the cellular level, on the level of the organism, which includes host genetics but also on the level of the pathogen. Linking the results from these very different domains requires biostatistics already because not all processes are homogenous. Mathematical will be helpful for predictions, which are e.g. required if a phenomenon cannot be experimentally addressed.

In the mid-term range, I plan to investigate the molecular reasons and the impact of cell variability in the context of genomic viral variability. This requires high throughput microscopy after siRNA application and single cell RNAseq for quantitatively measure cellular and viral processes. Correlation with clinical data will help to identify key elements determining infection outcome. This research as far as HBV is concerned also needs support from immunological and if possible genetic departments.

Publications

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*paper derived from R&D of the start-up

Funding since 2006*

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|---|----------|
| ● 6 contracts of the ANRS (funding quota 12 %) | 411700 € |
| ● 3 fundings of the local government (funding quota 25 %) | 465000 € |
| ● 2 supports from the Fondation pour la Recherche Médicale (FRM)
This includes the prestigious “équipe label FRM” from which the FRM supports 8 – 11 per year. | 317000 € |
| ● CNRS – DFG (German Research Council) (funding quota 25 %) | 244000 € |
| ● ARC (funding quota 30 %) | 30000 € |
| ● 5 collaborative fundings from the Ministry of higher education | 97000 € |
| ● 1 collaborative funding from the CNRS (PICS – Canada)
(funding quota 25 %) | 45000 € |

* the sums shown above represent exclusively the support for my research team. Further 280000 € were obtained as subventions for the start-up since 2010 (sum exclusive industrial contracts).

Supervision in France

Aside of eight students during their first year of Master studies I supervised eight students in their second year during their practical training. I further supervise(d) eight PhD students; actually also two students in collaboration with other Universities (Tsukuba, Japan, co-supervisor: Kyosuke Nagata; Jyvaeskylae, Finland, co-supervisor: Majja Vihinen-Ranta). Of note, the graduate school of Bordeaux allows the supervision of just one PhD student at the same time. Exceptions are made if one student is already in his last year allowing to accept a second one or, if a student does his thesis in collaboration with a University outside France. The same rule excluding a second student is applied for Master students.

Teaching/training

My current teaching duty is c. 80 h/year, which comprise teaching in medicine but also in life sciences. I basically explain the disease by molecular mechanisms but with a focus on the branch of the study. For medical students this approach opens a perspective for understanding molecular processes and why these processes cause disease. Students of life sciences in contrast understand the medical background driving their mostly fundamental research. Evidently, this teaching is held on an advanced level of their studies.

Teaching in Bordeaux:

- Lectures for students in life sciences: 1st year of Master studies (40 h), basic Virology
- Lectures for students in life sciences: 2nd year of Master studies (5 h), infection processes of the cell
- Lectures for students in medicine: 3rd and 4th year of Master studies (12 h), replication of viruses, viral hepatitis, parvoviruses
- Training of MDs in hepatitis B (4 h)
- Lectures in scientific English for students in life sciences: 1st year of Master studies (9 h)

Teaching at the University Andres Bello, Santiago de Chile:

- Lectures for students in life sciences, medicine and veterinary medicine (12 h), basic virology

Responsibilities in teaching

Organization of teaching in Virology, Parasitology and Immunology for students in life sciences during their 1st year of Master studies.

Medical activities

The diagnostic services at the University Hospitals of Bordeaux are organized in technical platforms, which are in the cross responsibility of the different services. This means that e.g. PCRs – also those for bacteria - are performed under supervision of the virology service, while serological analyses are done on another platform, which is supervised by the service of biochemistry. Validation of the results, irrespectively of the platform, is done by the respective specialized service.

My current activity comprises the routine validation of the results but also the interpretation of the results in discussion with the clinicians. Further, I took the responsibility for HBV and HIV PCRs and I participate in the ongoing accreditation of the service activities concerning HBV and HIV. Organizational activities as the rotation of technicians are performed as well as special training for BSL4 pathogens as Ebola.

Evidently, hospital activities also affect my research activities allowing easier access to clinical samples and data. This is crucial as HBV infections with high viral loads are rare in France and mostly found in immune suppressed patients.

Other administration and responsibilities

Local

- Board member of the Federal Research Structure “Fundamental Biology applied to Medicine” (Biologie fondamentale et appliquée à la Médecine, UMS 3427, accredited by Inserm, CNRS, University of Bordeaux). This transversal structure comprises c. 500 staff members of 10 laboratories and coordinates science between basic and applied research.
<http://www.transbiomed.u-bordeaux2.fr/pages/anglais.html>
- Board member of the Medical Research Council (Direction de la recherche clinique et de l'innovation, DRCI) of the Hospitals in South-West France and the French overseas territories.

National

- Member of several boards at the ANRS (National Agency for Research on HIV and hepatitis) including the scientific board giving recommendations for hepatitis B and hepatitis D clinical trials.
- Board member of the CNRS (National Centre for Scientific Research, section Microbiology – Immunology) for hiring and evaluating permanent scientists in these domains nationwide.
- Member of the national evaluation committee of the Foundation on Cancer (Fondation ARC pour la recherche sur le cancer).
- Member of the national commission for the evaluation of French research structures (AERES/HCERES).

International

- Member of the International Committee on Taxonomy of Viruses (ICTV), division hepatitis B and D viruses.
- Invited professor at the University of Tsukuba, Japan.
- Head of a so-called “International Laboratory” on Virology, consisting of the department I am chairing, the Department of Immunology at the University of Bordeaux and the Heinrich-Pette-Institute for experimental Virology, Hamburg, Germany. The laboratory is accredited by the CNRS, France, and the Leibniz Association, Germany.
- Member of evaluation committees for different German research structures and institutions (Helmholtz Gesellschaft, DFG).
- Expert for various journals and funding agencies of different countries (France, Germany, UK, Belgium, Hong Kong); editor of the Journal of General Virology (UK), associated editor on Virology Journal (USA).
- Member of the scientific advisory board of the International Meetings on the Molecular Biology of Hepatitis B Viruses.
- Member of the organization committee of the 2016 International Workshop on Parvoviruses, Ajaccio, Corsica, June 19 – 23
- Organization of several conferences, including the co-organization of the 2014 International Meeting on the Molecular Biology of Hepatitis B Viruses 2014, Los Angeles and the International Workshop on Parvoviruses, which I organized in Bordeaux in 2014.