

Prion

ISSN: 1933-6896 (Print) 1933-690X (Online) Journal homepage: www.tandfonline.com/journals/kprn20

Introduction: Invited Speakers

To cite this article: (2013) Introduction: Invited Speakers, Prion, 7:sup1, 1-9, DOI: 10.4161/pri.26105

To link to this article: https://doi.org/10.4161/pri.26105

Copyright © 2013 Landes Bioscience

Published online: 01 Apr 2013.

Submit your article to this journal

Article views: 361

View related articles

Full Terms & Conditions of access and use can be found at
https://www.tandfonline.com/action/journalInformation?journalCode=kprn20

Prion 7: Supplement, 1-7; April/May 2013; © 2013 Landes Bioscience

Introduction

The Alberta Prion Research Institute, part of Alberta Innovates Bio Solutions, is proud to host the world's largest international prion research congress, PRION 2013: Conquering Frontiers, in Banff, Alberta, Canada from May 26–29, 2013. PRION 2013 will be only the second time this international meeting has been held outside of Europe since it began in 2004. The PRION 2013 International Scientific Advisory Committee includes leading international scholars and policy advisors in both human and animal protein misfolding research from 12 countries: Australia, Brazil, Canada, China, England, France, Germany, Japan, The Netherlands, Scotland, Spain and the United States. Prion and protein misfolding science can inform policy, risk management and mitigation, diagnoses and potential treatments in a range of areas from wildlife management to human dementias and neurodegenerative diseases. Compelling evidence is emerging that prion-like mechanisms may underlie a number of the human neurodegenerative diseases and dementias, providing the opportunity to seek out new treatments and for the cross-fertilization of ideas between the two related fields. This approach will be highlighted at PRION 2013. The theme of PRION 2013 is "Conquering Frontiers". It will be a continuation of the science covered in previous meetings with an emphasis on looking towards investigations in the new frontiers created by the relationships between prion diseases and human neurodegenerative diseases and dementias. The four-day session features scientific talks, workshops and posters on the following themes: Prion and Prion-like Diseases in Humans; Prion Diseases in Animals; Protein Structure and Biology; and Socioeconomic Impacts. The knowledge exchange that will take place at PRION 2013 will help to shape the future of prion and protein misfolding research and its application around the world.

Invited Speakers

Invited.01: Transmission of misfolded proteins in neurodegenerative disorders: A common mechanism of disease progression

Virginia M.Y. Lee

Center for Neurodegenerative Disease Research; Marian S. Ware Alzheimer Drug Discovery Program; Department of Pathology and Laboratory Medicine; Perelman School of Medicine; University of Pennsylvania; Philadelphia, PA USA

The accumulation of misfolded proteins is a fundamental pathogenic process in neurodegenerative diseases. These hallmark proteinaceous lesions include extracellular senile plaques comprised of the Aβ peptide and intracellular neurofibrillary tangles consisted of tau proteins in Alzheimer disease as well as α-synuclein (α-syn) containing Lewy bodies and Lewy neurites in Parkinson disease. We hypothesized that templated recruitment of endogenous proteins by misfolded conformers follow by cell-to-cell spreading of the pathology are a common disease mechanism that account for the progression of these age-related disorders. In both tauopathies and synucleinopathies, we demonstrate that pre-formed fibrils (pffs) generated from recombinant tau or α-syn enters cultured primary neurons as well as transgenic and wild-type mice, promoted recruitment of soluble endogenous proteins into insoluble protein aggregates resembling the pathology in their human counterparts. Pathologic misfolded aggregates propagated along major central nervous system (CNS) pathways to regions far beyond injection sites and appear to follow neuroanatomical interconnectomes. Thus, synthetic α-Syn or tau pffs are wholly sufficient to initiate neurodegenerative disease pathology and transmit disease in primary neurons in vitro and in mice in vivo. Thus, these data support a prion-like cascade in neurodegenerative disease protein spreading whereby cell-to-cell transmission and propagation of misfolded proteins underlie the CNS proliferation of disease pathology. These findings open up new avenues for understanding the progression of neurodegenerative diseases and for developing novel therapeutics.

Invited.02: Healthy animals, healthy Canada: An expert assessment of approaches to animal health risk assessment

Alastair Cribb

Faculty of Veterinary Medicine; University of Calgary; Calgary, AB Canada

Keywords: animal health, risk assessment, socioeconomic impacts

In September 2001, the Council of Canadian Academies released an expert panel assessment of approaches to animal health risk assessment in Canada.[1] The expert panel was asked to assess "the state and comprehensiveness of risk assessment techniques in animal health science, specifically pertaining to risks which may impact human health." This presentation will briefly summarize the key findings of this report.

The Panel's major finding was that an integrated, multi-dimensional approach that considers the appropriate range of

potential animal, human, socioeconomic and environmental consequences, as well as risk management outcomes, in the risk assessment process would contribute to assessments that provide increased value to risk managers, decision-makers, and stakeholders. Many risks to animal health have economic, ecological, and social implications beyond those directly affecting domestic animal health. A full range of potential consequences should be identified early in the risk assessment process using input from risk managers, risk assessors, and relevant stakeholders. Selection of consequences to consider in the risk assessment should be a formal element of the process. Risk-based decision-making and subsequent risk communication and management could benefit from a greater engagement of stakeholders in establishing risk assessment questions, scope, and consequences, and from improved access to expertise and knowledge among risk assessment practitioners. Because risk assessment is part of a broader risk analysis process that comprises hazard identification, risk assessment, risk communication, and risk management, all four phases need to be effectively performed to maximize the benefits of the risk assessment component.

Through the assessment process, the Panel found that Canada is well-equipped to meet the needs of importation and international trade obligations. However, adopting an integrated, multidimensional approach to risk assessment would help to serve both these areas and the broader goals of risk assessment—that is, to better inform decisions about current risks, emerging threats, and optimal risk management strategies. The majority of risk assessments conducted are qualitative and, while they may consider a range of consequences, the major focus is on the economic and trade consequences of introducing animal disease into Canada. In reviewing risk assessments from other countries, the Panel observed that several countries were taking a broader view of the consequences of animal health events. Canada is also moving toward this broader view.

References

1. Cribb A, et al. Healthy Animals, Healthy Canada: The Expert Panel on Approaches to Animal Health Risk Assessment. 2011, Council of Canadian Academies

Invited.03: Understanding knowledge mobilization in a prion science context

Ralph Matthews

Department of Sociology; University of British Columbia; Vancouver, BC Canada

The processes through which knowledge is created, communicated, evaluated, accepted and implemented are researchable social processes. These social processes involve far more than what is sometimes referred to as "knowledge translation" (KT) with its implication that medical scientists and other professionals have knowledge that others should learn to accept. In contrast, "knowledge mobilization" (KM) is a nonlinear, discursive, reflexive, multi-directional and socially constructed process. To understand KM requires an awareness of how the development and acceptance of scientific knowledge is influenced by: cultural values; assessments of benefits, risks and costs; social organizational structures; institutional cultures; and, political processes. That is, knowledge "in the wild" involves a constant series of translation and reconstructions about its meaning and relevance and it is these that are the subject matter of KM research.

This presentation will provide an overview of knowledge mobilization particularly as it relates to various aspects of prion science investigation, both in veterinary and medical science. In doing so, it will set out a framework for the study of KM, distinguishing between the "knowledge issues" and the "social impact issues" involved in prion science investigation. The result is a framework for assessing what is sometimes described as a "knowledge ecosystem".

Using the perspective so developed, the presentation will conclude with an overview of a complex of three studies (funded through PrioNet and other sources) that seek to examine the processes of KM in the prion science area. It will also point to the relevance of these studies to understanding innovation and the commercial application of scientific knowledge.

Invited.04: Toward rational, risk-based policies for BSE: Maintaining perspective

Noel Murray

Canadian Food Inspection Agency; Ottawa, ON Canada

While there may be some potentially important gaps in our knowledge, particularly for atypical strains of BSE, we have learnt a great deal since it first leapt onto the world stage in the 1980s. As our understanding of its pathogenesis continues to evolve in tandem with the development of increasingly sensitive assays, perhaps one of the greatest challenges is to ensure that new found knowledge does not lead to calls for measures that are disproportionate to the attendant risks. Excessive measures ultimately divert scarce and finite resources from other competing public and animal health priorities with potentially significant adverse socio-economic impacts.

Ultra-sensitive assays, whether they target PrP^{Sc} itself or infectivity are capable of detecting vanishingly small amounts that may be millions of times less than a single bovine oral infectious dose. Observations that PrP^{Sc} or infectivity is clearly present do not, in and of themselves, justify concerns that the scope of existing measures, such as the exclusion of specified risk materials (SRM) from the human food supply or the animal feed chain, may be inadequate. Perspective, as always, is essential. The fundamental risk-based question is how informative these results are to real life exposure scenarios, particularly those involving oral ingestion.

As assays have become increasingly more sensitive, there has been a growing list of tissues that for the first time have been identified as harboring PrP^{Sc} and/or infectivity. They include peripheral nerves, skeletal muscle, saliva, tongue as well as tissues all along the digestive tract from the esophagus to the rectum. Conclusions are invariably drawn that such findings may

represent previously unrecognized transmission risks. But do they?

It is perhaps worth re-visiting earlier work, which formed the basis for establishing the SRM list. Wild type mice were inoculated intra-cerebrally with an extensive range of tissues, many of which were the same as those now being reported for the first time to contain PrP^{Sc} and/or infectivity. Even though a species barrier was confirmed when cattle were also inoculated intracerebrally, infectious dose estimates indicate that these mice were still about 600 times more sensitive than orally challenged cattle. Considering this, it would be reasonable to conclude that those tissues in which infectivity was not detected in these mouse assays would likely pose a negligible risk under most, if not all realistic exposure scenarios.

Invited.05: Alzheimer disease: Future outlook

Joseph B. Martin

Harvard Medical School; Harvard University; Boston, MA USA

Despite the extraordinary advances in our appreciation of the biologic processes that result in Alzheimer disease, the most common of the neurodegenerative disorders, there remain huge unsettled issues about the next appropriate steps in finding effective treatments to not cure, but slow down the pace of the disease. The reality of this failure to discern a point of treatment deviation in the disease course in humans leads to the grave concerns about the extent of the costs anticipated for the care of an increasingly aging population, whose treatments for other conditions lead to a situation of chronic care and eventual requirement for long-term care for an increasing number of the population. This talk will review the economic factors we face, touch upon the current efforts in clinical trials seeking effective treatments, and conclude with a few points about whether AD is a prion-like disorder.

Invited.06: New approaches to understanding and preventing neurodegenerative diseases

Christopher M. Dobson

Department of Chemistry; University of Cambridge; Cambridge, UK

Neurodegenerative disorders such as Alzheimer and Parkinson diseases arguably represent the greatest challenge to the social fabric and health care systems of much of the modern world. The predominant reason for their rapidly increasing prevalence is the increase in longevity that has resulted from the tremendous advances in public health and hygiene and in medical and surgical interventions over the last century. But the nature of neurodegenerative disorders is quite different from those of most other types of disease, and indeed there are at present no cures or even highly effective treatments. Very significant advances have, however, been made recently in our understanding of the fundamental molecular origins of these conditions, and are now suggesting new and rational therapeutic strategies by which to combat their onset and progression. This talk will discuss recent approaches to this end that we are currently exploring in the context of molecular and cellular biophysics.

Invited.07: Cofactor molecules maintain infectious conformation and restrict strain properties in mammalian prions

Surachai Supattapone,[1,4] Nathan R. Deleault,[1] Daniel J. Walsh,[1] Justin R. Piro,[1] Fei Wang,[2] Xinhe Wang,[2] Jiyan Ma[2] and Judy R. Rees[3]

[1]Department of Biochemistry; Dartmouth Medical School; Hanover, NH USA; [2]Department of Molecular and Cellular Biochemistry; Ohio State University School of Medicine; Columbus, OH USA; [3]Community and Family Medicine; Dartmouth Medical School; Hanover, NH USA; [4]Department of Medicine; Dartmouth Medical School; Hanover, NH USA

Non-proteinaceous cofactor molecules are required for the propagation of infectious prions in vitro. Several recent discoveries in this area will be discussed, including: (1) The identification of a novel endogenous prion propagation cofactor from mouse brain (phosphatidylethanolamine = PE). Synthetic PE can serve as a solitary cofactor for the formation of infectious recombinant prions from multiple animal species.[1] (2) The role of cofactor molecules in maintaining the infectious conformation of PrP^{Sc}. Withdrawal of cofactor molecules during serial propagation of purified recombinant prions caused adaptation of PrP^{Sc} structure accompanied by > 10^5-fold reduction in specific infectivity to undetectable levels, despite the ability of adapted "protein only" PrP^{Sc} molecules to self-propagate in vitro.[2] (3) The role of cofactor molecules in maintaining prion strain properties. Propagation in the presence of only one functional cofactor (PE) induced the conversion of three distinct strains into a single strain with unique infectious properties and PrP^{Sc} structure.[2] Taken together, these in vitro studies show that cofactor molecules can regulate the defining features of mammalian prions: PrP^{Sc} conformation, infectivity, and strain properties.

References

1. Deleault NR, Piro JR, Walsh DJ, Wang F, Ma J, Geoghegan JC, et al. Isolation of phosphatidylethanolamine as a solitary cofactor for prion formation in the absence of nucleic acids. Proc Natl Acad Sci USA 2012; 109:8546-51; PMID:22586108; http://dx.doi.org/10.1073/pnas.1204498109.
2. Deleault NR, Walsh DJ, Piro JR, Wang F, Wang X, Ma J, et al. Cofactor molecules maintain infectious conformation and restrict strain properties in purified prions. Proc Natl Acad Sci USA 2012; 109:E1938-46; PMID:22711839; http://dx.doi.org/10.1073/pnas.1206999109.

Invited.08: The structure of the infectious prion protein: Experimental data and molecular models

Holger Wille,[1] Matthijn Vos,[3] Ester Vázquez-Fernández,[1] Ludovic Renault,[1] Peter J. Peters,[4] Markus Zweckstetter,[5] Howard Young[1] and Jesús R. Requena[6]

[1]Department of Biochemistry; University of Alberta; Edmonton, AB, Canada; [2]Centre for Prions and Protein Folding Diseases; University of Alberta; Edmonton, AB, Canada; [3]FEI Company; Eindhoven, The Netherlands; [4]Netherlands Cancer Institute; Amsterdam, The Netherlands; [5]Deutsches Zentrum für Neurodegenerative Erkrankungen; Göttingen, Germany; [6]CIMUS Biomedical Research Institute & Department of Medicine; University of Santiago de Compostela-IDIS; Santiago de Compostela, Spain

The structures of the infectious prion protein, PrP^{Sc}, and that of its proteolytically truncated homolog, PrP 27–30, have eluded experimental determination due to their insolubility and propensity to aggregate. Molecular modeling has been used to fill this void and to predict the structures of both forms. The various modeling approaches have produced vastly different models, which indicate the limitations of this methodology. Over the years, in absence of a three-dimensional (3D) structure, a variety of experimental approaches have been used to gain insights into the molecular fold of this medically important isoform.

Here, we present an overview of recently published experimental results, which provided new insights into the structures of PrP^{Sc} and PrP 27–30. Negative stain electron microscopy and X-ray fiber diffraction argued that the β-sheets of the infectious prion conformer form a β-helix or β-solenoid structure with a height of four β-strands (rungs) per molecule of PrP^{Sc}/PrP 27–30 (= 19.2 Å per molecule). Results obtained by hydrogen/deuterium exchange and limited proteolysis followed by mass spectrometry claimed that none of the α-helices, which are characteristic for the structure of PrP^{C}, remain after conversion to the infectious state. Analyses of misfolded, recombinant forms of PrP provided insights into the structural pleomorphism that characterizes PrP, and which has also been seen with other amyloidogenic proteins. Stop codon mutants of PrP were found to adopt a β-helical conformation, supporting earlier predictions.

New approaches are being employed to analyze the structures of PrP^{Sc}, delta-GPI PrP^{Sc}, and of other variants. In particular, the helical periodicity that is inherent to most amyloid fibrils can be used to generate a 3D structure from two-dimensional (2D) images. Higher-resolution structures require electron micrographs to be recorded using cryo low-dose imaging techniques. Image processing based on the helical periodicity of fibrillar aggregates then allows the reconstruction of a 3D volume from 2D images. Once the parameters of the helical periodicity are determined, the image data can be averaged and back-projected into a 3D volume. Preliminary, helical reconstructions of PrP 27–30 fibrils show repeating densities along the fibril axis spaced at ~20 Å, in good agreement with the earlier X-ray fiber diffraction results.

Invited.09: Mapping the early steps in the conversion of PrP^{C} to PrP^{Sc}

Valerie Daggett

Department of Bioengineering; University of Washington; Seattle, WA, USA

Characterization of the PrP^{C} to PrP^{Sc} conversion process and identifying the various intermediates en route are critical to understanding and combating TSEs. These converted species have eluded detailed experimental characterization. A theoretical approach provides a means to predict the elusive infectious forms of PrP^{Sc}. So, we are using computational and modeling techniques to address this problem. Structural models of early soluble prion oligomers may help explain infectivity and provide tangible targets for drug and diagnostic development efforts. Since conversion can be triggered by mutations and low pH, molecular dynamics (MD) simulations can model the required environment for conversion. Consequently, we aim to map the molecular basis of conversion through realistic simulations of PrP and to develop reasonable, testable models for aggregated forms of PrP^{Sc} based on the MD-generated converted forms, as well as investigate interactions between the monomeric and oligomeric forms to better understand transmission and species barriers.

Since the central hypothesis in prion diseases is that it is a protein-only disease, whereby the prion protein is the only agent required for propagation and transmission of the disease, recombinant (rec) PrP is the primary construct used in experimental studies. However, PrP is a glycosylated membrane-associated protein. The non-protein moieties, such as the protein's N-linked glycans, its glycosylphosphatidylinositol (GPI) anchor, and the lipid environment affect the disease process in vivo. Nonetheless, based on structure alone, rec-PrP^{C} appears to be a good model for biologically relevant forms of PrP^{C}. The detailed effects of the GPI anchor and membrane have been harder to determine experimentally. Also, copper binding is important in terms of PrP function and can modulate conversion. Consequently we are also pursuing simulations of a more realistic system including the membrane and glycans and we have observed interactions with the membrane that may modulate conversion of PrP.

Invited.10: Epigenetic dominance of prion conformers

Eri Saijo,[1,2,7] Jifeng Bian,[1] Hae-Eun Kang,[1] Sehun Kim,[1] Jürgen A. Richt,[3] Jason Bartz,[4] Tracy Nichols,[5] Terry Spraker,[1] Nora Hunter[6] and Glenn C. Telling[1]

[1]Prion Research Center (PRC) and Department of Microbiology; Immunology and Pathology; Colorado State University; Fort Collins, CO USA; [2]Department of Microbiology; Immunology and Molecular Genetics; University of Kentucky; Lexington, KY USA; [3]Kansas State University College of Veterinary Medicine; Manhattan, KS USA; [4]Department of Medical Microbiology and Immunology; Creighton University; Omaha, NE USA; [5]US Department of Agriculture; National Wildlife Research Center; Fort Collins, CO USA; [6]The Roslin Institute and the University of Edinburgh; Midlothian, UK

To address the poorly understood mechanism by which distinct prion conformations and host prion protein primary structures interact to influence pathogenesis, we produced transgenic (Tg) mice encoding different scrapie susceptibility alleles. Tg mice expressing OvPrP-A136 infected with SSBP/1 scrapie prions propagated a relatively stable (S) prion conformation, which accumulated as punctate aggregates in the brain, and produced prolonged incubation times, while infected Tg mice expressing OvPrP-V136 developed disease rapidly, and the converted prion was comprised of an unstable (U), diffusely deposited conformer. Infected Tg mice expressing both alleles manifested properties consistent with the U conformer, suggesting that this dominant effect resulted from exclusive conversion of OvPrP-V136 but not OvPrP-A136. Surprisingly, however, studies with mAb PRC5, which discriminates OvPrP-A136 from OvPrP-V136, demonstrated substantial conversion of OvPrP-A136, and that the resulting prion acquired the characteristics of the U conformer. These results, substantiated by in vitro analyses as well as studies in the natural host, indicate that co-expression of OvPrP-V136 altered the conversion potential of OvPrP-A136 from the S to the otherwise unfavorable U conformer by physical interaction of allele products during infection. This epigenetic mechanism expands the range of conformations adoptable by a PrP primary structure, and thus the variety of options for strain propagation.

Invited.11: BSE: What else is new?

Stefanie Czub[1,2]

[1]Canadian Food Inspection Agency; Lethbridge, AB Canada; [2]University of Calgary Veterinary School; Calgary, AB Canada

Keywords: C-type & atypical BSE, regulation, science

Almost 30 years after the initial detection of classical (C-type) BSE and its subsequent spread through the western hemispheres, the number of C-type BSE cases are now steadily declining related to the implementation of effective control measures. This seems to be a regulatory success story and there is a strong push to call the case of "Bovine Spongiform Encephalopathy" solved and to be closed. While this might be true from a regulatory point of view, this presentation provides evidence that—in the presence of many open questions—from a scientific point of view BSE is far from being solved and why a precautionary approach remains necessary.

Invited.12: Polymorphic and polyphenotypic behavior of scrapie

Jan Langeveld

Central Veterinary Institute of Wageningen UR Centre; Lelystad, The Netherlands

Keywords: scrapie, goat, sheep, prion

In sheep and goats, prion disease (or TSE) is known for a long time as scrapie. In classical scrapie infection occurs horizontally in the field through ingestion (especially placenta) or during lactation or sometimes vertically during pregnancy; Nor98/atypical scrapie seems to develop spontaneously. The effectiveness of transmission is influenced by polymorphisms in prion protein (PrP), tissue tropism, PrP expression levels, and possibly additional host factors.

Phenotypic parameters of TSEs in the natural host are e.g., incubation time, brain lesion profile, tissue tropism, PrP^{Sc} tissue distribution, PrP^{Sc} biochemical properties, and rodent bioassay characteristics. In this way different strains have been identified, which even can change their phenotype. Mixtures of phenotypes are also being considered. One example is CH1641 scrapie in sheep and goat, a form of classical scrapie that has some PrP^{Sc} molecualr resemblance to BSE but differing from it in its tissue tropism and transmissibility to rodents. These cases though rare do occur probably on different continents.[1-4] Because of some similarities in rapid tests between CH1641 scrapie and BSE, and the uncertainty of the source of the BSE epidemic that arose since the 1980s, TSEs in small ruminants remain a subject for alertness. Also, in contrast to scrapie, BSE exhibits a very stable phenotype and is transmissible to many mammalian species including primates (vCJD in humans).

In sheep, breeding for genetic resistance to disease has been shown possible with a selective strategy for PrP with arginine on position 171 (171R in ARR sheep). This unique strategy has led to efficient reduction in classical scrapie prevalence in sheep within 6–7 y, while it also would have been preventive to BSE spread if it were to enter this species. Unfortunately, for atypical/Nor98 scrapie a decrease is not visible, and breeding programs will not be effective to reduce it since ARR allele carriers also are susceptible to this TSE type. In goats 171R does not occur, yet recently PrP with lysine on position 222 (222K) appears to be a good alternative candidate, though it has a low frequency and is not observed in some breeds.

The polymorphic variability of PrP in small ruminants allows choices to breed for genetic resistance in both sheep and goats.

References

1. Foster JD, Dickinson AG. The unusual properties of CH1641, a sheep-passaged isolate of scrapie. Vet Rec 1988; 123:5-8; PMID:3140468; http://dx.doi.org/10.1136/vr.123.1.5.
2. Jeffrey M, González L, Chong A, Foster J, Goldmann W, Hunter N, et al. Ovine infection with the agents of scrapie (CH1641 isolate) and bovine spongiform encephalopathy: immunochemical similarities can be resolved by immunohistochemistry. J Comp Pathol 2006; 134:17-29; PMID:16324707; http://dx.doi.org/10.1016/j.jcpa.2005.06.005.
3. Yokoyama T, Masujin K, Schmerr MJ, Shu Y, Okada H, Iwamaru Y, et al. Intraspecies prion transmission results in selection of sheep scrapie strains. PLoS One 2010; 5:e15450; PMID:21103326; http://dx.doi.org/10.1371/journal.pone.0015450.
4. Vulin J, Biacabe AG, Cazeau G, Calavas D, Baron T. Molecular typing of protease-resistant prion protein in transmissible spongiform encephalopathies of small ruminants, France, 2002-2009. Emerg Infect Dis 2011; 17:55-63; PMID:21192855; http://dx.doi.org/10.3201/eid1701.100891.

Invited.13: Multiple effects of prion protein membrane anchoring on prion disease pathogenesis: Interaction of PrP^{res} amyloid with the brain interstitial fluid (ISF) drainage pathway

Bruce Chesebro, Alejandra Rangel, James Striebel and Brent Race

Laboratory of Persistent Viral Diseases; Rocky Mountain Laboratories; NIAID; National Institutes of Health; Hamilton, MT, USA

Prion protein (PrP) is a host-encoded glycoprotein, which is required for susceptibility to prion diseases in humans, ruminants, rodents and other species. Normally PrP is attached to the cell surface by a glycophosphatidylinositol (GPI) linkage; however, in some human families, a PrP mutation consisting of a stop codon at positions 145, 160, 163, 226 or 227 results in synthesis of C-terminally truncated secretable PrP lacking the GPI moiety. Individuals with these mutations develop a fatal GSS-like disease with PrP amyloid plaques in brain. To model these patients and to study the role of PrP membrane anchoring, we previously generated a transgenic mouse model ($Tg44^{+/+}$) where only the GPI-negative anchorless form of PrP is expressed. In uninfected $Tg44^{+/+}$ animals, we have not seen clinical or pathological brain disease; however, scrapie-infected $Tg44^{+/+}$ mice develop a slow fatal neurological disease lasting 320–360 d with high infectivity in CNS, heart, brown fat and colon. The neuropathology consists of extensive perivascular PrP^{res} amyloid deposition with cerebral amyloid angiopathy (CAA) in both gray and white matter accompanied by severe astrogliosis and microgliosis. However, these mice lack typical gray matter vacuolation seen in prion diseases of humans and animals with anchored PrP suggesting that a different pathogenic mechanism is present. In previous studies by other groups in humans and mouse models of Alzheimer disease-associated CAA, Aβ amyloid distribution and deposition appeared to be influenced by interactions between Aβ and the brain interstitial fluid (ISF) system. In our experiments using scrapie-infected $Tg44^{+/+}$ mice, study of interactions between the ISF system and PrP^{res} amyloid found that clearance of ISF tracers was delayed significantly by PrP^{res} amyloid. We now hypothesize that in the absence of membrane-anchored PrP, ISF bulk flow might contribute to concentration of PrP^{res} amyloid precursor fibrils in perivascular regions within the CNS, and subsequent generation of additional amyloid fibrils in these areas might cause damage by partially blocking ISF drainage from the brain.

Invited.14: Preclinical downregulation of PrP^{C} precursor suggests a fundamental mechanism for the slow progression of prion infections

David Westaway,[1,2,3] Charles E. Mays,[1] Chae Kim,[4,5] Tracy Haldiman,[4] Jacques van der Merwe,[1] Qingzhong Kong,[4,5] Jan Langeveld,[5] Debbie McKenzie[1,7] and Jiri G. Safar,[2,3]

[1]Centre for Prions and Protein Folding Diseases; University of Alberta; Edmonton, AB, Canada; [2]Division of Neurology; University of Alberta; Edmonton, AB, Canada; [3]Department of Biochemistry; University of Alberta; Edmonton, AB, Canada; [4]National Prion Disease Surveillance Center; School of Medicine; Case Western Reserve University; Cleveland, OH, USA; [5] Department of Pathology; School of Medicine; Case Western Reserve University; Cleveland, OH, USA; [6] Central Veterinary Institute of Wageningen UR; Lelystad, The Netherlands; [7] Department of Biological Sciences; University of Alberta; Edmonton, AB, Canada

Keywords: conformation dependent immunoassay, scrapie cell assay, substrate depletion

Background. Prion diseases are unconventional neurodegenerative disorders characterized by incubation periods lasting for up to decades followed by rapid progression in the CNS within a matter of months because no treatment or cure is available.

Objectives. We hypothesized that the downregulat/ion of the PrP-like shadoo protein observed pre-clinically during prion infections[1,2] might also apply to $PrP^{C.}$ Our objective was to specifically measure PrP^{C} levels in different types of prion disease to determine if it was indeed downregulated·

Materials and Methods. To specifically separate PrP^{C} from oligomeric and disease-associated forms, we used sucrose gradient fractionation of infected brains in conjunction with quantification by conformation dependent immunoassays, scrapie cell assays and PMCA titrations.

Conclusion. Our data reveal that PrP^{C} is (1) reduced quantitatively in in vitro models for infection and at endpoint in rodent models used to study scrapie, Creutzfeldt-Jakob disease and chronic wasting disease and (2) altered qualitatively in terms of glycotype profile. Furthermore, in the case of mouse-adapted scrapie, quantitative reduction occurs pre-clinically, as it does for shadoo, implying activation of a generalized host defense mechanism. Since PrP^{C} is an obligatory precursor for the generation of misfolded forms of the prion protein and is also required for pathogenic signaling from misfolded PrP, down-regulation likely impacts disease pathogenesis. Specifically, we assert that preclinical depletion of PrP^{C} may be a major factor contributing to the slow evolution of prion diseases.

References

1. Westaway D, Genovesi S, Daude N, Brown R, Lau A, Lee I, et al. Down-regulation of Shadoo in prion infections traces a pre-clinical event inversely related to PrP(Sc) accumulation. PLoS Pathog 2011; 7:e1002391; PMID:22114562; http://dx.doi.org/10.1371/journal.ppat.1002391.
2. Watts JC, Stöhr J, Bhardwaj S, Wille H, Oehler A, Dearmond SJ, et al. Protease-resistant prions selectively decrease Shadoo protein. PLoS Pathog 2011; 7:e1002382; PMID:22163178; http://dx.doi.org/10.1371/journal.ppat.1002382.

Invited.15: The challenges of policy development to manage prion diseases: A reflection on the past to guide us into the future

Linda A. Detwiler

College of Veterinary Medicine; Mississippi State University; Starkville, MS USA

"If you wait, you are too late." Diseases with long incubation periods (years) and no or limited preclinical tests pose a unique challenge for animal and human health policy makers. The emergence of new strains or disease in different species prompts the need for actions of prevention and control. In the past, regulators and public health officials often had to wait years to obtain information on pathogenesis, transmission, species susceptibility and other aspects of the disease. The ramifications between the choices of delaying until study results were known or taking prompt action might result in allowing the silent spread of infection vs. imposing drastic, costly and perhaps unnecessary prohibitions on certain industries. The presentation will examine the relationship between science and the historical policy decisions for the risk management of scrapie, bovine spongiform encephalopathy, chronic wasting disease and variant Creutzfeldt-Jakob disease. Advances in research have definitely aided in our ability to make more informed decisions, but there are still significant gaps. The presentation will also discuss the challenges of the future, potential solutions and ask if public policy regarding the prion diseases is still relevant.

Invited.16: Studies of chronic wasting disease transmission in cervid and non-cervid species

Edward A. Hoover,[1] Candace K. Mathiason,[1] Davin M. Henderson,[1] Nicholas J. Haley,[1] Davis M. Seelig,[1] Nathaniel D. Denkers,[1] Amy V. Nalls,[1] Mark D. Zabe,[1] Glenn C. Telling,[1] Fernando Goni[2] and Thomas Wisniewski,[2]

[1] Prion Research Center; Colorado State University; Fort Collins, CO USA;
[2] New York University School of Medicine; New York, NY USA

How and why some misfolded proteins become horizontally transmitted agents and occasionally cross species barriers are issues fundamental to understanding prion disease. Chronic wasting disease (CWD) of cervids is perhaps a prototype of horizontal prion transmission, encompassing efficient mucosal uptake, lymphoid amplification, neuroinvasion, peripheralization, and dissemination via mucosal excretion. Efficient mucosal transmission of CWD in deer has been demonstrated by oral, nasal, aerosol, and indirect contact exposure. In addition, other studies (Mathiason CK, et al.) reported at the symposium support a significant role for pre- and/or postnatal transmission of CWD from doe to offspring. Accumulating, yet still incomplete, evidence also suggests that the period of relatively covert CWD infection may be longer than originally thought. Given the above, minimally invasive sensitive assays based on body fluids from live animals would aid substantially in understanding the biology of CWD. We have been applying seeded realtime quaking-induced amplification of recombinant PrP substrates (i.e., RT-QuIC methodology) to: (1) investigate antemortem CWD detection, and (2) model PrP-based species barriers and trans-species adaptation–topics we previously explored using sPMCA and in vivo bioassays. At this symposium, we report sensitive and specific detection CWD prions in saliva, urine, blood (Mathiason lab), and rectal and pharyngeal lymph node samples (Haley NJ, et al.) from pre-symptomatic and symptomatic experimentally and naturally exposed deer. Other ongoing studies are employing RT-QuIC methodology to model amplification barriers among CWD, FSE, BSE, and CJD prions using cervine, feline, bovine, human, and promiscuous rPrP substrates and the above species prion seeds, cellular co-factors, and transgenic mice. Finally, in collaboration with the Wisniewski laboratory, we are conducting of experimental CWD vaccination studies in deer employing oral administration of an attenuated Salmonella vector expressing cervid PrP epitopes.

Invited.17: A unifying role for prions in neurodegenerative diseases

Stanley B. Prusiner

Institute for Neurodegenerative Diseases; University of California, San Francisco; San Francisco, CA USA

Alzheimer disease, Parkinson disease, fronto-temporal dementias, Creutzfeldt-Jakob disease and amyotrophic lateral sclerosis are all neurodegenerative diseases that share two remarkable characteristics. First, more than 80% of cases are sporadic. Second, the inherited forms of these disorders have a late onset, despite the disease-specific mutant proteins being expressed from early in embryogenesis. This suggests that some event occurs with aging that renders the disease-specific proteins pathogenic; I argue that this event involves a stochastic refolding of the etiologic protein into an alternatively folded, self-propagating state known as a prion. Over the past two decades, studies from many different laboratories have accumulated data arguing that a half dozen proteins producing neurodegeneration are prions: synthetic Aβ peptides have been refolded into prions and bioassayed in transgenic mouse models of Alzheimer disease. Similarly, α-synuclein prions responsible for Parkinson disease and tau prions causing frontotemporal dementias have been produced from recombinant proteins and bioassayed in transgenic mice. The convergence of data

implicating prions in the pathogenesis of common neurodegenerative maladies has been remarkable. Many mysteries can now be explained within the paradigm of the prion concept including the steady progression of the disease process as well as the spread from one area of the CNS to another. From our growing knowledge of prions, strategies are emerging for developing informative molecular diagnostics and effective therapeutics for these elusive disorders. Early diagnosis will require reporters, such as positron emission tomography (PET) ligands, to identify prions long before symptoms appear. Meaningful treatments are likely to require drugs that diminish the precursor protein, interfere with the conversion of precursors into prions, and/or clear existing prions.

Invited.18: Propagated misfolding of SOD1 in ALS: A new prion-like disorder

Neil Cashman

Brain Research Centre; Department of Medicine; University of British Columbia; Vancouver, BC Canada

Approximately 10% of ALS cases are familial, with ~20% of these due to mutations in the gene encoding Cu/Zn superoxide dismutase (SOD1), a ubiquitous free-radical defense enzyme. We sought to molecularly dissect the effects of intracellular obligately misfolded SOD1 mutant proteins on natively structured wild-type SOD1. Expression of the enzymatically inactive, natural familial ALS SOD1 mutations G127X and G85R in human mesenchymal and neural cell lines induced misfolding of wild-type natively-structured SOD1, as indicated by: (1) acquisition of immunoreactivity with SOD1 misfolding-specific monoclonal antibodies; (2) markedly enhanced protease sensitivity suggestive of structural loosening; and (3) non-native disulfide-linked oligomer and multimer formation. Cytosolic mislocalizing mutations of FUS and TDP43, two proteins implicated in familial and sporadic ALS, also triggered SOD1 misfolding. Expression of G127X and G85R in mouse cell lines did not induce misfolding of murine wtSOD1, and a species restriction element for human wtSOD1 conversion was mapped to a region of sequence divergence in loop II and β-strand 3 of the SOD1 β-barrel (residues 24–36), then further refined surprisingly to a single tryptophan residue at codon 32 in human SOD1. Culture medium from cells transiently transfected with wild-type or mutant SOD1 induced misfolding of endogenous SOD1 when added to naive cell cultures, and this process was stably propagated in serial passage. Nonspecific uptake of misfolded SOD1 was excluded by siRNA knockdown of SOD1 in the fresh recipient cells, indicating a requirement for endogenously expressed SOD1 as a substrate. The agent responsible for induction of misfolding was determined to be a misfolded SOD1 aggregate which pelleted by ultracentrifugation of 100,000 × g for 1 h. Transmission of SOD1 misfolding in vitro was abrogated by extracellular pan- and misfolding-specific SOD1 antibodies. G37R Tg mice treated with misfolding-specific SOD1 antibodies displayed prolonged survival of ~11 d ($p < 0.001$). On quantitative immunoprecipitation, misfolded wtSOD1 was found to constitute ~5% of total SOD1 in spinal cord samples from SOD1 familial as well as sporadic ALS. SOD1 misfolding and toxicity can propagate within and between cells, prompting novel targeted therapies for all forms of ALS. ALS now joins company with Alzheimer, Parkinson, and other neurodegenerative and systemic diseases as a "prion-like" disorder that transmits from cell to cell in the CNS.

Invited.19: Prion-like propagation of α-synuclein as a novel therapeutic target in Parkinson disease

Edward A. Fon

Department of Neurology and Neurosurgery; McGill University; Montreal, QC Canada

Recent findings point toward the tantalizing possibility that aggregated α-synuclein can spread from one neuron to another in a prion-like fashion. This process is believed to occur via the release of α-synuclein from one cell followed by its uptake into another. Regardless of the ultimate mechanism of α-synuclein toxicity, we believe that limiting its spread would have major therapeutic implications for patients suffering from PD because it would have the potential to slow disease progression. We have recently developed a cell-based α-synuclein uptake assay that we are using to screen for genes and small-molecules that modulate α-synuclein uptake. Several promising hits obtained so far as well as those that will be obtained from our ongoing screening will be used to help understand how α-synuclein is taken up and processed in cells and to test whether they can influence the spread of α-synuclein in neurons and in vivo. Together, the work has the potential to uncover key regulators and therapeutics targeting the progression of α-synuclein pathology in PD.

Invited.20: Prion-like aspects of Alzheimer pathology

Mathias Jucker

Department of Cellular Neurology; Hertie-Institute for Clinical Brain Research; University of Tübingen; German Center for Neurodegenerative Diseases; Tübingen, Germany

Many neurodegenerative disorders are characterized by a predictable temporal progression of specific aggregated proteins in the brain. The hallmark proteopathy is Alzheimer disease in which Abeta is deposited in brain. Abeta-amyloidosis can be exogenously induced by the application of Abeta-containing brain extracts (Meyer-Lühmann et al., Science 2006; Eisele et al., Science 2010). The amyloid-inducing agent is likely Abeta itself, although in a conformation generated most effectively in the living brain. Once induced, Abeta lesions spread within and among brain regions. The induced amyloid is dependent on the nature of the Abeta seed and of the host, an observation reminiscent

of prion strains. Recently, the concept of prion-like induction of pathogenic proteins has been expanded to include intracellular lesions (Jucker and Walker, Ann Neurol 2011). Nevertheless, the clinical implications of these observations are not yet clear. Our finding that the Abeta-inducing agent is partly soluble (Langer et al., J Neurosci 2011) intensifies the search for protein seeds in bodily fluids that may have diagnostic value and be a novel target for early therapeutic intervention.

Invited.21: Interneuronal spreading of tau pathology in chronic traumatic encephalopathy

Ann C. McKee

Boston University School of Medicine; VA Boston Healthcare System; Boston, MA, USA

Keywords: chronic traumatic encephalopathy, tau protein, traumatic brain injury

Chronic traumatic encephalopathy (CTE) is a progressive tauopathy that occurs as a consequence of repetitive mild traumatic brain injury.[1] In the earliest stages of CTE, focal perivascular clusters of hyperphosphorylated tau (p-tau) neurofibrillary tangles are found at the depths of the sulci in the cerebral cortex. Even in the absence of additional trauma, CTE appears to progress over decades to become a severe tauopathy affecting widespread regions of the cerebral cortex, basal ganglia, diencephalon and brainstem and medial temporal lobes. How focal tau pathology spreads slowly to involve other brain regions in CTE might involve multiple mechanisms, including a prion-like templated misfolding of tau.

Under normal conditions in the mature human central nervous system, tau is primarily associated with microtubules in axons, where it is neither toxic nor associated with neurofibrillary pathology. Brain trauma causes some tau to become dissociated from microtubules in axons via mechanisms that probably include intracellular calcium influx, glutamate receptor-mediated excitotoxicity, and kinase activation mediating hyperphosphorylation of intracellular tau. Tau dissociated from microtubules becomes abnormally phosphorylated, misfolded, aggregated and proteolytically cleaved by calpains and caspases, all of which are associated with neurotoxicity. Direct and indirect evidence for interneuronal tau transfer in animal models has recently suggested that interneuronal spreading of tau pathology may be due to transfer of toxic tau species between neurons.[2-5] This might be mediated by either a prionlike templated misfolding of tau, or by calcium dysregulatory effects of oligomeric or toxic N-terminal tau in the receiving neuron.[6] While spreading of tau pathology is generally thought to occur in association with neuronal synapses, glial to glial spread, periventricular and diffuse extracellular tau migration patterns involving the cerebrospinal fluid represent additional pathways by which lesion spreading could occur in CTE.[7] Cerebrospinal fluid enters the brain parenchyma along the Virchow-Robin spaces surrounding penetrating arteries and brain interstitial fluid is cleared along paravenous drainage pathways. Recent studies have demonstrated that Aß peptide is cleared through this route.[8] Clearance through paravenous flow and the cerebrospinal fluid might also regulate extracellular levels of p-tau and explain the frequent perivascular, subpial and periventricular localization of tau protein in CTE. Interneuronal spreading of tau pathology in CTE is complex and likely involves a variety of non-synaptic mechanisms as well as synaptically mediated mechanisms.

References

1. McKee AC, Stein TD, Nowinski CJ, Stern RA, Daneshvar DH, Alvarez VE, et al. The spectrum of disease in chronic traumatic encephalopathy. Brain 2013; 136:43-64; PMID:23208308.
2. Clavaguera F, Bolmont T, Crowther RA, Abramowski D, Frank S, Probst A, et al. Transmission and spreading of tauopathy in transgenic mouse brain. Nat Cell Biol 2009; 11:909-13; PMID:19503072; http://dx.doi.org/10.1038/ncb1901.
3. Liu L, Drouet V, Wu JW, Witter MP, Small SA, Clelland C, et al. Trans-synaptic spread of tau pathology in vivo. PLoS One 2012; 7:e31302; PMID:22312444; http://dx.doi.org/10.1371/journal.pone.0031302.
4. de Calignon A, Polydoro M, Suárez-Calvet M, William C, Adamowicz DH, Kopeikina KJ, et al. Propagation of tau pathology in a model of early Alzheimer's disease. Neuron 2012; 73:685-97; PMID:22365544; http://dx.doi.org/10.1016/j.neuron.2011.11.033.
5. Hall GF, Patuto BA. Is tau ready for admission to the prion club? Prion 2012; 6:223-33; PMID:22561167; http://dx.doi.org/10.4161/pri.19912.
6. Frost B, Jacks RL, Diamond MI. Propagation of tau misfolding from the outside to the inside of a cell. J Biol Chem 2009; 284:12845-52; PMID:19282288; http://dx.doi.org/10.1074/jbc.M808759200.
7. Le MN, Kim W, Lee S, McKee AC, Hall GF. Multiple mechanisms of extracellular tau spreading in a non-transgenic tauopathy model. Am J Neurodegener Dis 2012; 1:316-33; PMID:23383401.
8. Iliff JJ, Wang M, Liao Y, Plogg BA, Peng W, Gundersen GA, et al. A paravascular pathway facilitates CSF flow through the brain parenchyma and the clearance of interstitial solutes, including amyloid β. Sci Transl Med 2012; 4:ra111; PMID:22896675; http://dx.doi.org/10.1126/scitranslmed.3003748.