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Thermodynamic Stabilization of the Folded Domain of Prion Protein Inhibits Prion Infection in Vivo

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SUMMARY

Prion diseases, or transmissible spongiform encephalopathies (TSEs), are associated with conformational conversion of the cellular prion protein, PrP^C, into a protease-resistant form, PrP^{Sc}. Here we show that mutation-induced thermodynamic stabilization of the folded, α -helical domain of PrP^C has a dramatic inhibitory effect on the conformational conversion of prion protein in vitro, as well as the propagation of TSE disease in vivo. Transgenic mice expressing human prion protein variant with an increased thermodynamic stability were found to be much more resistant to infection with the TSE agent than those expressing wild-type human prion protein, both in the primary passage and three subsequent subpassages. These findings not only provide a novel line of evidence in support of the protein-only model of TSEs, but also yield insight into the molecular nature of the PrP^C→PrP^{Sc} conformational transition, and suggest an approach to the treatment of prion diseases.

INTRODUCTION

Transmissible spongiform encephalopathies (TSEs) are a group of neurodegenerative disorders such as Creutzfeldt-Jakob disease in humans, scrapie in sheep, chronic wasting disease in cervids and bovine spongiform encephalopathy in cattle (Aguzzi and Polymenidou, 2004; Caughey et al., 2009; Cobb and Surewicz, 2009; Collinge, 2001; Prusiner, 1998; Weissmann, 2004). The prion hypothesis asserts that the transmission of TSEs does not require nucleic acids, and that the infectious TSE agent is proteinaceous in nature, consisting of a misfolded form of the prion protein (Prusiner, 1982). Once heretical,

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ACCESSION NUMBERS

The coordinates and structural restraints for V209M HuPrP have been deposited under BMRB accession number 19268, RCSB ID code rcsb103353 and PDB ID code 2m8t.

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this protein-only model is now supported by growing body of evidence, most notably the recent success in generating infectious prions *in vitro* from brain-derived (Castilla et al., 2005; Deleault et al., 2007) or bacterially-expressed prion protein (Kim et al., 2010; Legname et al., 2004; Makarava et al., 2010; Wang et al., 2010). However, the mechanisms of conformational conversion of the normal form of the prion protein, PrP^C, to the misfolded PrP^{Sc} conformer remain largely unknown, hindering understanding of the molecular basis of the disease as well as the development of therapeutic approaches.

Cellular human PrP^C is a glycoprotein consisting of an unstructured N-terminal region and a folded C-terminal domain comprised of three α -helices and two very short β -strands (Zahn et al., 2000). Conversion of this protein to an abnormal PrP^{Sc} isoform occurs by a posttranslational process involving a major conformational change that results in an increased proportion of β -structure (Caughey et al., 1991; Pan et al., 1993). Although the three-dimensional structure of PrP^{Sc} remains unknown, a body of evidence suggests that this conformational transition involves at least partial refolding of the helix-rich C-terminal domain (Cobb et al., 2007; Govaerts et al., 2004; Smirnovas et al., 2011). This, together with recent findings that mutations which reduce thermodynamic stability of PrP^C greatly increase the PrP^C propensity to undergo a conversion to oligomeric β -sheet forms *in vitro* (Apetri et al., 2005; Vanik and Surewicz, 2002), prompted us to search for amino acid substitutions that stabilize the native α -helical structure, with the expectation that—if the protein only hypothesis is correct—such mutations should suppress the PrP^C→PrP^{Sc} conversion and, thus, attenuate replication of the infectious prion agent.

RESULTS AND DISCUSSION

A particularly dramatic increase in thermodynamic stability of PrP^C was found upon replacement of valine (V) at position 209 with methionine (M). As shown in Figure 1A, equilibrium unfolding of the full-length wild-type recombinant human prion protein (HuPrP23-231) in guanidinium chloride (GduCl) at pH 7 is characterized by a midpoint unfolding GduCl concentration of 2.1 M and a free energy difference between the native and unfolded state, ΔG° , of 20.6 kJ/mol. For the V209M variant, the unfolding curve is shifted to much higher denaturant concentrations (midpoint at 2.8 M), and the ΔG° value is increased to 31.9 kJ/mol. A similar effect was observed for N-truncated HuPrP90-231, with ΔG° increasing from 20.9 to 30.0 kJ/mol. The observed increase of ~10 kJ/mol in the free energy of unfolding is remarkably high, to the best of our knowledge among the largest reported for a single residue mutation in any protein. Thermodynamic stabilization of the native PrP structure by the Val209→Met substitution was further confirmed by thermal unfolding experiments using differential scanning calorimetry (Figure S1).

It has been previously shown that, under mildly acidic conditions in the presence of low concentrations of GduCl, the N-truncated recombinant prion protein HuPrP90-231 undergoes a transition to an oligomeric β -sheet structure mimicking certain properties of PrP^{Sc} (Apetri et al., 2005; Vanik and Surewicz, 2002). Under the present experimental conditions (sodium acetate buffer, pH 4, 1 M GduCl, protein concentration of 24 μ M) the α -helix→ β -sheet transition for the wild-type HuPrP90-231 was complete within ~60 min. In contrast, the V209M mutant was highly resistant to this conversion, remaining in a monomeric α -helical form even after 24 h incubation under identical conditions (Figure 1B).

Incubation of the recombinant PrP in the presence of GduCl at neutral pH is known to result in formation of thioflavine T-positive amyloid structures with fibrillar morphology (Apetri et al., 2005; Baskakov, 2004). Under the present experimental conditions, the conversion to amyloid fibrils for the wild-type HuPrP23-231 was characterized by a lag phase of 6.5 ± 0.5 h. Again, upon the replacement of Val209 with Met, this reaction became much slower, with

an increased lag phase of 16.3 ± 1.4 h (Figure 1C). For the N-truncated HuPrP90-231, the conversion reactions were slower compared to the full-length protein. However, also in this case the V209M mutation reduced the rate of the conversion reaction (lag phase of 18 ± 2 and 42 ± 3 h for wild-type HuPrP90-231 and V209M HuPrP90-231, respectively (Figure 1C). Collectively, this data demonstrates that the V209M mutation greatly increases the thermodynamic stability of PrP^C, resulting in a remarkably reduced propensity of the protein to undergo a conversion to PrP^{Sc}-mimicking β -sheet-rich aggregates in vitro.

Inspection of NMR data indicates that the structure of wild-type human PrP (Zahn et al., 2000) is characterized by the presence of three cavities (PDB ID 1QM0). Two of these cavities (with volumes of 57 and 14 Å³ and surface areas of 76 and 29 Å²) are surrounded by residues of the second and third α -helix and the loops connecting α -helix 1 with β -strands 1 and 2 (Figure 2). The third cavity (18 Å³, 34 Å²) is located at the packing interface of helices 1 and 3. The presence of such cavities within the hydrophobic core of proteins is known to have a destabilizing effect (Eriksson et al., 1992). Our initial modeling suggested that the substitution of Met in place of Val 209 should largely eliminate the cavities in PrP, providing a rationale for improved thermodynamic stability. This prediction has been verified by the NMR determined structure (Figure 2 and Figure S2 and Table S1). Indeed, as shown in Figure 2, the structure of the V209M variant shows remarkably improved packing within the hydrophobic core, resulting in a complete removal of the two larger cavities near residue 209. This is a consequence of different side chain geometry of residue 209 and subtle changes in the packing and geometry of helices 1 and 3. Apart from this minor difference, the overall fold of the mutant protein remains unaltered.

To test whether thermodynamic stabilization of the folded domain of PrP is sufficient to confer resistance to prion replication in vivo, we have created two lines of transgenic mice in the FVB/PrP-null background: one expressing wild-type human PrP [denoted Tg(HuPrP)] and the other expressing the superstable variant [denoted Tg(HuPrP^{V209M})]. Western blot analysis indicates that both lines of transgenic mice express PrP in the brain at a level similar to that observed for wild type FVB mice, and with comparable electrophoretic profiles dominated by the diglycosylated form (Figures 3A and 3C). Confocal microscopy of primary neurons derived from Tg(HuPrP) and Tg(HuPrP^{V209M}) mice (Figure 3B), as well as of human neuroblastoma cell line M17 transfected with either wild type human PrP (HuPrP) or the V209M variant (HuPrP^{V209M}) (data not shown), demonstrates that HuPrP^C and HuPrP^{V209M} have similar cellular distributions, residing both at the cell surface and in intracellular compartments. Furthermore, treatment of M17 cells expressing PrP^{V209M} with phosphatidylinositol-specific phospholipase C (PI-PLC) released HuPrP^{V209M} into the culture medium, indicating that, like wild-type PrP^C, PrP^{V209M} is attached to the cell membrane by a GPI anchor (Figure S3). Thus, all the data indicates that Tg(HuPrP) and Tg(HuPrP^{V209M}) mice express comparable amounts of the prion protein, and that the cellular localization of PrP^{V209M} is indistinguishable from that of the wild-type protein.

After intracerebral inoculation with brain homogenates derived from subjects with sporadic Creutzfeldt-Jacob disease (sCJD), all inoculated Tg(HuPrP) mice fell ill after incubation time of approximately 263 days (Table 1), exhibiting classical symptoms of TSE disease. In sharp contrast, only two of six sCJDMM1-inoculated Tg(HuPrP^{V209M}) mice [and none of seven sCJDMM2-inoculated Tg(HuPrP^{V209M}) mice] became symptomatic, after a very long incubation time of nearly 700 days (Table 1). As expected, Western blot analysis revealed that brains of all inoculated Tg(HuPrP) mice accumulated relatively large quantities of proteinase K (PK)-resistant prion protein, PrP^{Sc}, which electrophoretically reproduced the pattern of the original sCJD PrP^{Sc} (Figure 3C). In contrast, PrP^{Sc} was found in brains of only two symptomatic Tg(HuPrP^{V209M}) mice, but not in the remaining eleven symptom-free animals, even after sodium phosphotungstate precipitation treatment of brain homogenate to

enrich PrP^{Sc} (Safar et al., 1998). The electrophoretic profile of PrP^{Sc} from the two infected Tg(HuPrP^{V209M}) mice differed from that of Tg(HuPrP) mice with regard to gel mobility and the ratio of bands representing different PrP^{Sc} glycoforms (Figure 3C). Furthermore, compared to the inoculated Tg(HuPrP) mice, the two affected Tg(HuPrP^{V209M}) mice displayed much less severe overall spongiform neurodegeneration, reduced PrP immunostaining and significantly different lesion profiles (Figure 3D and Figure S4A–D). Altogether, this data indicates that, compared with transgenic mice expressing wild-type human PrP, Tg(HuPrP^{V209M}) mice are highly resistant to infection with sCJD prions. However, the question must be raised as to whether the enhanced resistance of Tg(HuPrP^{V209M}) mice is intrinsic or due to the ‘mutation barrier’ related to the mismatch in the amino acid sequence between the wild type sCJD PrP^{Sc} of the inoculum and the mutated PrP^{V209M} expressed by the recipient Tg(HuPrP^{V209M}) mice.

The availability of two sCJD-affected Tg(HuPrP^{V209M}) mice provided us with the opportunity to probe this question by performing a second passage experiment. Upon inoculation with the Tg(HuPrP^{V209M})-adapted sCJD preparations (that contain only the newly generated PrP^{Sc(V209M)} isoform), all Tg(HuPrP) mice (that express wild-type PrP^C) became infected with an average incubation of 316 days, longer than the 263 days of incubation needed after the inoculation of the original (not-passaged) sCJD preparation (Table 1). This increase in incubation time most likely can be attributed to the mutation barrier now existing between the PrP^{V209M} of the inoculum and the PrP^C expressed by the recipient Tg(HuPrP) mice. Remarkably, despite the lack of any mutation barrier between the inoculum and Tg(HuPrP^{V209M}) mice in this second-passage experiment, Tg(HuPrP^{V209M}) mice required a much longer incubation of ~431 days, although, this time, all of them succumbed to the disease (Table 1). Given that passage of prions in mutant mice might be associated with strain adaptation phenomenon (Bartz et al., 2000), two additional passages were performed. While the incubation time in the third passage in Tg(HuPrP^{V209M}) mice decreased from 431 to 366 days, no further reduction in the incubation time was observed in the fourth passage, indicating that the adaptation process has been completed. Importantly, even at this point the incubation time was still much longer for Tg(HuPrP^{V209M}) mice than for Tg(HuPrP) mice (366 and 399 days versus 267 and 295 days in third and fourth passages, respectively) (Table 1). Thus, this data clearly demonstrates an inherently high resistance of Tg(HuPrP^{V209M}) mice to sCJD prion infection.

Intriguingly, second-fourth passage Tg(HuPrP) mice inoculated with PrP^{Sc(V209M)} were characterized by PrP^{Sc} electrophoretic patterns and lesion profiles indistinguishable from those observed in the first passage experiment with sCJD-inoculated Tg(HuPrP) mice, whereas distinct electrophoretic characteristics of PrP^{Sc(V209M)} and lesion profiles were consistently maintained in passages in Tg(HuPrP^{V209M}) mice (Figure S4C–E). This data strongly suggest that the PrP^{Sc} isoforms associated with the V209M mutation can be faithfully propagated only in the host containing this mutation, whereas in Tg(HuPrP) mice they ‘adapt back’ to the characteristics apparently dictated by the wild-type PrP host.

Tg(HuPrP^{V209M}) mice were specifically generated to test whether thermodynamic stabilization of the folded domain of PrP^C as observed *in vitro* is sufficient to inhibit prion replication *in vivo*. The answer to this question is clearly yes, providing a new line of evidence in support of the protein-only model of TSEs. While the requirement for PrP^C in TSE pathogenesis has been demonstrated in seminal experiments with PrP-knockout mice (Bueler et al., 1993), the present data shows that this requirement is directly related to the ability of PrP^C to undergo a conversion to the PrP^{Sc} state, and that prion propagation *in vivo* can be effectively inhibited by stabilizing the normal α -helical conformation of PrP^C. Given the similar electronic and hydrophobic properties of Val and Met residues, the reduced conversion propensity of the mutant protein is highly unlikely due to factors other than

thermodynamic stabilization. Furthermore, since residue 209 is buried within the hydrophobic interior of the protein, its substitution should not affect the interaction of PrP^C with other cellular cofactors in vivo.

The finding that thermodynamic stabilization of the native α -helical domain of PrP^C inhibits prion propagation in mice impacts the ongoing debate regarding critical, yet still unresolved, issues in prion research: the mechanism of prion protein conversion and the structure of the infectious PrP^{Sc} conformer. While some models postulate that the C-terminal region of PrP^{Sc} retains at least partial native α -helical structure of PrP^C (DeMarco and Daggett, 2004; Govaerts et al., 2004), recent data indicate that prion protein conversion involves major refolding of the entire C-terminal region, and that this region in PrP^{Sc} consists of β -strands and short turns/loops, with no α -helices present (Smirnovas et al., 2011). The present finding is consistent with the latter scenario, providing strong support to the notion that prion protein conversion in vivo involves a major rearrangement of the α -helical domain of PrP^C.

Finally, the present data suggests a strategy for pharmacological intervention in prion diseases. While a number of immuno- and chemotherapeutic approaches have been proposed (Cashman and Caughey, 2004), there is currently no effective treatment for TSEs. A promising new strategy has recently emerged based on down-regulating PrP^C expression using siRNA (Pfeifer et al., 2006). However, this approach may carry significant risks given the reported role of PrP^C in cell signaling, neuroprotection and other physiological processes (Westergard et al., 2007). The finding that prion replication in vivo can be effectively reduced by stabilizing the native conformation of PrP^C without manipulating its expression level offers an alternative and, potentially, more practical strategy based on screening and/or rational design of small molecules that can thermodynamically stabilize the normal conformation of monomeric PrP^C. A generally similar approach has been recently successfully used for the development of a clinically effective drug against transthyretin amyloidosis, even though in the latter case the stabilization is kinetic rather than thermodynamic, preventing dissociation of the transthyretin tetramer (Bulawa et al., 2012).

EXPERIMENTAL PROCEDURES

Protein purification

Recombinant human prion protein 90-231 (HuPrP90-231) and the V209M mutant (both 129M variants) were prepared and purified as described previously (Apetri et al., 2005). Uniformly ¹⁵N- and ¹³C/¹⁵N-labeled proteins for NMR spectroscopy were expressed in *E. coli* using a minimal medium containing ¹³C₆ glucose (3 g/l) and/or ¹⁵N NH₄Cl (1 g/l) as the sole carbon and nitrogen sources, respectively.

Biophysical experiments

Equilibrium unfolding experiments were performed by circular dichroism spectroscopy (50 mM phosphate buffer, pH 7) by monitoring GduCl-induced changes in ellipticity at 220 nm as described previously (Apetri et al., 2005). The unfolding curves were analyzed using a two-state transition model (Santoro and Bolen, 1988). The conversion of prion protein variants to β -sheet oligomers was performed in 50 mM sodium acetate buffer containing 1 M GduCl, pH 4, and monitored by circular dichroism spectroscopy as described previously (Apetri et al., 2005). The concentration of each protein in these experiments was 24 μ M. The conversion of the proteins to amyloid fibrils at neutral pH (50 mM phosphate buffer, 1.5 M GduCl, pH 7, protein concentration of 30 μ M) was performed and monitored by thioflavine T assay as described previously (Apetri et al., 2005).

Structural Studies

The structure of V209M human prion protein was determined by NMR spectroscopy. Details of these experiments are provided in Supplemental Experimental Procedures.

Transgenic mice

HuPrP and HuPrP^{V209M} transgene constructs were based on the murine half-genomic PrP clone (HGPRP) (Fischer et al., 1996). Tg40, a Tg(HuPrP) line that expresses wild type human PrP-129M at the same level as that of the murine PrP in wild type FVB mice, was described previously (Kong et al., 2005). Tg(HuPrP^{V209M}) mice were created in the same fashion and bred with FVB/*Prnp*^{0/0} mice to obtain Tg(HuPrP^{V209M})*Prnp*^{0/0} mice. The transgene expression in brain was examined by Western blotting analysis using mAb 3F4 or 8H4 as described below. Tg20, a Tg(HuPrP^{V209M}) line expressing the mutant PrP at the wild type FVB mouse level, was used for all transmission experiments. All transgenic mice used were in the *Prnp*^{0/0} background.

Inoculation and examination of transgenic mice

Frozen brain tissues from human subjects with sCJD or prion-infected transgenic mice were homogenized in phosphate buffered saline (PBS) and inoculated intracerebrally into brains of Tg(HuPrP) and Tg(HuPrP^{V209M}) mice as reported (Kong et al., 2005). Thirty microliters of 1% brain homogenate was injected into each animal. Monitoring of prion symptoms was done as previously described (Kong et al., 2005), and the animals were sacrificed within 2–3 days after appearance of symptoms. Each brain was sliced sagittally; half was frozen for Western blot analysis (see below), and half was fixed in formalin for staining with haematoxylin and eosin or anti-PrP antibody 3F4 (Castellani et al., 1996; Kong et al., 2005). The prion titers of the sCJD or mouse brain tissues were calculated according to the incubation time using the previously described method based on end-point titration of sCJDDMM1 in the Tg40 mice (Prusiner et al., 1982).

Western blotting analysis and detection of proteinase K (PK)-resistant PrP

Total protein concentrations of brain homogenates in the lysis buffer (100 mM Tris, 150 mM NaCl, 0.5% Nonidet P-40, 0.5% sodium deoxycholate, 10 mM EDTA, pH 7.8) were measured with the BCATM Protein Assay Reagents (Thermo Fisher Scientific, Rickford, IL). Total PrP as well as proteinase K-resistant PrP^{Sc} were examined by Western blotting using precast SDS-PAGE gels with 8H4 or 3F4 antibodies in conjunction with HRP-conjugated goat anti-mouse IgG Fc antibody essentially as described previously (Pan et al., 2001). Proteinase K digestion was performed for 1 h at 37 °C using 100 µg/ml of the enzyme.

Confocal immunofluorescence imaging of primary neurons

Primary cortical neuron cultures were prepared from day14-day16 embryos of Tg(HuPrP) and Tg(HuPrP^{V209M}) mice (Yuan et al., 2008). Cell surface and intracellular PrP was examined with a Zeiss LSM510 inverted confocal microscope using monoclonal antibody 3F4 and goat anti-mouse IgG (H+L) conjugated with highly cross-absorbed Alexa fluor 488 (Invitrogen, Carlsbad, CA) as described previously (Mishra et al., 2002).

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Highlights

- Stabilization of α -helical domain of PrP inhibits prion protein conversion in vitro
- Transgenic mice expressing superstable PrP variant are resistant to prion infection
- The findings suggest a strategy for pharmacological intervention in prion diseases

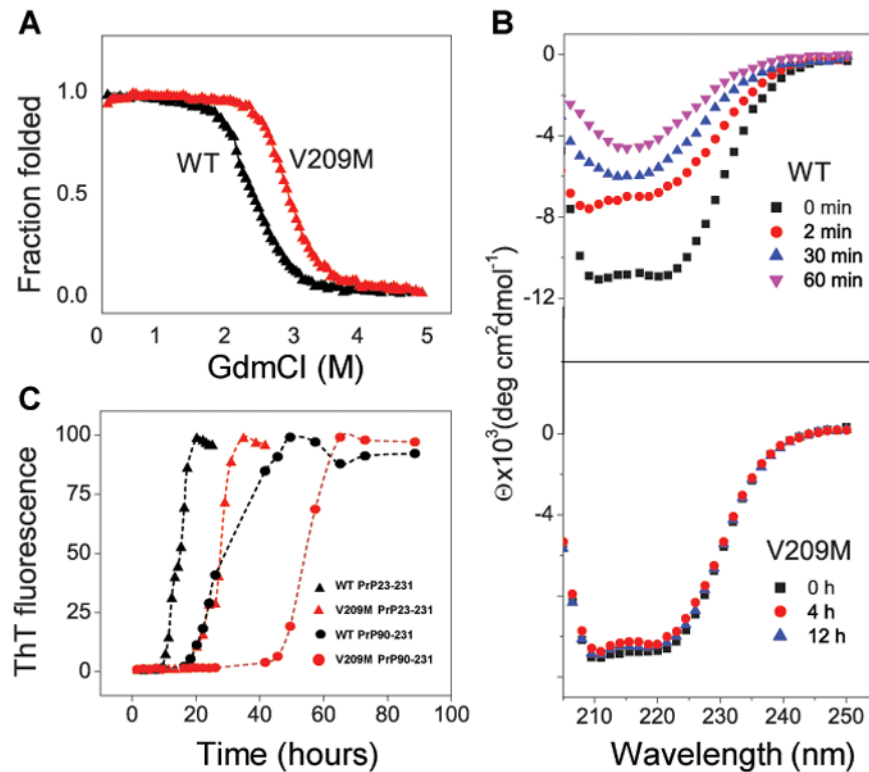


Figure 1. The effect of V209M mutation on biophysical properties of human prion protein (A) GdmCl-induced equilibrium unfolding for WT full-length human PrP (HuPrP23-231) and the V209M variant. The unfolding curves were obtained in 50 mM phosphate buffer, pH 7.

(B) Time-dependent transition of WT HuPrP90-231 and the V209M variant from α -helical structure to β -sheet oligomers as monitored by circular dichroism spectroscopy. Spectra were recorded in 50 mM sodium acetate, pH 4 in the absence of the denaturant and at different time points after the addition of 1 M GdmCl. The spectrum of α -helical monomer shows characteristic 'double minimum' at ~210 and 220 nm, whereas the spectrum of β -sheet oligomers is characterized by lower intensity and a broad minimum around 215 nm.

(C) Time-course of amyloid fibril formation for wild-type HuPrP and the V209M variant as monitored by thioflavine T fluorescence. Data for both full-length protein (HuPrP23-231) and HuPrP90-231 are shown. The lag phases (mean \pm SD) based on 3–4 experiments are 6.5 \pm 0.5 and 16.3 \pm 1.4 h for HuPrP23-231 and V209M HuPrP23-231, respectively, and 18 \pm 2 and 42 \pm 3 h for HuPrP90-231 and V209M HuPrP90-231, respectively. See also Figure S1.

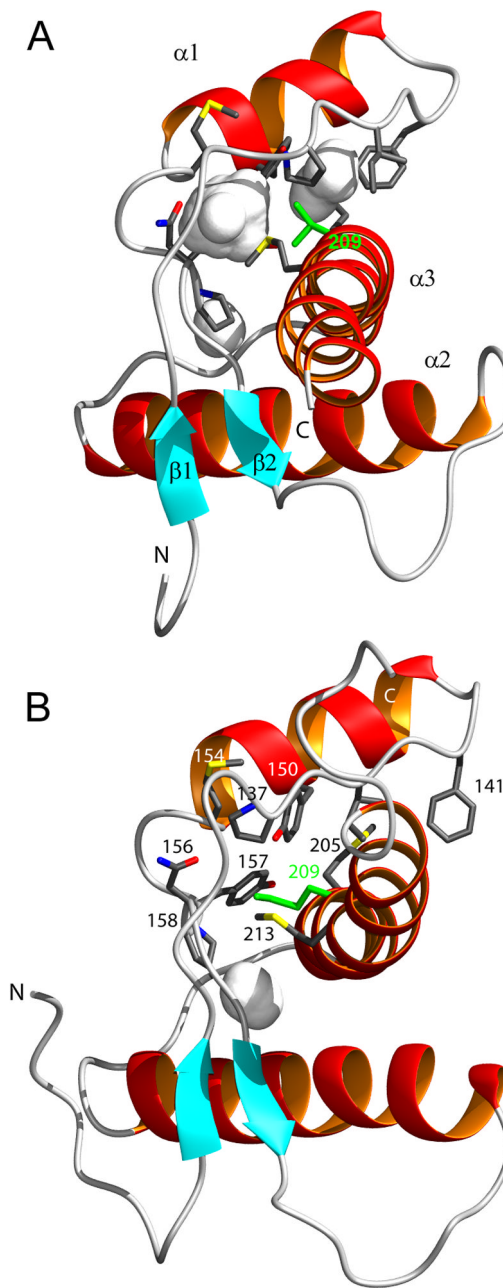


Figure 2. NMR-determined structures (ribbon representations) of prion protein folded domain (A) Wild-type human prion protein (Zahn et al., 2000) (PDB ID 1QM0). (B) The V209M variant of human PrP. In the wild-type protein, two cavities (displayed as white spheres) are present near residue V209. In the V209M variant, these cavities are eliminated as a result of altered side chain geometry of residue 209 and subtle changes in the packing and geometry of helices $\alpha 1$ and $\alpha 3$. A third cavity with nearly equal size in both proteins is found near Pro 158 between helices $\alpha 2$ and $\alpha 3$. Side chains surrounding the cavities are shown and labeled with residue numbers. The structure shown for the V209M variant represents the lowest energy structure of the ensemble of 20 water refined conformers. Additional structural details and statistics are provided in Figure S2 and Table S1.

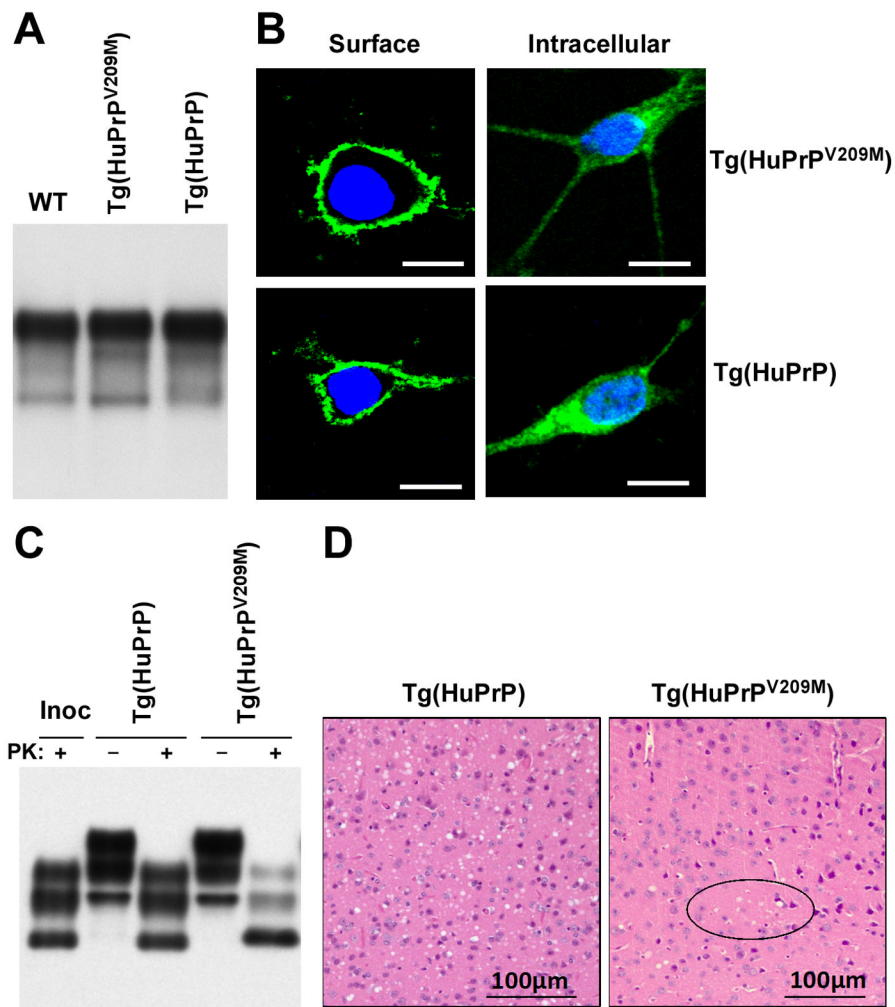


Figure 3. Transmissions of CJD prions in Tg(HuPrP) and Tg(HuPrP^{V209M}) mice
 (A) PrP expression levels in brains of Tg(HuPrP), Tg(HuPrP^{V209M}), and wild type (WT) FVB mice as probed by Western blotting using mAb 8H4.
 (B) Cell surface and intracellular localization of PrP in primary neurons prepared from Tg(HuPrP^{V209M}) and Tg(HuPrP) mice. Cells were probed for PrP with mAb 3F4, counterstained for nuclei with Hoechst, and examined with a confocal microscope. Scale bars: 10µm.
 (C) PrP^{Sc} in brains of sCJDMM1-infected Tg(HuPrP) and Tg(HuPrP^{V209M}) mice. Transgenic mice were intracerebrally inoculated with brain homogenate from a subject with sCJDMM1. Brain homogenates from symptomatic mice and the inoculum (Inoc) were subjected to Western blot analysis with mAb 3F4 before (–) and after (+) proteinase K (PK) treatment.
 (D) Spongiform degeneration in brains of sCJDMM1-infected Tg(HuPrP) and Tg(HuPrP^{V209M}) mice. Fixed brain sections from cerebral cortex of Tg(HuPrP^{V209M}) mice show small and scattered areas with vacuoles (circled area), whereas in Tg(HuPrP) mice spongiform degeneration is much more widespread and severe. Brain sections were stained with haematoxylin and eosin. Scale bars: 100 µm. See also Figure S3.

Table 1

Primary and secondary transmissions of sCJD in transgenic mice

Tg Line	Inoculum	Attack rate	Incubation Time (days) ^a	Titers (ID ₅₀ units/g)
Tg(HuPrP)	sCJDMM1 ^b	9/9	263±13	4.6 x 10 ⁷
	sCJDMM2 ^b	9/9	267±17	3.2 x 10 ⁷
Tg(HuPrP ^{V209M})	sCJDMM1	2/6	685, 696	
	sCJDMM2	0/7	798	
Tg(HuPrP)	Tg(HuPrP ^{V209M})- passaged sCJDMM1	5/5	316±16	8.3 x 10 ⁵
Tg(HuPrP ^{V209M})	Tg(HuPrP ^{V209M})- passaged sCJDMM1	6/6	431±30	
Tg(HuPrP)	sCJDMM1 passaged twice in Tg(HuPrP ^{V209M})	7/7	267±12 ^c	
Tg(HuPrP ^{V209M})	sCJDMM1 passaged twice in Tg(HuPrP ^{V209M})	7/7	366±18 ^d	
Tg(HuPrP)	sCJDMM1 passaged thrice in Tg(HuPrP ^{V209M})	10/10	295±7 ^c	
Tg(HuPrP ^{V209M})	sCJDMM1 passaged thrice in Tg(HuPrP ^{V209M})	4/6 ^e	399±6 ^d	

^aAverage values and standard errors are shown.

^bDenote the MM1 and MM2 subtypes of sCJD according to the classification of Parchi et al. (Parchi et al., 1999).

^cThe difference in incubation times for third and fourth passage in Tg(HuPrP) mice is statistically insignificant (p=0.11).

^dThe difference in incubation times for third and fourth passage in Tg(HuV209MPrP) mice is statistically insignificant (p=0.28).

^eTwo mice are still alive with no apparent symptoms (at ~580 days post inoculation).

See also Figure S4.