Structural biology of PrP prions





Distorted membrane

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100

nm





- Cross-section: single monomer with β-strands and loops
- Monomers stacked with parallel in-register intermolecular β -sheet (PIRIBS) architecture
- Glycans and GPI anchor project outward
- Cofactors on periphery?

Interspecies variation: hamster 263K vs mouse aRML prion cryo-EM structures



Variations in shared motifs and sequence (at 8 residues within core region):

- distinct templates for faithful propagation of strain conformers
- bases for differential transmission (e.g. species) barriers.

Kraus et al., *Mol Cell*Hoyt et al., *Nature Comm*Manka et al., *Nature Comm*Caughey et al., *PLoS Path*, 2022

Interspecies variation: hamster 263K vs mouse aRML prion cryo-EM structures



Variations in shared motifs and sequence (at 8 residues within core region):

- distinct templates for faithful propagation of strain conformers
- bases for differential transmission (e.g. species) barriers.
- Needed comparison of strains from same host genotype to identify purely conformational determinants of prion strain phenotypes
 - Same PrP sequence
 - Same cofactor pool

Kraus et al., *Mol Cell*Hoyt et al., *Nature Comm*Manka et al., *Nature Comm*Caughey et al., *PLoS Path*, 2022

Strain variation: a22L & aRML prion strains from the same genotype of mouse



- Conformationally conserved regions, especially near N-terminus
- Strain-dependent variations within shared motifs outside of conserved region



Kraus et al., *Mol Cell* 2021; Hoyt *et al.*, *Nat Comm* 2022 & *PLoS Path* 2022

- **Conformationally conserved regions**, especially near N-terminus
- Strain-dependent variations within shared motifs outside of conserved region



Hoyt et al., Nat Comm 2022 & PLoS Path 2022

- Conformationally conserved regions, especially near N-terminus
- Strain-dependent variations within shared motifs outside of conserved region
- Similar themes from comparison of RML & ME7 strains (Manka et al, Nat Comm 2022 & Nat Chem Biol 2023)

Distinct conformational templates provide a molecular basis for the "encoding" of prion strain characteristics

Influence of GPI anchor & N-linked glycans?

aRML (GPI-anchorless, underglycosylated)





Solution of RML strain Glycans & GPIs have **little effect** on core conformation of RML strain

Influence of GPI anchor & N-linked glycans?



Influence of GPI anchor & N-linked glycans?



How might distinct structures mediate strain-dependent pathogenesis?

A Charge



B Hydrophobicity-hydrophilicity



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B Hydrophobicity-hydrophilicity









Atomic model embedded in EM density map





Comparison to other *ex vivo* prion structures

229

227







Minimal stable size of the infectious prion core: Molecular dynamics simulations of *dimeric* (n=2) to *tetradecameric* (n=14) fragments



Efrosini Artikis **Minimal stable size of the infectious prion core:** Molecular dynamics simulations of *dimeric* (n=2) to *tetradecameric* (n=14) fragments



dimer

Efrosini Artikis

Minimal stable size of the infectious prion core: Molecular dynamics simulations of *dimeric* (n=2) to *tetradecameric* (n=14) fragments



dimer

Efrosini Artikis

Minimal stable size of the infectious prion core: Molecular dynamics Backbone RMSD (Å) 01 dimer simulations of *dimeric* (n=2) to *tetradecameric* (n=14) fragments 14-mer Fibril % Δβ-Strand -K105 14-mer N-arch (cross-section) -30 Disulfide B-arch dimer Middle arch -60 .00 N-term Lobe C-term Lobe Time (ns) E) **Multimers** ~10 Å ~660 Å Octamer, 2.5 Å MD Dimer, 17.9 / Decamer ~1 µsec Tetramer Decamer, 3.1 Å Trimer, 9.1 Å Pentamer ~35 Å Tetradecamer Tetramer, 5.9 Å Tetradecamer, 2.2 Å Octame

- Cross-β core oligomers appear stable as small as a (and do not have to look or behave like fibrils)
- No signs of fragmentation of these oligomers (or 2 (even at temperatures up to 127°C)

Efrosini

Artikis

Also, biochemically: no sign of disassembly of PrP^{Sc} aggregates into small oligomers under non-inactivating conditions (in our hands)
➢ Prion fragmentation in vivo may require physiological assistance

Summary

- High-resolution structures of brain-derived PrP fibrils:
 - Experimentally rodent-adapted scrapie (263K, RML, aRML, 22L, ME7)
 - Natural CWD from naturally infected white-tailed deer
 - Human GSS F198S
- PIRIBS-based architectures
 - All brain-derived or synthetic PrP fibrils with unambiguously determined architectures to date are PIRIBS-based (n>13)
- Complete refolding of PrP^c is required.
- **Glycans and GPI anchors** of wildtype prions project outwards but have little effect on core structure (RML)
- Distinct templating surfaces on ends of fibrils encipher strains
- Transmission barrier mechanisms?
 - 263K hamster → mice (Kraus et al., Mol Cell 2021)
 - CWD → humans (Alam et al., Acta Neuropath 2024)
- Non-infectious PrP fibrils have smaller ordered cores
- **aRML core structure** is mostly stable when as small as a **tetramer** (*in silico*)
 - PIRIBS prions do not have to look like fibrils!
- We've seen **no evidence efficient spontaneous disassembly** of PrPSc aggregates into small oligomers
- Many more prion structures (fibrillar & non-fibrillar?) remain to be determined...



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Current Caughey lab



Christina Orrú Hughson



Sabiha Parveen Samantha King



Efrosini Artikis Parvez Alam

Jakub Soukup



National Institute of Allergy and Infectious Diseases

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Transmission barrier mechanism?



Efrosini Artikis in Kraus et al., *Mol Cell*, 2021

Transmission barrier mechanism?



Efrosini Artikis in Kraus et al., *Mol Cell*, 2021

Transmission barrier mechanism?





Temperature 300K



Last frame of 500ns at 300K – cubic water box, 150mM NaCl



aRML at 400K showing a transient kink, but runs need more sampling time