The FT-IR spectra of abnormal prion protein from different scrapie strains show distinct secondary structure

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Strain diversity in the transmissible spongiform encephalopathies (TSEs) has been suggested to be "coded" by variations in the structure of the misfolded prion protein isoform (PrP^{Sc}). PrP^{Sc} is derived from the cellular prion protein (PrP^{C}) by posttranslational modifications and it is assumed to be the main component of the infection unit. The PrP^{Sc} from all TSE strains is characterised with partial proteinase K (PK) resistance and unusual stability to physical and chemical denaturation.

We have investigated the secondary structure of the protease-resistant core of PrP^{Sc} (PrP27-30), derived from four different TSE isolates (263K, ME7-H, 22A-H, and BSE-H) adapted to Syrian hamsters, each showing different incubation time and distinct disease specific symptoms. The PrP27-30 samples obtained by repeated independent purification procedures for each strain were used. FT-IR spectra were obtained from PrP27-30 samples suspended in D_2O or H_2O and from samples resuspended in water and dried for FT-IR microscopic measurements.

As seen from the protein FT-IR second derivative spectra, all three scrapie strains possessed consistent specific infrared patterns in the secondary structure sensitive amide I region. The variations observed were based mainly on distinct differences in the amide I band components which are assigned to different β-sheet conformations. These variations could be supplemented with strain dependent variations in the amide II and amide A absorption regions and results from the different hydrogen/deuterium (H/D) exchange behaviour of the protein samples. The strain differentiation capacity of the FT-IR approach could be objectively proven also by multivariate cluster analysis.

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