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UK Iatrogenic Creutzfeldt–Jakob disease: investigating human prion transmission across genotypic barriers using human tissue-based and molecular approaches

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Abstract Creutzfeldt–Jakob disease (CJD) is the prototypic human prion disease that occurs most commonly in sporadic and genetic forms, but it is also transmissible and can be acquired through medical procedures, resulting in iatrogenic CJD (iCJD). The largest numbers of iCJD cases that have occurred worldwide have resulted from contaminated cadaveric pituitary-derived human growth hormone (hGH) and its use to treat primary and secondary growth hormone deficiency. We report a comprehensive, tissue-based and molecular genetic analysis of the largest series of UK hGH-iCJD cases reported to date, including in vitro kinetic molecular modelling of genotypic factors influencing prion transmission. The results show the interplay of prion strain and host genotype in governing the molecular, pathological and temporal characteristics of the UK hGH-iCJD epidemic and provide insights into the adaptive mechanisms involved when prions cross genotypic barriers. We conclude that all of the available evidence is consistent with the hypothesis that the UK hGH-iCJD epidemic resulted from transmission of the V2 human prion strain, which is associated with the second most common form of sporadic CJD.

Keywords Creutzfeldt–Jakob disease · Prion · Iatrogenic · Growth hormone · Disease phenotype · Agent strain

Introduction

Prion diseases are a group of fatal transmissible neurodegenerative disorders that occur naturally in man and a range of other species [12]. All are associated with the conversion of a normal host cellular protein, the prion protein (PrPC), into a misfolded disease-associated form, PrPSc, which accumulates in the central nervous system (CNS) [29]. The prion hypothesis states that PrPSc is the principal (if not the sole) component of the transmissible agents responsible for this group of diseases [30]; this hypothesis is supported by an increasing body of experimental evidence [9]. However, the precise relationship between the conformation of PrPSc in different forms of prion disease and the biological properties of the transmissible agents (strain characteristics) in different prion diseases is still unresolved.

Unlike the more common forms of human neurodegenerative diseases, human prion diseases occur in sporadic, genetic and acquired forms [12]. The acquired human prion diseases that have resulted from human-to-human transmission include kuru (now considered to be extinct) and iatrogenic Creutzfeldt-Jakob disease (iCJD), with variant Creutzfeldt–Jakob disease (vCJD) resulting from bovine to human transmission of the bovine spongiform encephalopathy (BSE) agent. Iatrogenic transmission of Creutzfeldt–Jakob disease (CJD) has occurred in many countries across the world as a consequence of transmission...
40 years have been reported [8]. In contrast, only eight
[31]; these prolonged incubation periods are reminiscent of
in the UK hGH-iCJD patients range from 7 to 40 years
[33]. Estimated incubation periods in human pituitary hormone recipients (1.3–30 years), and human pituitary-derived hGH and
gonadotrophin recipients (5–42 years) [5]. Estimation of
incubation periods in human pituitary hormone recipients is
difficult, since the patients are often treated over a period of
years; the time period from the mid-point of pituitary hor-
mone treatment to the onset of clinical symptoms of iCJD
is often used as an estimate for the incubation period [33].

The use of pituitary-derived hGH in the treatment of
primary and secondary growth hormone deficiency in the
United Kingdom (UK) began as a clinical trial in 1959 and
became a centrally administered National Health Service
activity in 1976 [33]. In 1985, the first cases of iCJD in
patients treated with pituitary-derived hGH were reported
in the United States of America (USA) and in the UK [10,
28]. Consequently, the use of pituitary-derived hGH for the
treatment of growth hormone deficiency was abandoned in
the UK, USA and many other countries and biosynthetic
growth hormone is now used for this purpose. The pres-
ence of prion infectivity in hGH preparations in the USA
was confirmed by experimental intracerebral inoculation
of samples of pituitary-derived hGH into primates, which
resulted in the onset of neurological symptoms in a squir-
rel monkey after an incubation period of over 5.5 years
[11]. Post-mortem examination of the brain of this animal
confirmed the presence of a subacute spongiform encephalopathy.

In the UK, 1849 patients were treated with hGH in the
national scheme from 1959 until 1985 [33]. Since 1985, 78
deaths from iatrogenic CJD have occurred in this cohort,
and it has been identified that one particular prepara-
tion of UK pituitary-derived hGH (the Hartree-modified
Wilhelmi preparation) had been administered to all hGH
recipients who had developed iCJD [31, 33]. It has also
been estimated that the risk of developing iCJD in the UK
hGH recipient cohort was greatest in those patients who
received treatment at ages 8-10 years with a peak incuba-
tion period of 20 years [33]. Estimated incubation periods
in the UK hGH-iCJD patients range from 7 to 40 years
[31]; these prolonged incubation periods are reminiscent of
those occurring in kuru, where incubation periods of over
40 years have been reported [8]. In contrast, only eight
cases of iCJD in hDM graft recipients (hDM-iCJD) have
been reported in the UK, with incubation periods ranging
from 3.8 to 14.8 years [13].

Incubation periods in prion diseases have been studied
extensively under experimental conditions and appear to
be significantly influenced by both recipient (host) genetic
factors and the strain properties of the infectious agent [12].
The principal human genetic factor influencing this incu-
bation period is the codon 129 polymorphism in the prion
protein gene (PRNP) of the recipient. It has long been rec-
ognised that homozygosity at this locus may predispose to
both iCJD and sporadic CJD (sCJD), but differences in the
frequency of the three possible genotypes (MM, MV and
VV) have been reported in hGH-iCJD cohorts in different
countries; in particular, most cases of hGH-iCJD in France
have belonged to the MM subgroup, whilst in the UK the
VV and MV subgroups predominate [4]. These differences
may also reflect the nature of the strain(s) of CJD (presum-
ably sCJD) that were responsible for the iatrogenic disease
transmission.

Despite the fact that iCJD in hGH recipients has
occurred in over 200 patients across the world, there have
been very few detailed studies of the neuropathology, prion
protein biochemistry and prion protein seeding activity in
this form of human prion disease. Most reports describe
only small numbers of cases that are not necessarily rep-
resentative of the cohort in question, particularly with
respect to the year of diagnosis in relation to the evolving
time period since iatrogenic exposure to contaminated hGH
ceased. We now report a detailed study of the largest cohort
of hGH-iCJD cases reported to date, with detailed char-}
acterisation of PrP Sc in the brain, correlation with genetic
and pathological factors and an exploration of the in vitro
PrP seeding activity present in different genetic subgroups.
These cases are compared with a limited number of cases
of hDM-iCJD in the UK, but also a very much larger group
of sCJD cases drawn from the UK population over a simi-
lar time period. The detailed examination of these cohorts
has allowed us a unique opportunity to ask fundamental
questions about person-to-person transmission of prion dis-
ease and the molecular mechanisms involved.

Materials and methods

Cases, inclusion criteria and tissue specimens

All CJD cases examined were of UK origin and were
referred to the National CJD Research and Surveillance
Unit (NCJDRSU) between 1991 and 2015. Diagnoses were
made according to WHO criteria [35]. Inclusion criteria for
biochemical investigation of iCJD cases were the availabil-
ity of frozen CNS tissue taken at post-mortem, appropriate
consent and ethical approval for retention and research use and the availability of basic clinical data. All patients referred to the NCJDRSU with a diagnosis of CJD who had received hGH therapy or a hDM graft and met these criteria were included in the study. The study identification number and basic patient demographic data for 21 hGH-iCJD and three hDM-iCJD cases are detailed in Online Resource Table 1. Where available, samples of both frozen grey matter and the corresponding fixed samples from the cerebral cortex (frontal, parietal, temporal and occipital cortex), cerebellum, thalamus and spinal cord were examined. Data from a larger subset of the UK hGH-iCJD cases, including some of those for which frozen tissues were not available were included in genetic analyses. Data from 1080 unselected cases of UK sCJD of known genotype, PRNP codon 129, with deaths between 1990 and 2015 were used for genetic comparison with the UK hGH-iCJD cases. A smaller group of UK sCJD cases (n = 108) that were referred to the NCJDRSU during the period 1990–2011 were used for biochemical comparison with the hGH-iCJD group. These cases were selected on the basis of consent for research use, availability of clinical information and sufficient frozen tissue available (minimal set comprising temporal cortex, occipital cortex, parietal cortex and thalamus) for PrPres tissue available (minimal set comprising temporal cortex, availability of clinical information and sufficient fro-

cases were selected on the basis of consent for research use, and the corresponding fixed samples from the cerebral cortex (frontal, parietal, temporal and occipital cortex), cerebellum, thalamus and spinal cord were examined. Data from a larger subset of the UK hGH-iCJD cases, including some of those for which frozen tissues were not available were included in genetic analyses. Data from 1080 unselected cases of UK sCJD of known

Western blot analysis and classification of PrP\textsuperscript{res} types

PrP\textsuperscript{res} types present in brain samples from the hGH-iCJD, hDM-iCJD and sCJD cases were determined using the refined Western blot protocol of Parchi et al. [23]. Briefly, 100 mg samples of frozen CNS samples were subjected to stringent sample preparation (including strong buffering to pH 6.9 at 37 °C) and digestion with proteinase K (Roche, Lewes, UK) using 10 U/ml corresponding to ~200 µg/ml (depending on the batch) at 37 °C for 1 h prior to Western blot analysis. Immunodetection of PrP was carried out using monoclonal antibody 3F4 (Millipore, Watford, UK; Catalogue number MAB1564) at a final concentration of 75 ng/mL for 1 h, or the monoclonal antibody 12B2 (Central Veterinary Institute of Wageningen UR, Lelystad, The Netherlands) at a final concentration of 200 ng/mL for 1 h. This protocol allows a distinction to be made between PrP\textsuperscript{res} types based on the migration of the unglycosylated (bottom) band of the typical triplet glycoform pattern. Three different unglycosylated PrP\textsuperscript{res} fragment mobilities are recognised within the 21–19 kDa range: type 1 in which the unglycosylated PrP\textsuperscript{res} has a molecular mass of ~21 kDa, type 2 in which the unglycosylated PrP\textsuperscript{res} fragment has a molecular mass of ~19 kDa, and an additional type with a mobility of ~20 kDa migrating between type 1 and 2, and therefore referred to as type i (for intermediate). PrP\textsuperscript{res} types 1, i and 2 are not mutually exclusive. Certain individual samples and cases contain more than one PrP\textsuperscript{res} type. This diversity is recognised by classifying such samples and cases as 1 + 2 or i + 2.

Real-time quaking induced conversion (RT-QuIC)

The method used for the RT-QuIC in vitro conversion assay was the one used previously [26, 27] with minor modifications. Full length hamster recombinant PrP (recPrP,
were performed on each patient sample. The RT-QuIC
was performed by mixing the wells in a 96-well microplate
and then dispensing into the wells in 96-well microplates.
RecPrP was the final addition to the master mix, which was
diluted by gently inverting the tube and then dispensed into
the wells of a clear-bottomed black 96-well microplate
at 5200 g for 5 m. Further serial tenfold dilutions of
the cleared tissue homogenate were made using PBS. The
to give a final tissue concentration of 10% (w/v). Cellular
debris was cleared from the homogenates by centrifugation
at 5200 g at 4 °C for 5 m. Further serial tenfold dilutions of
the cleared tissue homogenate were made using PBS. The
100 μl RT-QuIC reactions were set up in quadruplicate
in the wells of a clear-bottomed black 96-well microplate
(Fisher Scientific, Loughborough, UK). Stock solutions
containing the reaction components were filtered through a
0.22 μM Millex PES filter prior to making a master mix. RecPrP
was the final addition to the master mix, which was
mixed by gently inverting the tube and then dispensed into
the wells in 98 μl volumes. At least four replicate analyses
were performed on each patient sample. The RT-QuIC
reactions (final volume = 100 μl, recPrP final concentra-
tion = 0.1 mg/ml) were initiated by the addition of 2 μl of
a 10-fold dilution of the 10% (w/v) homogenate, which is
equivalent to 2 × 10^{-7} g brain (wet mass) per 100 μl reaction.
After adding this volume of diluted brain homogenate,
the final reactions contained PBS, 324 mM NaCl (includ-
ing the NaCl present in PBS), 1 mM EDTA, 10 mM ThT,
1 × 10^{-5} % Triton™ X-100 and 0.1 mg/ml recPrP. The
plates were sealed with film, incubated at 42 °C and shaken
intermittently (87 s shaking at 900 rpm in a double orbital
configuration followed by a 33 s rest) using a FLUOstar
OMEGA microplate reader (BMG Labtech). Fluorescence
readings were taken at 480 nm every 15 min from the bot-
tom of the wells after excitation with 20 flashes per well
at 450 nm. To quantify prion seeding efficiency we used a
method based on the one described by Shi et al. [32]. In
this method, the lag time to conversion is used as an inverse
measure of seeding potential. The lag period to the start
of conversion was taken to be the time (in hours) from the
start of the assay to when the RT-QuIC fluorescence read-
ing was three times the average reading at 0.5 h (the base-
line). A mean lag period for four replicate analyses
was thus obtained for each patient.

**Protein misfolding cyclic amplification**

Normal brain homogenates, from humanised transgenic
mice of the PRNP codon 129 methionine homozygous
(129MM) and valine homozygous (129VV) genotypes,
were prepared using a manual homogenizer and convers-
ion buffer (Phosphate-Buffered Saline 1X, 150 mM NaCl, 1% Triton X-100 and 1X protease inhibitors)
to obtain a final 10% weight/volume solution (termed
the PMCA “substrate”). The homogenized tissue was
cleared by centrifugation at 2000 rpm for 40 s in a refrig-
erated centrifuge (4 °C), and the supernatant was ali-
quoted and stored at −80 °C. The CJD brain homogen-
ates (termed PMCA “seeds”) were prepared following
the same method used for substrate preparation. PMCA
experiments were carried out as described previously
[1]. Briefly, aliquots of 10% brain homogenate substrate
were mixed with 10% CJD brain homogenates seeds in
PCR tubes. Low molecular weight heparin was included
at 100 μg/ml for all PMCA reactions. Prior to the ampli-
ification procedure, 19 μL of the PMCA reaction mixture
were taken (from the final volume of 120 μl) for each
reaction (referred to as the “frozen” sample) for com-
parison with the sonicated samples (referred to as the
“sonicated” sample). Amplification employed cycles of
sonication and incubation in a programmable sonicator
(Qsonica, model Q-700) at 37 °C. A total of 96 PMCA
cycles were performed comprising 20 s of sonication (at
an amplitude of 38%, wattage: 278–299) followed by
29 min 40 s of incubation for each cycle. Frozen and soni-
cated samples were digested with proteinase K, and
analysed by Western blotting using the monoclonal antibody
3F4 as described previously [1]. Amplification efficiency
was expressed as the increase in PrPres signal in the soni-
cated compared to the frozen sample, as judged by den-
sitometry of Western blot images acquired and analysed
using the ChemiDoc™ System with Image Lab Software
(Bio-Rad, Hemel Hempstead, UK).

**Statistics**

In the statistical analysis of the clinical patient information
statistical significance was determined between the differ-
tent PRNP codon 129 genotypes using a one-way ANOVA
and Tukey’s multiple comparisons test. Statistical analysis of all clinical data was performed using
GraphPad Prism software 7.00. In the statistical analysis of
RT-QuIC data, a two sided Mann–Whitney test was used to
assess the statistical significance of differences between the
median RT-QuIC lag periods of sCJD versus hGH-iCJD or
hDM-iCJD cases. The Kruskal–Wallis test was used for the
combined analysis of sCJD (VV2, MV2, MM1) and hGH-
iCJD (VV2, MV2) subgroups. These non-parametric tests
were employed on the basis that the shapes of the distribu-
tions of the lag periods were similar for various subgroups.
Statistical analysis and graphing of the data was performed
using GraphPad Prism 7.00.
Results

PRNP codon 129 genotype of the hGH-iCJD cases

There have been 78 cases of hGH-iCJD identified in the UK from 1985 to the present day. 43 of these had fixed and/or frozen tissue referred for diagnosis at the NCJDRSU. Of these 43 cases, 40 were autopsy cases and three were biopsy cases. 37 of these 43 cases had available codon 129 genotype data. 21 of the autopsy cases had frozen CNS tissues that were available for research use. The study identification numbers with clinical and pathological features of these 21 autopsy cases are shown in Online Resource Tables 1 and 2, respectively. When the hGH-iCJD patient PRNP codon 129 status is considered by year of death the following becomes apparent: first, the 21 cases of hGH-iCJD with frozen tissue analysed in this study died during the period from 1990 to 2012, and consequently these cases provide examples from the leading edge, the peak and the tail of the epidemic (Fig. 1a, b). Second, the UK hGH-iCJD group is dominated by patients of the MV and VV PRNP codon 129 genotypes; the few hGH-iCJD cases that occurred in individuals with an MM PRNP codon 129 genotype tended to occur later than those of the MV and VV PRNP codon 129 genotypes (Fig. 1a, b). In contrast, the MM PRNP codon 129 genotype is the most frequently occurring group within the UK sCJD group overall, and in every year during the hGH-iCJD epidemic (Fig. 1c). Finally, when considered as a whole, the distribution of codon 129 genotypes of the 21 available hGH-iCJD cases and the 108 sCJD cases selected for study here differ from each other and from the normal UK population, but they appear to be broadly representative subsets of the larger hGH-iCJD and sCJD cohorts (Fig. 1d). The three hDM-iCJD cases were all of the PRNP codon 129 MM genotype (Online Resource Table 2).

hGH-iCJD patient information in relation to PRNP codon 129 genotype group

Age at death, duration of hGH treatment and estimated incubation periods were similar between the PRNP codon 129 MV and VV genotype hGH-iCJD groups, but the incubation periods in the two MM cases were longer. In
contrast, the mean disease duration of illness of the MV group was longer than that of both the VV and MM groups (Online Resource Table 3).

**PrP**

**Pres** types found in the hGH-iCJD cases

Western blot analysis of all available CNS tissue from the 21 cases of hGH-iCJD for protease resistant prion protein (PrP**Pres**) was performed. Four PrP**Pres** types were identified in the hGH-iCJD cases, differing in the mobility and in the number of unglycosylated bands found. Representative examples of the PrP**Pres** types 1, i, i + 2 and 2 in these cases are shown in Fig. 2a, example Western blots for each individual case are shown in Fig. 3, and the data compiled with the **PRNP** codon 129 genotype are shown in Online Resource Tables 1 and 2. The majority of cases were characterised by the presence of the 19 kDa type 2 PrP**Pres** band (19/21 cases). However, in 12 out of these 19 cases the 20 kDa type i PrP**Pres** band was also present. The relative abundance of the 19 kDa type 2 PrP**Pres** band and the 20 kDa type i PrP**Pres** band was variable, but the 19 kDa type 2 PrP**Pres** band usually predominated (Fig. 3a). Type i was found to predominate overall in only one hGH-iCJD case (hGH-iCJD20) and the 21 kDa type 1 PrP**Pres** was found in only one hGH-iCJD case (hGH-iCJD21). In contrast to the hGH-iCJD cases, all three cases of hDM-iCJD cases had type 1 PrP**Pres** exclusively (Fig. 3b). Where it could be assessed, regional variation within the brain was largely confined to the presence or absence of the PrP**Pres** type i band and the relative abundance of PrP**Pres** types i and 2 bands (Online Resource Table 4). Comparison of the immunoreactivity of the 21 kDa type 1, 20 kDa type i, and 19 kDa type 2 bands using the 3F4 antibody (epitope 106-112) with the 12B2 antibody (epitope 89-93) showed that the 21 kDa type 1 PrP**Pres** and the 20 kDa type i PrP**Pres** fragments both retain the 12B2 epitope, whereas type 2 PrP**Pres**
fragments do not (Fig. 2a, b). Analysis of the PrPres types found in the CNS of 108 sCJD cases showed type 1, type 2, type 1 + 2 and cases in which type 1 and type 2 were found in individual brains, either in the same or in different regions (Online Resource Table 5). These latter cases were designated type 1 + 2, irrespective of the relative abundance and location of the two types. The breakdown of these 108 sCJD cases according to the combination of CNS PrPres type and PRNP codon 129 genotype is shown in Online Resource Table 6, while the histotypes and PrPres types associated with the PRNP codon 129 MV sCJD cases are shown in Online Resource Table 7.

**PrPres type and PRNP codon 129 genotype of the hGH-iCJD cases**

When the 21 cases of hGH-iCJD were grouped according to the combination of PRNP genotype and CNS PrPres type (Online Resource Table 2; Fig. 4a) all PRNP codon 129 VV hGH-iCJD cases (7/7) were found to have type 2 PrPres exclusively. All of the hGH-iCJD PRNP codon 129 MV genotype cases were found to have type i + 2 PrPres (12/12). Of the two PRNP codon 129 MM genotype cases found within the hGH-iCJD cohort, one had type 1 PrPres and the other had type i PrPres. In contrast, within the 108 sCJD cases, those with type 1 PrPres and a PRNP codon 129 MM genotype predominated (50/108) and cases with type 1 + 2 PrPres were relatively common (26/108), but no examples of type i PrPres alone were found (Online Resource Table 6; Fig. 4b). The three hDM-iCJD cases were in individuals of the PRNP codon 129 MM genotype and each had PrPres type 1 in the CNS (Fig. 3b).

**Neuropathology of hGH-iCJD**

The neuropathological features were reviewed in the 21 hGH-iCJD patients (fixed tissue from case hGH-iCJD1 was not available for PrP immunohistochemistry). All cases showed a general widespread spongiform encephalopathy of a predominantly microvacuolar type accompanied by neuronal loss and gliosis, with amyloid plaques in the cerebellum in 13/21 cases. The patterns of accumulation of the disease-associated prion protein on immunohistochemistry were recorded in the 20 cases with available material. A summary of the neuropathological features of each hGH-iCJD case is added to the PRNP codon 129 genotype and PrPres type in Online Resource Table 2 and example micrographs are shown in Fig. 5 (the neuropathological features in this cohort will be described more fully in a separate manuscript). Overall, the patterns of pathology in the hGH-iCJD patients showed close similarities with sCJD patients of the corresponding PRNP codon 129 genotype.

Immunohistochemistry on tissue sections from PRNP codon 129 VV hGH-iCJD patients showed a combination of synaptic, perineuronal and plaque-like deposits of PrP in the cerebral cortex often in a distinctive linear distribution in the deeper cortical layers, a pattern of PrP pathology very similar to that in the VV2 subtype of sporadic CJD (Fig. 5a, i). The cerebellum in these cases showed a coarser deposition of PrP with occasional plaque-like deposits (Fig. 5e, m). In contrast, all PRNP codon 129 MV hGH-iCJD patients were characterised by a pathology dominated by the accumulation of large and numerous kuru-type amyloid plaques in the cerebellar cortex and frequently in the cerebral cortex and basal ganglia, consistent with that observed in the sCJD MV2 subtype (Fig. 5b, f, j, n). The two hGH-iCJD PRNP codon 129 MM cases available for analysis showed strikingly different patterns of neuropathology. In patient hGH-iCJD20, the spongiform change comprised a mixture of both microvacuolar and confluent types, with PrP staining showing a combination of synaptic, perineuronal and perivascular PrP deposits (Fig. 5c). In addition, plaque-like deposits and kuru plaques were a prominent feature in the cerebral and cerebellar cortex from this case (Fig. 5g). In contrast, hGH-iCJD21 showed spongiform change of predominantly the microvacuolar type with a widespread synaptic/granular pattern of PrP deposition, a pattern more consistent with that observed in the sCJD MM1 subtype (Fig. 5d, h, k, o). In the two hDM-iCJD cases in which fixed tissue was available for immunohistochemical analysis, both showed a synaptic deposition of PrP throughout the brain. Kuru-type amyloid plaques or plaque-like PrPres deposits were not observed in either case (Fig. 5l, p).

**Comparison of the amyloid seeding potential of hGH-iCJD and sCJD**

The amyloid seeding activity of hGH-iCJD and sCJD cases was compared using the real-time quaking induced conversion assay (RT-QuIC). hGH-iCJD cases were selected on the basis of the availability of frozen cerebral cortex samples (n = 20). sCJD cases (n = 28) were selected on the basis of PrPres type and PRNP codon 129 genotype to match, as far as possible, those found in the hGH-iCJD cohort. RT-QuIC assays were seeded with CJD cerebral cortex homogenate diluted by a factor of 2 × 10−5 (each 100 μl RT-QuIC reaction was seeded with the equivalent of 2 × 10−7 g brain) and the seeding activity for each patient was assumed to be inversely proportional to the mean lag period (Table 1). The hGH-iCJD and sCJD seed amounts were determined empirically to be within the range for quantifying seeding activity by the lag time method. The hGH-iCJD group as a whole (and their subgroups) have a lower median seeding activity than the sCJD group (and their matched subgroups). The
difference is significant for the hGH-iCJD group as a whole and for the VV and MV subgroups. The two PRNP codon 129 MM hGH-iCJD cases had noticeably different lag times in this assay (hGH-iCJD20 at 43.5 h and hGH-iCJD21 at 27.5 h). Three hDM-iCJD cases were also analysed by RT-QuIC and their median lag period (34.2 h) was also greater than the sCJD MM1 subgroup, but this difference was not statistically significant. Although these experiments were conducted with recombinant hamster PrP, and therefore with a substrate containing methionine at the position equivalent to human codon 129, our previous experience with RT-QuIC indicates that it is less sensitive than PMCA to the biologically relevant effects of seed and substrate sequence matching or mismatching [26].

**Comparison of the in vitro amplification of hGH-iCJD and sCJD**

The seeding characteristics of the two divergent hGH-iCJD PRNP codon 129 MM cases (hGH-iCJD20 and hGH-iCJD21) were further examined using protein misfolding cyclic amplification (PMCA). Samples of cerebral cortex were used to seed matched (PRNP codon 129 MM, designated HuMM) and mismatched (PRNP codon 129 VV, designated HuVV) PRNP transgenic mouse brain substrates and the results compared with those of sCJD subtypes. PMCA reactions seeded with cerebral cortex samples from cases of sCJD of the MM1 subtype amplified poorly under these conditions, whereas hGH-iCJD20 more closely resembled the sCJD MM1 subtype (and the limited number of hDM-iCJD cases analysed), whereas hGH-iCJD21 resembled the sCJD MV2 or VV2 subtypes, despite its PRNP codon 129 MM genotype. These data are summarised in Table 2 and Fig. 7.

**Discussion**

This study provides a thorough molecular genetic description of the largest series of UK hGH-iCJD epidemic published to date, including as it does a large number of cases (21 compared to seven in a recent study [31]) in which the pathology, biochemistry and genetics can be compared. It also provides a description of the leading edge, peak and tail of the epidemic, rather than focussing largely on the tail of the epidemic [31]. In doing so, this study provides a unique opportunity to investigate the molecular epidemiology of prion transmission within a species, but across PRNP codon 129 polymorphic barriers.
The UK hGH-iCJD epidemic is widely thought to result from contamination of hGH batches with prions present in tissue (either pituitary or brain) collected from one, or more cases of “classical” Creutzfeldt-Jakob disease. On the balance of probabilities, this is more likely to be a form of sCJD (rather than a genetic form) since sCJD accounts for ~85% of human prion disease cases [12]. Although it cannot be known with certainty, the thesis proposed here is that the epidemiology of the epidemic is consistent with contamination with a single major prion strain.

Prion transmission (susceptibility, incubation period and phenotype) can be considered as an interaction between agent strain and host genotype, mediated in part by the related properties of abnormal prion protein conformation (for which PrPres type is a surrogate marker) and the PRNP polymorphism that encodes the residue at position 129 of the prion protein (either M or V). At present, five sCJD prion strains (designated M1, M2(c), M2(t), V1 and V2) have been distinguished by transmission studies in PRNP humanised transgenic mice and nonhuman primates and the V2 strain has been proposed to account for both MV2 and VV2 sCJD [3, 21, 24]. The surfeit of PRNP codon 129 MM hGH-iCJD cases in France, compared to the predominance of PRNP codon 129 VV hGH-iCJD cases in the UK as of 2003 was suggested to be attributable to different contamination events by different strains of agent [4]. Given that the two most frequently occurring subtypes of sCJD are the MM1 and VV2 subtype, the simplest hypothesis is that the French hGH-iCJD epidemic was caused primarily by contamination with MM1 sCJD (i.e. the M1 sCJD strain) and the UK hGH-iCJD epidemic caused primarily by VV2 or MV2 sCJD contamination (i.e. the V2 sCJD strain).

The data presented here and those of Rudge et al. [31] are consistent with that explanation, coupled with the PRNP genotype frequency of the at-risk hGH treated patient group, which if similar to UK control (e.g. blood donor) groups would be 44% MM, 45% MV and 11% VV [2]. Hence, the early surfeit of PRNP codon 129 VV UK hGH-iCJD cases could reflect the absence of a genotypic barrier and shorter incubation periods, albeit in a small subset of the hGH treated patient group. The appearance of more numerous cases in PRNP codon 129 MV individuals may reflect the larger numbers of PRNP codon 129 MV individuals in the hGH treated patient group. The appearance of a limited number of PRNP codon 129 MM hGH-iCJD cases, comparatively late in the epidemic, even although the hGH treated patient group would be expected to be ~40%, could be interpreted as evidence of a substantial PRNP codon 129 genotypic barrier to transmission of sCJD of the VV2 or MV2 subtypes, or a very prolonged incubation period. Although we cannot completely discount a mixture of contaminating strains including M1 in the form of sCJD MM1/MV1 subtype, the late appearance of these MM cases argues against a second minor M1 contaminating strain.

Our comprehensive data set coupled with the use of in vitro molecular conversion systems can be used to refine that model and provides a possible molecular mechanism for cross-genotype transmission. Within sCJD cases with PRNP codon 129 MV and PrPres type 2, some cases have kuru plaques (the MV2K subtype), whereas others do not (the MV2C subtype). The MV2K sCJD subtype is characterised by PrPres type i + 2 (a doublet of approximately 20 kDa and 19 kDa), whereas the MV2C subtype is reported to be characterised by the 19 kDa band only, and

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**Fig. 4** PrPres type and PRNP codon 129 genotype of the hGH-iCID and sCID groups. a Shows the numbers of cases found within the hGH-iCID group (n = 21) according to the combination of PrPres type (inner ring) and PRNP codon 129 genotype (outer ring). b Shows the numbers of cases found within the sCID group (n = 108) according to the combination of PrPres type (inner ring) and PRNP codon 129 genotype (outer ring)
termed type 2 [17, 23, 24]. We note that all PRNP codon 129 MV UK hGH-iCJD cases had PrPres type i + 2 (12/12) and kuru plaques. One of the two PRNP codon 129 MM hGH-iCJD cases described (hGH-iCJD20) also had kuru plaques (not normally found in PRNP codon 129 MM sCJD cases) and an intermediate ~20 kDa PrPres type (type i), perhaps suggestive of a causal link to the MV2K subtype of sCJD. Moreover, the in vitro amplification characteristics of PrPres from this case when used to seed the cell free prion protein conversion assay PMCA were not
consistent with its PRNP codon 129 MM genotype, instead showing a preference for a substrate containing PrP\(^C\) with valine rather than methionine at position 129. This situation is highly reminiscent of the molecular trace-back phenomenon proposed by Kitamoto and coworkers to explain the phenotypic diversity of the MV2 sCJD cases, and the transmission properties and origin of dura mater-associated CJD in Japan [15, 16, 18]. Furthermore, Kobayashi et al. [19, 20] have proposed that kuru plaques in PRNP codon 129 MM apparent sCJD cases can be used as an indication of an iatrogenic rather than idiopathic/sporadic aetiology. The characterisation of our case hGH-iCJD20 here extends the trace-back phenomenon of Kitamoto and coworkers from dura mater-associated transmissions in Japan to UK growth hormone associated transmissions. One of our PRNP codon 129 MM hGH-iCJD cases has some similarities to one case recently described in a group of three hGH-iCJD cases in the USA [6]. The association of a PRNP codon 129 MM genotype with kuru plaques in three national independent iCJD cohorts adds weight to the trace-back hypothesis. Moreover, our data using PMCA also confirms that evidence of the trace-back phenomenon in hGH-iCJD can be acquired from cell free systems, in addition to animal transmission studies, as predicted for hDM-iCJD by Kobayashi et al. [20] and subsequently demonstrated by Takeuchi et al. [34].

The molecular mechanism of the trace-back phenomenon is not fully understood, but the data of Kitamoto and coworkers points to a key role for the intermediate PrPres type, termed type i. In this light, it is also tempting to suggest that our data points to the sCJD MV2K subtype as the source of the UK hGH-iCJD epidemic. It is plausible that the combination of the 20 kDa type i and 19 kDa type 2 PrPres conformational variants found in sCJD MV2K might engender enhanced genotypic host range according to the principles of the conformational selection model proposed by Collinge and Clarke [7]. In this scheme, the MV2K subtype would transmit efficiently to MV individuals resulting in hGH-iCJD with a recognisable MV2K phenotype involving kuru plaques. The presence of type 2 PrPres in the type i + 2 isoform would also facilitate efficient transmission to PRNP codon 129 VV individuals and result in the recognisable VV2 phenotype lacking kuru plaques. Finally, the coexistence of type i with type 2 PrPres within the type 2d or 2 doublet isoform might render MV2K more compatible with transmission to PRNP codon 129 MM individuals, but only with extended incubation periods and producing a phenotype with PrPres type i and kuru plaques or, if molecular adaptation is complete, type 1 PrPres and an MM1 phenotype.

Alternatively, a sCJD VV2 source of infection in the hGH-iCJD cohort would involve a molecular strain adaptation-based model (rather than a molecular strain

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**Table 1** Lag period analysis of RT-QuIC reactions seeded with cerebral cortex from cases of sCJD and iCJD

| Patient subgroup | All subtypes | VV2 | MV2 | MV2 +i | MV1 | MM1 | MMi | Median lag periodc (h) | Number of patients | IQRd | Mann–Whitney teste | Kruskal–Wallis testf |
|-----------------|-------------|-----|-----|-------|-----|-----|-----|------------------------|-------------------|------|-----------------|-------------------|
| sCJD            | 14.7        | 22.0| 11.9| 17.9  | 15.0| 12  | 10.7| 12.3                   | 11                | 10.6–17.1| 0.0001          | 0.005             |
| hGH-iCJD        | 27.4        | 17.4| 12  | 11.2  | 6   | 10  | 16.3| 16.6                   | 27.5              | 16.6–27.5| 0.027           | 0.007             |
| sCJD            | 10.6–17.1   | 11.2| 17.3| 9.2–16.5| 10.7–20.5| 7   | 10.7–20.5| 15.0                   | 3                 | 10.7–20.5| 0.0001          | 0.005             |
| hGH-iCJD        | 12.3        | 17.9| 10  | 13.85 | 24.5| 19.3| 16.3| 16.6                   | 34.2              | 16.3–24.5| 0.00007         | 0.00007           |
| sCJD            | 10.7–20.5   | 17.3| 9.2–16.5| 10.7–20.5| 7   | 10.7–20.5| 15.0                   | 3                 | 10.7–20.5| 0.0001          | 0.005             |
| hGH-iCJD        | 16.3–24.5   | 13.85| 9.2–16.5| 10.7–20.5| 7   | 10.7–20.5| 15.0                   | 3                 | 10.7–20.5| 0.00007         | 0.00007           |
| sCJD            | 19.3–62.0   | 16.3| 9.2–16.5| 10.7–20.5| 7   | 10.7–20.5| 15.0                   | 3                 | 10.7–20.5| 0.0001          | 0.005             |
| hGH-iCJD        | 27.5        | 16.3| 9.2–16.5| 10.7–20.5| 7   | 10.7–20.5| 15.0                   | 3                 | 10.7–20.5| 0.00007         | 0.00007           |

*The patients were separated into subgroups according to PRNP codon-129 genotype and PrPres type.

b Cases in the sCJD MV2 group were chosen to be representative of all sCJD cases with an MV PRNP codon-129 genotype that have type 2 PrPres. Therefore, this group includes three type i + 2 cases, four type 2 cases and three type 1 + 2 cases.

c The mean of at least four replicate analyses of one sample of cerebral cortex.

d IQR = Interquartile range

e The Mann–Whitney test was used to assess the statistical significance of the difference in the median lag periods in pairwise comparisons of patient subgroups on the basis that the shapes of the distributions of lag periods were similar for the patient subgroups.

f The Kruskal–Wallis test was used for the combined analysis of sCJD (VV2, MV2, MM1) and hGH-iCJD (VV2, MV2) subgroups.
selection-based model) in which the \( PRNP \) codon 129 polymorphism of the host imposes a modified \( \PrP^{Sc} \) conformation on the infectious agent. In vitro \( \PrP^{Sc} \) type switching we observed when sCJD VV2 was amplified in a mismatched substrate (MM) is entirely consistent with this second VV2 source adaptation-based model. These scenarios are summarised in Fig. 7a and the epidemic is plotted according to estimated incubation periods in

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Fig. 6 \( \PrP^{Sc} \) analysis of PMCA reactions seeded with cerebral cortex from case of sCJD and iCJD. a hGH-iCJD, hDM-iCJD and sCJD brain homogenate (seeds) were diluted in humanised transgenic mouse brain homogenate (substrate) of the \( PRNP \) codon 129 MM (red dots) or VV (blue dots). Amplification factor is shown as the relative increase (fold) in \( \PrP^{Sc} \) signal after a single round of PMCA as determined by densitometry of the Western blotting signal. PMCA reactions were normalized by seed \( \PrP^{Sc} \) amount. PMCA of serial dilution of the hGH-iCJD MM seeds were also performed (hGH-iCJD20: 1/50, 1/100, 1/200, 1/400 and hGH-iCJD21: 1/4, 1/8, 1/16, 1/32). PMCA experiments seeded with hGH-iCJD, hDM-iCJD and sCJD samples were performed twice independently and repeated at least four times for the reactions seeded with the hGH-iCJD MM cases. b \( \PrP^{Sc} \) type of MM hGH-iCJD cases 20 and 21 assessed before and after PMCA. PMCA reactions employed matched (MM) and mismatched (VV) \( PRNP \) transgenic mouse brain substrates. Each sample was run between a type 1 (left lane) and type 2 (right lane) reference standards from sCJD MM1 and VV2 subtype cases, respectively (T1 and T2). Study identification numbers of the hGH-iCJD MM cases are indicated. c \( \PrP^{Sc} \) analysis of sCJD VV2 PMCA products detected by Western blot. \( \PrP^{Sc} \) type of MM hGH-iCJD cases 20 and 21 assessed before and after PMCA. PMCA reactions employed matched (MM) and mismatched (VV) \( PRNP \) transgenic mouse brain substrates. Each sample was run between a type 1 (left lane) and type 2 (right lane) reference standards from sCJD MM1 and VV2 subtype cases, respectively (T1 and T2). Study identification numbers of the hGH-iCJD MM cases are indicated. d \( \PrP^{Sc} \) analysis of sCJD VV2 PMCA products detected by Western blot. sCJD VV2 brain homogenate was amplified in matched (MM) and mismatched (VV) codon 129 substrate by a single round of PMCA. Samples corresponding to unamplified (Frozen) and amplified (PMCA) aliquots are shown with reference standards as described above. A total of 25 biological replicates of hGH-iCJD, hDM-iCJD and sCJD were analysed.

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Fig. 7b. The most relevant published humanised transgenic mouse model transmission data do not help in resolving the VV2/MV2 question, because the VV2 sCJD and MV2 sCJD cases used transmitted with indistinguishable characteristics in these mice. However, it is noteworthy that the most efficient transmission with the shortest incubation period was with the V2 strain (both VV2 and MV2 sCJD) in \( PRNP \) codon 129 VV mice [3]. Distinguishing between
sCJD VV2 and MV2K as the source of UK hGH-iCJD may be more than a formal difficulty given our recent finding that the proportion of PrPres derived from the two PRNP M and V alleles can vary dramatically in sCJD, such that some heterozygous sCJD cases might in effect contain only PrPres derived from the 129 V or the 129 M alleles [22]. Irrespective of mechanisms, the chronological sequence of cases (as judged by date of death and by estimated incubation period) involves a gradual change from predominantly PRNP codon 129 VV cases first, then MV cases during the peak and finally MM cases later and a corresponding change from predominantly PrPres type 2, to more complex type i + 2 and then the two cases with PrPres type i and type 1.
Implications for person-to-person transmission

The RT-QuIC and PMCA comparisons performed here did not support the hypothesis that human-to-human transmission of CJD results in acquired replicative efficiency [36]. Indeed, the RT-QuIC assay showed reduced rather than enhanced seeding activity in hGH-iCJD compared to the matched subtypes of sCJD suggesting that hGH-iCJD is not markedly more of a public health concern than its presumed source, sCJD. However, CJD surveillance systems in countries where contaminated batches of growth hormone were used should remain vigilant for further cases of hGH-iCJD. Some of these cases may be identifiable by the presence of kuru plaques and the presence of PrPres type i. However, others cases may appear closely similar to the most common form of sCJD (MM1), and the only
indication of an iatrogenic aetiology may be in their medical history. The overriding message from the UK experience with hGH-iCJD and perhaps human prion diseases, more generally, is that poorly assessed risks can continue to have ramifications for patients years to decades after the risk source is itself recognised and removed. This point is underscored by a further case of hGH-iCJD being identified during the writing of this report in 2016, some 30 years after treatment with pituitary-derived hGH was abandoned in the UK.

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Conflict of interest The authors declare that they have no conflicts of interest.

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