

Complementation between pathological prion protein subassemblies to cross existing species barriers

Angélique Igel-Egalon, Florent Laferrière, Philippe Tixador, Mohammed Moudjou, Laetitia Herzog, Fabienne Reine, Juan Maria Torres, Hubert Laude, Human Rezaei, Vincent Béringue

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- 3 Angélique Igel-Egaloni, Florent Laferrièrei, Philippe Tixadori, Mohammed Moudjoui,
- 4 Laetitia Herzogi, Fabienne Reinei, Juan Maria Torres2, Hubert Laudei, Human Rezaeii*, and
- 5 Vincent Béringue1*

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- 7 1VIM, INRA, Université Paris-Saclay, 78350, Jouy-en-Josas, France,
- 8 2Centro de Investigación en Sanidad Animal (CISA-INIA), Valdeolmos, Madrid, Spain
- 9 #Current address: Institute of Neurodegenerative diseases, CNRS UMR5293, University of
- 10 Bordeaux, Bordeaux, France
- 12 *Corresponding authors:
- 13 E-mail: <u>vincent.beringue@inra.fr</u> (VB), <u>human.rezaei@inra.fr</u> (HR)
- 14 ¶Equal contributors

Abstract **Background:** prion replication results from the autocatalytic templated assisted conversion of the host-encoded prion protein PrPc into misfolded, polydisperse PrPsc conformers. Structurally distinct PrPsc conformers can give rise to multiple prion strains. Within and between prion strains, the biological activity (replicative efficacy and specific infectivity) of PrPsc assemblies is size-dependent and thus reflects an intrinsic structural heterogeneity. The contribution of such PrPsc heterogeneity across species prion adaptation, - which is believed to be based on fitadjustment between PrPsc template(s) and host PrPc -, has not been explored. Methods: to define the structural-to-fitness PrPsc landscape, we measured the relative capacity of size-fractionated PrPsc assemblies from different prion strains to cross mounting species barriers in transgenic mice expressing foreign PrPc. Results: in the absence of a transmission barrier, the relative efficacy of the isolated PrPsc assemblies to induce the disease is superimposable to the efficacy observed in the homotypic context. However, in the presence of a transmission barrier, size fractionation overtly delays and even abrogates prion pathogenesis in both neural and extraneural, prion-permissive tissues, for reason independent of the infectivity load of the isolated assemblies. This suggests that a synergy between structurally distinct PrPsc assemblies in the inoculum is requested for crossing the species barrier. We further strengthen this hypothesis by showing that altering, by serial dilution, PrPsc assemblies content of unfractionated inocula reduce their specific infectivity in an aberrant manner, solely in the presence of a transmission barrier. **Conclusions**: our data support a mechanism whereby overcoming prion species barrier requires complementation between structurally distinct PrPsc assemblies. This work provides key insight into the "quasi-species" concept applied to prions, which would not necessarily rely on prion sub-strains as constituent but on structural PrPsc heterogeneity within prion population.

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Keywords

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Prion / species barrier / transgenic mice / quasi-species / sedimentation velocity / assemblies

Background

5 Mammalian prions are proteinaceous pathogens formed from misfolded assemblies (PrPsc) of 6 the host-encoded prion protein PrPc. Prions self-replicate by templating the conversion and 7 polymerization of PrPc [1]. Prions cause inexorably fatal neurodegenerative diseases such as 8 human Creutzfeldt-Jakob disease (CJD), sheep scrapie, bovine spongiform encephalopathy 9 (BSE) and chronic wasting disease of cervids [2]. 10 The prion strain phenomenon which is due to a structural polymorphism of PrPsc assemblies is 11 defined by the physiopathological and biochemical characteristics of prior disease within these 12 host species and in experimental models [3-10]. The strain-specified physiopathological 13 differences include duration of disease in the challenged or affected species, vacuolation 14 distribution and pattern of PrPsc deposition in the brain, tropism for the lymphoid tissue and 15 biochemical properties of PrPsc, including resistance to denaturation and to proteases [3]. How 16 PrPsc structural polymorphism causes such distinct phenotypes remains poorly understood. 17 A broad panel of experimental observations, including by size fractionation supports the 18 existence of structurally different PrPsc subsets within a given prion strain [11-19]. This intra-19 strain structural heterogeneity results from the intrinsic and deterministic properties of the prior 20 replication process to generate structurally diverse PrPsc subsets [20]. Structural diversity can 21 be observed at different levels. Size-fractionation studies by sedimentation velocity (SV) 22 indicate that variability in PrPsc quaternary structure is strain-specific [15,18,17,21,22]. Within 23 a given prion strain, PrPsc assemblies with differing quaternary structure exhibit markedly 24 different templating and biological activities, which are a hallmark of the existence of 25 structurally distinct PrPsc subpopulations, as previously discussed [23]. The biological and biochemical consequences of PrPsc structural heterogeneity during prion replication and propagation are poorly understood. Maybe one of the most intriguing and unpredictable change in prion replicative environment is the interspecies transmission. In certain host/strain combinations, prions will propagate readily as in an intraspecies transmission. In other host/strain combinations, only a fraction of the exposed animals will develop the disease with variable incubation periods, reflecting a 'species' or 'transmission' barrier. Attaining full attack rate and minimal incubation periods will require iterative transmissions. At that stage, prions are considered to be adapted to the new host [3]. Two main theoretical models have been developed to describe the transmission barrier at the molecular level. Both propose that the species barrier is governed by a misfit between PrPsc contained in the infecting prion and host PrPc folding landscape [5,24]. Schematically, the first one called 'deformed templating' consider that PrPc will progressively adopt, -due to its specific conformational dynamic-, the "quasi-right" conformation to be selected during the templating process [24]. As a consequence, a switch to a new strain structural determinant can occur, which combines structural information from the inoculated PrPsc assemblies with the folding landscape of the new host PrPc [25-29]. A major limitation of this model resides in the assumption that all PrPsc assemblies are structurally equivalent, despite experimental counterevidence. The second model called 'conformational selection' considers the existence of structurally distinct PrPsc subsets within a strain or isolate, the species adaptation resulting from the selection of the best replicator [5]. The two models are not mutually exclusive. They at least have the merit to highlight the role of structural diversity of PrPc and/or PrPsc in prion adaptation and evolution. Here, we aim at defining the contribution of PrPsc (quaternary) structure polydispersity to across species prion fitness. We compare the relative capacity of size-fractionated PrPsc assemblies to propagate in transgenic mice expressing homotypic versus heterotypic PrPc, used as proxy of

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1 mounting species barriers (one with prion 'mutation'). We show that fractionating PrPsc 2 assemblies strengthens existing species barrier, to a degree of magnitude independent of their 3 infectivity load. Coexistence of heterogeneous PrPsc quaternary structure in the inoculum may 4 thus be requested to cross species barriers. We strengthen this hypothesis by showing that 5 altering, by serial dilution, PrPsc assemblies content overtly reduces the specific infectivity from 6 unfractionated inocula during cross-species transmission events. Our data support a mechanism 7 whereby overcoming prion species barrier requires complementation between structurally 8 distinct PrPsc subsets within the inoculum, refining the current prion adaptation models. 9 Methods 10 Transgenic mouse lines The transgenic mouse lines expressing ovine, hamster and bovine PrP have been described 11 12 previously [30-33]. The bovine PrP tg540 [30] and tg110 [31] lines showed equivalent 13 susceptibilities to classical BSE prions [30]. 14 **Prion sources** 15 LA19K, LA21K fast and 127S scrapie prions are cloned prion strains. They have been obtained 16 by serial transmission and subsequent biological cloning by limiting dilutions of classical field 17 scrapie isolates to tg338 transgenic mice expressing the VRQ allele of ovine PrP [32,18]. Pooled 18 tg338 mouse brain homogenates (20% wt/vol. in 5% glucose) were used in centrifugation 19 analyses, as indicated. 20 The transmission properties of the L-type BSE isolate (designated BASE by the authors [34]) 21 in tgBov mice (tg540 line) and tgOv mice have been previously described [26]. The same brain

material from the same isolate was transmitted to tgBov line (tg110) line by intracerebral route

by using 20 µl of a 10% (wt/vol. in 5% glucose) brain homogenate.

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Fractionation by sedimentation velocity

2 The sedimentation velocity procedure has been previously and comprehensively described

[15,18,20,13]. Briefly, detergent-solubilized brain homogenates were loaded atop a continuous

10–25% iodixanol gradient (Optiprep, Axys-shield). The gradients were centrifuged at 285 000

g for 45 min in a swinging-bucket SW-55 rotor using an Optima LE-80K ultracentrifuge

(Beckman Coulter). Gradients were then manually segregated into 30 equal fractions of 165µl

from the bottom using a peristaltic pump. Fractions were aliquoted for immunoblot and

bioassays. Gradient linearity was verified by refractometry. To avoid any cross-contamination,

each piece of equipment was thoroughly decontaminated with 5 M NaOH followed by several

rinses in deionised water after each gradient collection.

Bioassays

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12 Fractions were diluted extemporarily in 5% glucose (1:5) in a class II microbiological cabinet

according to a strict protocol to avoid any cross-contamination. Individually identified 6- to 10-

week-old mice were inoculated intracerebrally with 20 µl of the solution, using a 27-gauge

disposable syringe needle inserted into the right parietal lobe. At terminal stage of disease or at

end-life, mice were euthanized and analyzed for proteinase K (PK) resistant PrPsc (PrPres)

content in brains and spleens tissues (as indicated), using the Bio-Rad TsSeE detection kit [26]

before immunoblotting, as described below.

Endpoint titration

For titration purposes, groups of indicator mice were inoculated intracerebrally (20 µl) with

serial ten-fold dilutions of the indicated brain homogenates. Animals inoculated with the initial

dose at 10% (w/v) solution were assigned an infectious dose of 0. The mice were monitored

daily, euthanized at terminal stage and analyzed as above for PrPres content. The survival times

of tgBov or tgHa reporter mice was measured for each tenfold dilution tested and the relative

infectious dose / survival time relationship was reported, when available. It allows translating

survival times of the inoculated fractions in infectious dose (i.e., equivalent to that found in

brain homogenate dilutions) as estimate of infectivity.

Immunoblots

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4 Aliquots of the collected fractions were treated with a final concentration of 50 μg/ml PK (1

5 hour, 37°C). Samples were then mixed in Laemmli buffer and denatured at 100°C for 5 min.

6 The samples (15 μl) were run on 12% Bis-Tris Criterion gels (Bio-Rad, Marne la Vallée,

France) and analyzed by immunoblots, using the Sha31 anti-PrP antibody (human PrP epitope

at residues 145 to 152 [35]). Immunoreactivity was visualized by chemiluminescence (GE

Healthcare). The amount of PrP present per fraction and the PrPsc glycoforms ratios were

determined with the GeneTools software after acquisition of chemiluminescent signals with a

GeneGnome digital imager (Syngene, Frederick, Maryland, United States).

Histoblots

For histoblotting procedure, brains were rapidly removed from euthanized mice and frozen on

dry ice. Cryosections were cut at 8–10 μm, transferred onto Superfrost slides and kept at -20°C

until use. Histoblot analyses were performed on 3 brains per experiment, using the 12F10 anti-

PrP antibody (human PrP epitope at residues 145 to 160 [36]).

Results

Transgenic modelling of prion species barrier

We used a previously developed SV protocol to separate different populations of PrPsc

assemblies according to their quaternary structure [13,15,18]. To determine the potential role

of the SV-isolated PrPsc subpopulations in prion adaptation and evolution, we included in the

present study three well-characterized ovine prion strains termed LA19K, LA21K fast and

127S. These cloned strains markedly differ according to the specific infectivity of their

respective PrPsc subpopulations in the homotypic PrP transmission conditions. For LA21K fast

and 127S strains, a discrete population of small oligomers (pentamers) exhibit the highest

specific infectivity values. For LA19K, the highest specific infectivity values are associated with larger-size oligomers (>40 PrP-mers) [23]. We also included atypical L-BSE prions in the study, because of their mutability on cross-species transmission [37]. We transmitted SV fractionated-PrPsc assemblies from the aforementioned strains to transgenic mouse models expressing heterotypic PrP. The models were chosen according to the transmission barrier observed with unfractionated material, as examined by gold-standard criteria [38-40], including disease attack rate on primary passage, reduction of incubation durations (ID) on serial passaging, and establishment of prion strain properties. The same analyses were performed on back-passage to mice expressing the parental host PrPc. For the sake of clarity, these data are comprehensively summarized as Additional file 1, supplementary text and supplementary Fig. 1-4. However, to provide a straightforward estimator of the stringency of the species barrier, we used the reduction factor between the mean ID on first to second passage in the heterotypic context and on retrotransmission [40]. These data are shown as Fig. 1a. A magnitude of 1 signifies prion straight adaptation. As model of prion transmission without species barrier, LA19K scrapie prions from ovine PrP (tgOv) mice was passed to bovine PrP mice (tgBov). As model of prion transmission with species barrier and 'mutation', we passed L-BSE prions onto tgOv mice. As models of prion transmission with strong species barrier, we passed LA21K fast and 127S scrapie prions onto hamster PrP mice (tgHa). Impact of size-fractionation on prion pathogenesis in the heterotypic PrP context Brain homogenates from tgOv mice containing LA19K prions, LA21K fast or 127S prions and from cattle containing L-BSE prions were solubilized and fractionated by SV [15,18]. The fractions were then intracerebrally inoculated in the heterotypic PrPc context to determine the specific transmission propensity of each fraction. (Fig. 1b). As controls, some fractions were transmitted in the homotypic PrP context and confirmed our previous results ([18]; vide infra).

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In the absence of any apparent species barrier, as determined for LA19K inoculated to tgBov mice, the infectivity sedimentograms in the homotypic and heterotypic passage conditions, tended to superimpose, in terms of distribution and infectivity values amongst the fractions (Fig. 2a). Each LA19K isolated PrPsc assembly thus exhibited quasi-equivalent specific infectivity in both transmission contexts. The strain-specified PrP_{res} electrophoretic profile and pattern of cerebral PrPres deposition [33] were conserved amongst the tgBov mice inoculated with the different fractions or unfractionated LA19K brain material (Fig. 2b and additional file 1, supplementary Fig. 5), suggesting phenotypic invariance of the isolated LA19K assemblies on heterotypic transmission. In the presence of a strong species barrier, as determined for LA21K fast and 127S inoculated to tgHa mice, SV-fractionation had a strong negative impact. None of the mice inoculated with the fractions from three independent gradients developed any neurological symptoms up to endlife. Only 3 out of the 221 tested mice (i.e., 1%) accumulated PrPres in the brain. These 3 mice were inoculated with fractions 10 and 13 from one LA21K fast gradient (Fig. 2, Table 1). In particular, none of the tgHa mice inoculated with the PrPsc assemblies with the highest specific infectivity values from fractions 1-2 accumulated any detectable PrPres (n=43, Table 1). These results were confirmed by a second passage with individual or pooled (by 2) tgHa brains, covering the entire LA21K fast gradient. All the secondary transmissions with PrPres-negative brains were negative (neurological signs and PrP_{res}; Table 2), indicating absence of a subclinical disease [41,42] and/or of infectious, PK-sensitive PrPsc species [16,43] in the non-responder mice. Oppositely, serial transmissions from PrPres-positive brains led to isolation of prions with strains properties identical to those obtained on adaptation of unfractionated LA21K fast prions to tgHa mice (Table 2, Fig. 2b, Additional file 1, supplementary Fig. 3). To discard the possibility that the loss of tgHa-transmissibility of the isolated PrPsc was due to an insufficient infectivity load, we estimated the infectivity levels of the top and middle

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1 fractions of one LA21K fast gradient. Fractions 2 and 12 induced disease in tgOv mice in 68 \pm 2 3 days (5/5) and 82 ± 1 days (5/5), respectively (Fig. 3a), meaning, according to LA21K fast 3 dose/response curve (Fig. 3a, Table 3), that their infectivity levels were equivalent to 10-1.2 and 4 10-3.2 dilutions of LA21K fast brain material, respectively. These values were fully consistent 5 with the mean (±SEM) relative infectious dose contained in LA21K fast most infectious upper 6 fractions and middle fractions established from seven independent bioassays (top fractions: 7 mean: 10-1.36 (10-1.08 to 10-1.64); middle fractions: between 10-2.9 and 10-4.65 depending on the 8 middle fractions). To estimate the infectivity load of these factions in the heterotypic PrP 9 context, we established a dose/response curve of LA21K fast in tgHa mice by transmitting by 10 intracerebral route serial tenfold dilutions of a LA21K fast tgOv-brain to reporter tgHa mice. 11 The limiting dilution value of LA21K fast prions in tgHa mice was surprisingly low (vide infra), 12 establishing at 10-2 (Table 3). Nevertheless, this value was below the infectivity value of the 13 top fractions of the gradient. Those were thus sufficiently infectious per se to induce or transmit 14 disease, at least partly in tgHa mice. This was not observed in 3 independent experiments with 15 a sufficient number of inoculated mice. Almost counterintuitively, the sole fractions eliciting 16 asymptomatic replication in a very low number of mice had infectivity values below the limiting 17 dilution. This suggests a stochastic transmission process and lends support to the view that 18 infection is possible at doses below the limiting dilution [44]. 19 Together, these observations indicate that PrPsc subassemblies segregation by SV-fractionation 20 alters their replication efficiency in the PrP transmission barrier context, for reasons 21 independent of their infectivity load. This suggests synergetic interactions between PrPsc 22 subsets for an efficient heterospecies transmission.

1 Dilution of LA21K fast prion-infected brain homogenate strengthens existing 2 transmission barriers 3 LA21K fast prions are composed of at least two structurally PrPsc subsets in different 4 proportion, each with distinct specific infectivity [23,15,18]. Dilution experiments constitute a 5 relevant method to explore the contribution of each PrPsc subtype. Over a certain dilution factor, 6 the minor population will be quasi-eliminated from the inoculum leading to explore the effect 7 of the major species. The dilution approaches should also allow dissociating biochemical 8 complex(es) between different PrPsc subsets due to equilibrium displacement toward 9 dissociation [13]. 10 We thus further analyzed the titration of LA21K fast prions in tgHa mice. Neat brain 11 homogenate (20 µL 10%) containing LA21K fast prions induced disease in all tgHa mice with 12 a mean ID of 153 days (Table 3; Additional file 1., supplementary Fig. 3a). At the 10-1 dilution, 13 the mean ID increased to 181 days (6/6 mice affected). The limiting dilution value resulting in 14 positive transmission established at the 10-2 dilution, with 2 out of 6 tgHa mice developing the 15 disease at 192 and 230 days (Table 3). In homotypic transmission, LA21K fast limiting dilution 16 value established at 10-7 (Table 3). There was thus a considerable 10s-fold reduction of this 17 value in the heterotypic PrP transmission context. For comparison, in the absence of a 18 transmission barrier, as for LA19K prions in tgBov mice, there was no significant variations in 19 the limiting dilution value between the homotypic and heterotypic contexts (Table 3). 20 The inefficacy of LA21K fast diluted material to infect tgHa mice appeared further discrepant 21 when considering the fold increase between the IDs at the lowest and at the limiting dilution. 22 There was here a 1.37-fold increase for LA21K fast in tgHa mice (from 153 to 211 days, Table 23 3) whereas the mean±SD fold increase value observed in all the titrations we performed so far 24 in our laboratory in homotypic conditions, including in tgHa mice, was statistically higher at 25 2.17±0.32 (p<0.05, One-sample z test; Fig. 4a). Applying this value to LA21K fast titration in

- tgHa mice would result in a theoretical limiting dilution value at \sim 10-5 and a \sim 330 days ID (Fig.
- 2 4b).

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- 3 Collectively, these data suggest that the dilution leads to the quasi elimination of at least one
- 4 compound and/or the dissociation of a complex mandatory for the efficacy of the heterotypic
- 5 transmission and consolidate our SV-based observations.

PrPc level and/or tissue environment imposes the species barrier stringency

7 When isolated L-BSE SV-fractions were transmitted to tgOv mice, only fractions 8 to 14

induced disease at complete or near-complete attack rate, with an overt delay compared to

unfractionated material (Fig. 5a, Table 4). Mice inoculated with the top and bottom fractions

transmitted the disease only erratically, suggesting unfavorable transmission conditions (Fig.

5a, Table 4). Isolated L-BSE assemblies had therefore altered transmission capacities in the

heterotypic PrP transmission context, as observed with LA21K fast and 127S. The western blot

profile on primary passage (Fig. 5b) and the strain phenotype obtained on 2nd passage with

PrPres-positive mouse brains indicated that C-BSE like prions has emerged from all positive

transmissions (Additional File 1, supplementary Fig. 5; supplementary Table 1).

Previously, we reported that lymphotropic prions replicated easier in the spleen than in the brain

in both homotypic and heterotypic PrP context, despite 20-fold lowered PrPc levels [27,45].

This makes bioassays based on prion detection in the mouse spleen a highly sensitive method

to detect low dose of lymphotropic prions [45]. We thus examined further the capacity of SV-

fractionated L-BSE prions to propagate in the heterotypic PrP context by examining tgOv

spleens for PrPres content after inoculation with the different fractions. Of the 49 tgOv spleens

analyzed, only 3 (6%) accumulated low levels of PrPres (Table 4). Of the 13 mice for which

both the brains and spleens were analyzed for PrP_{res} content and the brain was positive (notably

fractions 10-12 with 100% attack rate), only 3 had also positive spleens (23%). For comparison,

all the spleens analyzed after inoculation of unfractionated L-type prions were strongly PrPres-

positive from the first passage onward (Table 4, [46]).

3 Strikingly, prion replication in the spleen was still altered on secondary passage of SV-

fractionated L-BSE assemblies. While all the spleens analyzed (n=15) were PrPres-positive, the

levels of accumulation were still reduced by ~4-fold as compared to those observed on serial

transmission of unfractionated material (Fig. 6a-b). It may be noted that in homotypic

transmissions, fractionating brain material had no significant influence on spleen colonization

by prions, with regards to the number of positive spleens and PrPres accumulation levels (Fig.

6b), indicating that, alone, the size of the infectious particles or PrPsc subpopulation segregation

were not causal. Therefore, we can conclude from the impairment observed over two serial

passages that the low barrier penetrance of the isolated fractions is not due to a low infectivity

load and that size fractionation impairs L-BSE replication in the spleen to an extent that is

higher than in the brain.

Discussion

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As conventional pathogens, prions are subject to adaptation and evolution. The concept of molecular quasispecies, as defined by Eigen in 1979 [47], has been applied to prions [5,48] to reconcile the structural diversity of prion assemblies (i.e. prion structural landscape) to the preferential selection based on the 'best replicator' selection concept of certain subassemblies during prion adaptation to new host or to a new environment/replicative conditions [49,27]. To refine this 'best replicator' hypothesis [50], we tested the capacity of isolated PrPsc subassemblies within a given prion strain to adapt to a new host. We show here with multiple PrP transgenic mouse models inoculated with both field-derived and biologically cloned prions, that cross-species prion transmission does not strictly involve the selection of an existing

subpopulation of optimized PrPsc assemblies. Rather, our observations suggest that the key determinant is a synergy between structurally distinct PrPsc subassemblies. There was a positive correlation between the magnitude of the transmission barrier and the difficulty for SV-individualized PrPsc assemblies to transmit the disease in the heterotypic PrP conditions. L-BSE prions fractionation significantly delayed priogenesis in the brain and even more negatively in the spleen of the challenged tgOv mice. Fractionated LA21K fast scrapie prions replicated asymptomatically in a very small proportion of tgHa mice and fractionated 127S prions failed to propagate in these mice. As shown previously and also demonstrated here, LA21K fast and 127S scrapie prion strains are composed of at least two structurally distinct PrPsc subpopulations according to their specific infectivity values (Fig. 3a and [15,18,23]). The loss of transmissibility of separately taken PrPsc assemblies to tgHa mice cannot be attributed to a global decrease of infectivity levels due to the solubilization/fractionation method as we previously reported that the cumulated infectivity of the SV fractions did not differ significantly from that present in the loaded material [18]. Further, for LA21K fast, the relative infectivity titer of the top 'most infectious' fractions was sufficiently high to induce disease in tgHa. The fact that PrPsc assemblies segregation affects prion heterospecies transmission suggests a synergy between PrPsc subassemblies to overcome the species barrier. This hypothesis implicates an unprecedented notion of complementation between structurally distinct prior assemblies. While the molecular mechanisms of such synergy between different PrPsc subsets remain to be elucidated, some simple biochemical considerations can bring basements on the biochemistry of the process. It implicates interactions between structurally distinct PrPsc subsets in order to create a new structural information absent in each individual PrPsc population and leading to heterologous PrPc integration. During the early stage of prion replication, we showed that two

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1 sets of structurally distinct PrPsc assemblies are generated, in fractions 1-5 and 10-18 [20]. 2 These sets are defined by their elementary subunit [13] as suPrPA and suPrPB, respectively [27]. 3 During the early step of prion replication, suPrPA and suPrPB form a suPrPA:suPrPB 4 heterocomplex involved in a secondary autocatalytic templating process generating de novo the 5 formation of suPrP_B, in a PrPc-dependent manner [27]. The synergetic effect between different 6 PrPsc subsets can reside in the formation of this complex, making therefore this secondary 7 templating process a pivot of prion adaptation to a new host. In the heterotypic PrP transmission 8 context, the suPrPa:suPrPB complex (likely present in the inoculum) may incorporate 9 heterologous PrPc, leading to the formation of a de novo suPrPB* formed by the heterologous 10 PrPc with a new templating interface different from the inoculum suPrPB (Fig. 7). This first 11 event would be a limiting step of the adaptation process. The entrance of suPrPB* in the 12 autocatalytic cycle makes its formation highly cooperative. Based on these assumptions, if the 13 stability of the complex is high enough (i.e., low dissociation constant), the reconstitution of 14 the initial composition by mixing different PrPsc subsets should allow recovering the 15 transmission efficiency. This approach has been unsuccessfully attempted in the case of LA21K 16 fast. This fail could be due to the weakness of the suPrPa:suPrPB complex, as previously 17 observed [20]. Indeed, size exclusion chromatography analysis of the 127S suPrPa:suPrPB 18 complex revealed that this last is highly labile and can be observed only in conditions where 19 the concentration of suPrPA and suPrPB were high. 20 The existence of a complex such as suPrPa:suPrPB within the inoculum is further supported by 21 the striking observation that endpoint dilutions aberrantly impaired LA21K fast prions transfer 22 to tgHa mice (1000-fold decreased efficacy); the dilution steps would make certain PrPsc 23 subpopulations disappearing given their ratio/amount and/or induce the dissociation of an 24 existing complex [51,15]. While cross-species transmission of prions has rarely been done at 25 high dilution, it may be noted that comparing the limiting dilution values of MM1 sporadic CJD prions (homozygous for Met at codon 129) in transgenic mice expressing human PrP with either

Met or Val at codon 129 resulted in 103-fold decrease [52], a negative impact quantitatively

comparable to our observations.

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If the synergy between structurally different PrPsc subsets involves the formation of a

suPrPa:suPrPB heterocomplex and the PrPc-dependent secondary templating pathway, the

magnitude of the species barrier would thus depend both on the strength of the heterocomplex

and on the amount of heterotypic PrPc which defines the rate of the secondary templating and

its cooperativity aspect [20]. Such prominent role of PrPc is experimentally supported by the

observation that L-BSE prion adaptation is more impaired in tg338 mouse spleen than brain,

despite a potentially favored local environment for heterotypic conversion as prion species

barrier is lower in the spleen than in the brain [27]. The lower concentrations of PrPc [53] in

the spleen [27] and/or the different structure (including the post-translational modifications)

may impact the secondary templating pathway and its autocatalytic nature.

Conclusion

Together, our data would expand the prion quasispecies concept to an ensemble of

macromolecular assemblies, -not necessarily associated to different substrains-, that

complement each other to adapt tissue-specific selection pressure and extend prion host range.

Such 'epistatic' behavior may provide new fundamental principles for understanding prion

distinctive properties to transfer between species [54] and can explain the relative inability of

recombinant PrP to generate high-titer prions [55], unless submitted to intense mechanisms of

polymerization/fragmentation which may generate aggregate polydispersity and/or a larger

portfolio of conformations [56] for complementation.

List of Abbreviations

2 Boy: boyine

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- 3 BSE: bovine spongiform encephalopathy
- 4 CJD; Creutzfeldt-Jakob disease
- 5 Ha: hamster
- 6 Ov: ovine
- 7 PrP: prion protein
- 8 PK: proteinase K
- 9 PrPres: proteinase K resistant PrPsc
- 10 PrPsc: pathological/abnormal form of the prion protein
- 11 suPrP: PrP elementary brick
- 12 SV: sedimentation velocity
- 13 tg: transgenic

14

15 **Declarations**

- 16 Ethics approval
- 17 All the experiments involving animals were carried out in strict accordance with EU directive
- 18 2010/63 and were approved by INRA local ethics committee (Comethea; permit numbers 12-
- 19 034 and 15-056).
- 20 Consent for publication
- 21 Not applicable.
- 22 Availability of data and material
- 23 All data supporting our findings are presented in the main paper and additional files.
- 24 Competing interests
- 25 The authors declare no competing financial interests.

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8 Author's contribution

- 9 Conceptualization, AIE, FL, PT, MM, HL, HR, and VB; Data curation and Analysis, AIE, FL,
- 10 PT, MM, LH, FR, JMT, HL, HR, and VB; Resources, HL, JMT, HR and VB; Writing Original
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- 6 Figures

5

- 7 Figure 1. Magnitude of the species barrier on transmission of scrapie prions (LA19K,
- 8 LA21K fast, 127S) and cattle prions (L-BSE) to transgenic mice expressing heterotypic
- 9 **PrP**
- 10 (a) Scrapie LA19K, LA21K fast, 127S prions and cattle L-BSE prions were transmitted
- iteratively to mice expressing bovine PrP (tgBov), hamster PP (tgHa) and ovine PrP (tgOv),
- respectively, before reisolation in transgenic mice expressing the parental PrP (Additional file
- 1). The magnitude of the transmission barrier in transgenic mice expressing heterotypic PrP
- 14 (blue color) and on reisolation in transgenic mice expressing the parental PrP (green color) was
- calculated as the ratio of the mean incubation durations (ID) on first to second passage in the
- new host PrP and on reisolation in mice expressing the parental PrP. A magnitude of 1 signifies
- 17 prion straight adaptation.
- 18 (b) Overview of the bioassays made with PrPsc assemblies fractionated by sedimentation
- 19 velocity.

- 21 Figure 2. Unaltered capacity of SV-fractionated PrPsc assemblies to propagate onto a new
- 22 host PrP sequence in the absence of a transmission barrier
- 23 (a) SV profiles of PrPres (black line) and infectivity in the homotypic PrP (green line) and
- 24 heterotypic PrP (blue line) transmission context. Brain homogenates from tgOv mice inoculated

with LA19K prions were solubilized before fractionation by SV. The collected fractions were analyzed for PrP_{res} content by immunoblot and for infectivity by an incubation time bioassay in tgOv and tgBov mice (tg110 line). In the homotypic context, plain and dotted symbols/lines refer to this study and to previous reports [18], respectively. The right logarithmic brown scale provides the LA19K-specific reciprocal relation between survival time in tgOv and tgBov mice and infectious dose, as established by limiting dilution titration (as from Table 3 and [18]). Animals inoculated with 10% infectious brain material are assigned an infectious dose of 0.

(b) PrP_{res} electrophoretic profiles in the brains of tgBov mice inoculated with size-fractionated

LA19K-tgOv PrPsc assemblies. The profile obtained with unfractionated (U) material is shown

for comparison.

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Figure 3. Altered capacity of size-fractionated PrPsc assemblies to propagate onto a new

host PrP sequence in the presence of a 'strong' transmission barrier

(a) SV profiles of PrP_{res} (black line) and infectivity in the homotypic PrP (green line) and heterotypic PrP (blue dots) transmission context. Brain homogenates from tgOv mice inoculated with LA21K *fast* prions were solubilized before fractionation by SV. The collected fractions were analyzed for PrP_{res} content by immunoblot and for infectivity by an incubation time bioassay in tgOv and tgHa mice. In the homotypic context, plain and dotted symbols/lines refer to this study and to previous reports [18], respectively. Because of the reduced penetrance of the disease in tgHa mice, the mean individual ID of the PrP_{res} positive mice are shown as blue dots. The right logarithmic brown scale provides the LA21K *fast*-specific reciprocal relation between survival time in tgHa and tgOv mice and infectious dose, as established by

limiting dilution titration (as from Table 3 and [18]). Animals inoculated with 10% infectious

2 brain material are assigned an infectious dose of 0.

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3 (b) PrPres electrophoretic profiles in the brains of tgHa mice inoculated with size-fractionated

LA21K fast prions at the 1st (p1) and 3rd (p3) passage. The profiles obtained with unfractionated

(U) LA21K fast and 127S material in tgOv and tgHa mice are shown for comparison.

Figure 4. Aberrant titration of LA21K fast prion in hamster PrP mice as compared to

other prion titrations in PrP transgenic mice

9 (a) Fold increase (x) between the mean IDs at the lowest and at the limiting dilution during

prion titrations. The prions titrated and the reporter mice are indicated on the graph. The

mean \pm SD value observed for all but the LA21K fast \rightarrow tgHa titrations established at 2.17 \pm 0.32

(mean \pm SD, dotted vertical line:mean; shadow square: SD). The 1.37-fold increase for LA21K

fast in tgHa mice is significantly lower (*p<0.05, One-sample z test).

14 **(b)** Titration curve of LA19K prions in tgOv and tgBov mice as compared to that of LA21K

fast in tgOv and tgHa mice. The theoretical curve of LA21K fast prions in tgHa mice is the

result of the 2.17-fold increase in the IDs at the lowest and at the limiting dilution.

Figure 5. Capacity of size-fractionated PrPsc assemblies to propagate onto a new host PrP

sequence in the presence of an 'intermediate' transmission barrier and with mutation

(a) SV profiles of PrP_{res} (black line) and infectivity in the homotypic PrP (green line) and

heterotypic PrP (blue dots) transmission context. Brain homogenates from cattle infected with

L-BSE prions were solubilized before fractionation by SV. The collected fractions were

analyzed for PrPres content by immunoblot and for infectivity by an incubation time bioassay in

tgBov and tgOv mice. The disease incidence in tgOv mice is presented on the right red graph.

Because of the reduced penetrance of the disease in tgOv mice, the mean individual ID of the

2 PrPres positive mice are shown as blue dots.

3 (b) PrPres electrophoretic profiles in the brains of tgOv and tgBov mice inoculated with size-

4 fractionated L-BSE PrPsc assemblies. The profiles obtained with unfractionated (U) material

5 from L-BSE or classical BSE (C-BSE) are shown for comparison.

7 Figure 6. Capacity of size-fractionated L-BSE prions to colonize the spleens of mice

expressing homotypic or heterotypic PrPc

9 (a) PrPres detection in the spleens of tgOv mice inoculated with unfractionated L-BSE or C-

BSE prions (primary passage) or with fractionated L-BSE prions (second passage, fractions

used for passaging are indicated).

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12 **(b)** PrP_{res} accumulation levels in the spleens of tgOv mice inoculated with unfractionated (2_{nd}

passage) or SV-fractionated L-BSE ((all fractions combined), 2nd passage) prions as compared

to unfractionated or SV-fractionated 127S prions. (*p<0.05, Mann-Whitney test).

Figure 7. The formation of heterocomplex between structurally distinct PrPsc subsets may

drive the conversion of heterologous PrPc by a secondary templating pathway process

(a) In the homotypic PrP transmission context, prion replication involves two templating

pathways: a primary templating pathway where structurally distinct PrPsc subsets, taken

individually (A_i and B_i), are able to perpetuate the strain information and a PrPc-dependent

autocatalytic secondary templating pathway contributing to structural diversification, which

- 1 requires the formation of a heterocomplex between the elementary subunits of two structurally
- distinct sets of PrPsc assemblies (suPrPa and suPrPB) [20].
- 3 (b) This autocatalytic secondary templating pathway could drive the incorporation of
- 4 heterologous PrPc during the species barrier passage, leading to de novo generation of suPrPB
- 5 (in red) more prone to replicate/propagate in the new host. PrPsc assemblies segregation or
- 6 dilution could drastically affect the formation of the suPrPa:suPrPB complex, compromising
- 7 this secondary templating pathway.

Tables

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Table 1. Survival time of hamster PrP mice inoculated with LA21K fast and 127S prions

4 fractionated by sedimentation velocity

	LA21K	. fast	127S			
Fractions	n/n01	Survival2 (days ± SEM)	n/n01	Survival2 (days ± SEM)	n/n 01	Survival2 (days ± SEM)
1	0/12	399-627	0/5	384-631	0/6	365-552
2	0/13	520-692	0/6	318-576	0/5	341-496
3	0/5	389-651	0/6	401-636	0/5	405-538
4	0/5	507-647	0/6	384-535	0/6	317-506
6	0/6	386-780				
8	0/6	375-713				
10	2/6	353; 386	0/6	461-531	0/6	331-510
11	0/5	536-937	0/6	378-517		
12	0/11	347-687	0/6	322-426	0/6	382-587
13	1/6	394				
14	0/6	556-720	0/6	344-629	0/6	481-631
15	0/6	323-854				
16	0/6	614-710				
18	0/6	325-839				
20	0/6	406-877				
22	0/6	371-751				
24	0/5	543-927				
26	0/6	413-602				
28	0/6	345-749				
30	0/6	383-665				
\mathbf{U}_3	8/8	157 ± 6			8/8	168 ± 7

⁶ In/no: Number of mice with neurological disease or positive for PrP_{res} in the brain by immunoblotting/number of intracerebrally inoculated mice.

9

^{8 2}For mice negative for PrP_{res} accumulation, only the range of survival time is given.

³U: unfractionated material (Additional File 1, supplementary Fig. 3).

Table 2. Serial passage of SV fractionated LA21K fast prions in hamster PrP mice

	LA21H	K fast				
Fractions	2nd passage		3rd passage		4th passage	
(mouse	n/n02	Survival3	n/n02	Survival3	n/n02	Survival ₃
no.1)						
1 (no. 2+3)	0/6	382-524				
2 (no.4+7)	0/6	301-605				
10	6/6	54 ± 1	6/6	50 ± 1	6/6	48 ± 1
(no.1+2)						
11	0/6	353-544				
(no.1+4)						
12	0/6	347-687				
(no.1+2)						
13 (no.1)	6/6	58 ± 1	6/6	48 ± 1		
20	0/6	361-518				
(no.2+5)						
26	0/6	405-587				
(no.1+3)						
\mathbf{U}_4	6/6	48 ± 1	6/6	47 ± 1	6/6	46 ± 1

³ mouse identification number inoculated as pools.

1 2

^{4 2}n/no: Number of mice with neurological disease or positive for PrPres in the brain by

immunoblotting/number of intracerebrally inoculated mice (the number of the mouse

⁶ inoculated is indicated).

^{7 3}For mice negative for PrP_{res} accumulation, only the range of survival time is given.

^{8 4}U: unfractionated material (Additional File 1, supplementary Fig. 3).

Table 3. Endpoint titration of LA19K and LA21K fast scrapie prions in transgenic mice

expressing homotypic and heterotypic PrP

Dilution	Survival time ₂ (n/n ₀) ₃					
	LA19K		LA21K fast			
	Ovine PrP	Bovine PrP ₄	Ovine PrP	Hamster PrP		
10-0	$128 \pm 2 \ (6/6)$	$196 \pm 3 \ (6/6)$	$60 \pm 2 (5/5)$	$153 \pm 6 \ (6/6)$		
10-1	$151 \pm 3 \ (6/6)$	$213 \pm 5 \ (6/6)$	$64 \pm 1(5/5)$	$181 \pm 11 \ (6/6)$		
10-2	$167 \pm 4 \ (6/6)$	$240 \pm 5 \ (6/6)$	$71 \pm 1 (5/5)$	192; 230 (2/6)		
10-3	$188 \pm 4 (6/6)$	$272 \pm 19 \ (6/6)$	$79 \pm 1 (6/6)$	371-591 (0/6)		
10-4	$223 \pm 15 \ (4/6)$	$361 \pm 90 \ (4/6)$	$85 \pm 1 (5/5)$	399-518 (0/6)		
10-5	245 (1/6)		$99 \pm 2 (5/5)$	367-636 (0/6)		
10-6			$112 \pm 2 (5/5)$			
10-7			148 (1/5)			

^{3 110%} brain material used as 10-0 dilution.

1

⁴ 2Days \pm SE of the mean. For mice negative for PrP_{res} accumulation, only the range of survival

⁵ time is given.

^{6 3}n/no: Number of mice with neurological disease or positive for PrPres in the brain by

⁷ immunoblotting/number of inoculated mice.

^{8 4}tg110 line.

⁹ Data in italic are from [18].

Table 4. Survival time and PrPres detection in the brain and spleen tissues of ovine PrP

mice intracerebrally inoculated with L-BSE prions fractionated by sedimentation velocity

Fractions	n/n01	Survival ₂	PrPres detection	
			Brain	Spleen
1	1/6	802	1/6	0/5
2	2/5	519;739	2/5	0/3
3	0/5	532-711	0/5	0/4
4	1/6	496	1/6	0/3
6	1/6	472	1/6	0/2
8	3/6	542 ± 67	3/6	0/2
10	5/6	625 ± 64	5/6	1/5
12	6/6	575 ± 38	6/6	1/4
14	4/6	577 ± 76	4/6	0/1
16	2/6	530;655	2/6	1/4
18	2/6	621;681	2/6	0/1
20	0/6	406-877	0/6	0/3
22	2/6	479;538	2/6	0/3
24	1/6	452	1/6	0/2
26	0/6	381-754	0/6	0/3
28	0/6	357-739	0/6	0/2
30	0/6	465-884	0/6	0/1
\mathbf{U}_3	9/9	423 ± 7	8/8	8/8

^{4 1}n/no: Number of mice with neurological disease or positive for PrP_{res} in the brain by immunoblotting/number of inoculated mice.

1

2

²Days \pm SE of the mean. For mice negative for PrP_{res} accumulation, only the range of survival time is given.

^{8 3}U: unfractionated material; data from [26,46] are in italic.

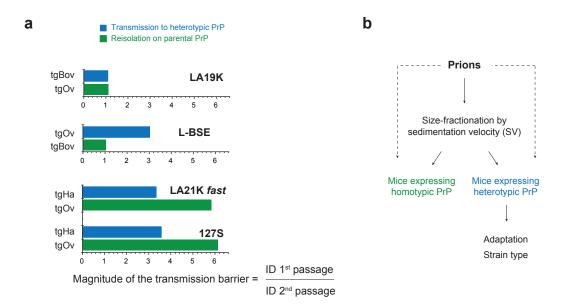


Figure 1

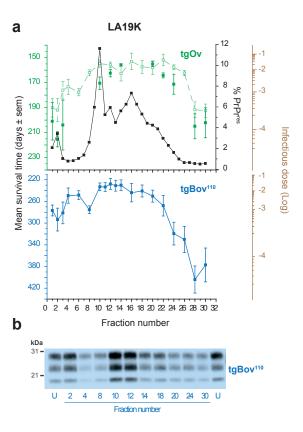


Figure 2

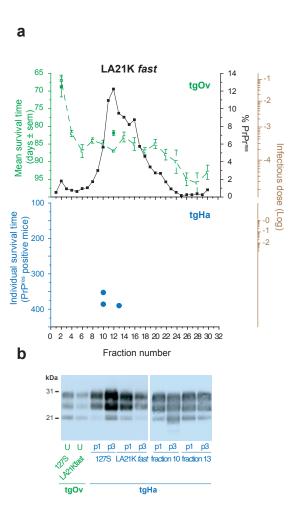
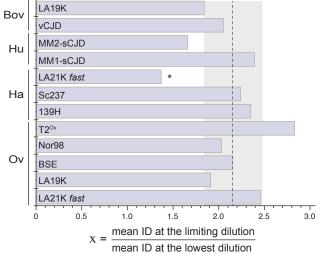


Figure 3



b



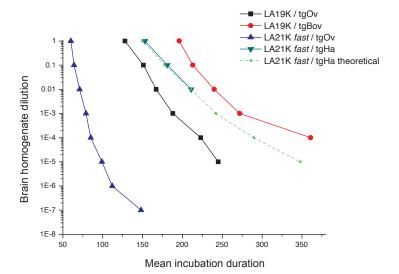


Figure 4

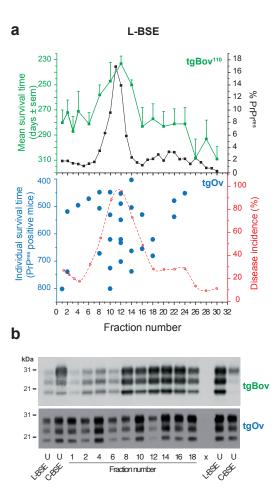
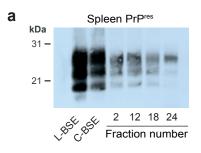


Figure 5



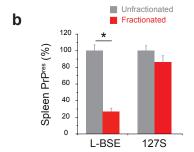
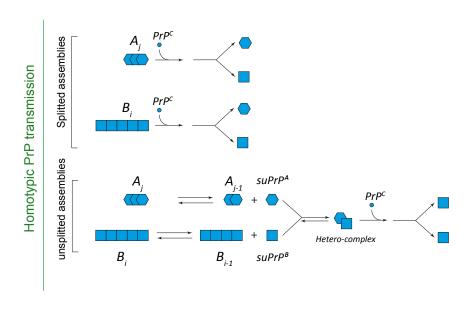


Figure 6



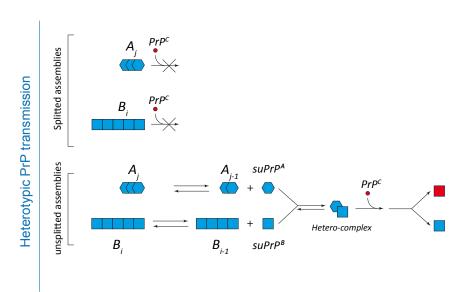


Figure 7