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Prion-like proteins sequester and suppress the toxicity of huntingtin exon 1

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Expansions of preexisting polyglutamine (polyQ) tracts in at least nine different proteins cause devastating neurodegenerative diseases. There are many unique features to these pathologies, but there must also be unifying mechanisms underlying polyQ toxicity. Using a polyQ-expanded fragment of huntingtin exon-1 (Htt103Q), the causal protein in Huntington disease, we and others have created tractable models for investigating polyQ toxicity in yeast cells. These models recapitulate key pathological features of human diseases and provide access to an unrivalled genetic toolbox. To identify toxicity modifiers, we performed an unbiased overexpression screen of virtually every protein encoded by the yeast genome. Surprisingly, there was no overlap between our modifiers and those from a conceptually identical screen reported recently, a discrepancy we attribute to an artifact of their overexpression plasmid. The suppressors of Htt103Q toxicity recovered in our screen were strongly enriched for glutamine- and asparagine-rich prion-like proteins. Separated from the rest of the protein, the prion-like sequences of these proteins were themselves potent suppressors of polyQ-expanded huntingtin exon-1 toxicity, in both yeast and human cells. Replacing the glutamines in these sequences with asparagines abolished suppression and converted them to enhancers of toxicity. Replacing asparagines with glutamines created stronger suppressors. The suppressors (but not the enhancers) coaggregated with Htt103Q, forming large foci at the insoluble protein deposit in which proteins were highly immobile. Cells possessing foci had fewer (if any) small diffusible oligomers of Htt103Q. Until such foci were lost, cells were protected from death. We discuss the therapeutic implications of these findings.

protein misfolding | prions

Protein misfolding and aggregation underlie many neurodegenerative diseases. The causes of protein misfolding are numerous and include single amino acid changes and expansions of amino acid repeats. Polyglutamine (polyQ) expansions are an infamous example of the latter and are responsible for at least nine neurodegenerative conditions, including Huntington disease (HD). In most of these diseases the polyQ-expanded protein is expressed throughout the body, but tissue damage is restricted to the nervous system and, often, to a subset of cells depending on the causal protein. Thus, there are important cell type-specific determinants of toxicity, and these are specific to particular proteins.

Despite these differences, disease severity is tightly linked to the number of glutamines. Progressively earlier onset occurs as the number of glutamines increases beyond a critical threshold of ∼35–45 residues (1). Moreover, in all cases, pathology is associated with misfolded forms of the polyQ-expanded protein. Thus, common features that arise from the expansions and result from shared aspects of polyQ-driven protein misfolding must contribute to pathology. Given the diverse nature of both the proteins bearing the polyQ tract and the pathologies they cause, understanding the nature of the interaction between misfolded polyQ-expanded proteins and the cellular environment is a complex but critical area of research.

The most prevalent polyQ disease, HD, is caused by an expansion of the polyQ tract in the protein huntingtin (Htt). A fragment of polyQ-expanded Htt, roughly encompassing exon 1 and including the polyQ tract, characteristically aggregates and accumulates in the cortex and striatum, the regions most sensitive to degeneration in HD (1, 2). The expanded polyQ tract promotes aberrant splicing of *HTT* exon 1 and results in the production of an exon 1 fragment of Htt protein (3). Overexpression of an exon 1 fragment alone is sufficient to cause neurodegeneration in mice (4) and is the basis for polyQ toxicity models in many other organisms, including yeast.

Neuron-specific vulnerabilities cannot be addressed in yeast models. However, these simple cells possess many archetypal aspects of protein homeostasis and other fundamental cell biology that are central to eukaryotes and are known points of susceptibility in neurodegenerative diseases. These include the full suite of eukaryotic chaperones and protein remodeling factors, the ubiquitin/proteasome system, autophagy, vesicle trafficking and the secretory pathway, the nuclear envelope and chromatin structure, and mitochondrial biology. The relationship between the length and toxicity of the polyQ region observed in human diseases is recapitulated in yeast, providing a strong indication that some aspects of polyQ toxicity are conserved (5).

Significance

Expansion of polyglutamine tracts in at least nine proteins causes neurodegeneration. Although the pathology caused by each protein is different, there must be common features of the polyglutamine expansion that contribute to toxicity. We modeled polyglutamine toxicity in yeast by expressing a 103-glutamine expanded fragment of huntingtin (Htt103Q) and screened the yeast genome to identify proteins that alter this toxicity. Surprisingly, our suppressors were proteins containing glutamine- and asparagine-rich segments typical of prion proteins. When we expressed just these segments with Htt103Q, the two proteins formed large, coaggregated particles, and smaller, more toxic aggregated forms were absent. Proteins with such segments may interact with polyQ-expanded proteins and thereby modulate their toxicity. These interaction partners provide targets for therapeutic intervention.

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Generally, polyQ-expanded proteins have altered protein–protein interactions, which either buffer or propagate the deleterious conformational changes of the polyQ-containing protein (6–11). However, the characteristics that distinguish beneficial from toxic interactions at a molecular level remain enigmatic. Taking advantage of the genetic tools available in yeast, we performed a genome-wide overexpression screen for modifiers of polyQ toxicity. Of the 5,532 proteins we tested, 10 were highly reproducible suppressors. These proteins were disparate in their physiological functions, yet seven of them contained segments of primary sequence that were enriched for asparagine and glutamine residues (N and Q) and had prion-like character (12). Prion-like domains in several other proteins have recently been implicated in many neurodegenerative diseases, raising interest in these unusual polypeptides (13). We used a variety of cell-based assays to investigate how prion-like domains can suppress or enhance the toxicity of polyQ-expanded Htt exon-1.

Results

Prion Domains Recovered from Genome-Wide Screen for Htt103Q Toxicity Modifiers. To model polyQ-expanded proteotoxicity in yeast, we created a diploid strain carrying two chromosomally integrated polyQ-expanded fragment of huntingtin exon-1 (Htt103Q) genes (encoding a FLAG tag, the first 17 amino acids of Htt, 103 repeats of glutamine, and a fluorescent protein) under control of the galactose-inducible promoter. This resulted in an intermediate level of Htt103Q toxicity and enabled us to screen for both suppressors and enhancers (Fig. 1*A*). Our ORF library covered 95% of the proteins encoded by the yeast genome. Each ORF encoded the protein without either *N*- or C-terminal additions and was borne on a single-copy plasmid under the control of the same galactose-inducible promoter as Htt103Q (14). The growth of each strain was compared with an Htt103Q strain carrying the same plasmid lacking an insert. An ORF was deemed to be a suppressor or enhancer if it affected growth of the Htt103Q-expressing strain but not a control strain without Htt103Q.

We identified ten genes that suppressed Htt103Q toxicity (Fig. 1*A*). (All genes that enhanced Htt103Q toxicity were also toxic in the control strain lacking Htt103Q and were not further investigated.) No single cellular process logically connected all of the proteins. However, inspection of the amino acid sequences of the suppressors revealed in many a region strongly enriched for glutamine- and asparagine-rich prion-like sequences. This finding was surprising because other proteins with such domains are implicated in the pathology of various neurodegenerative diseases (13) and not in protection against proteotoxicity.

In yeast, an individual domain confers the prion characteristics of most prion proteins. These prion domains (PrDs), both on their own and in the context of the full-length proteins, are capable of self-perpetuating conformational changes and can exist in either soluble or aggregated states (15). To date, over 25 proteins that possess prion-like characteristics have been identified in yeast, and most of their PrDs are highly enriched for the amino acids glutamine (Q) and asparagine (N). Many of these were identified by computational algorithms for ranking the likelihood that a given protein might function as a prion (12). In this ranking, seven of our Htt103Q toxicity suppressors (all but Mbp1, Bre5, and Ykr075c) reside within the top 150 of all proteins in the yeast genome. The likelihood that this occurred by chance is less than 1 in 10^{10} (hypergeometric distribution).

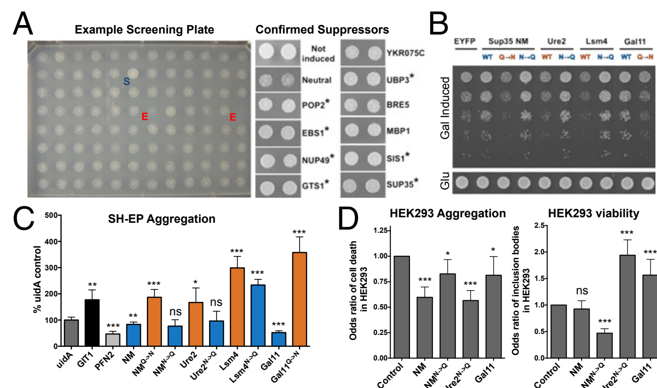

Fig. 1. Overexpression screen for modifiers of Htt103Q toxicity in yeast. (*A*) An example plate with (*Left*) representative suppressor (S) and enhancer (E) hits and (*Right*) the 10 confirmed hits in duplicate along with uninduced and neutral controls (EYFP). Hits with PrDs are marked with an asterisk. (*B*) Growth of cells expressing Htt103Q and PrD modifiers or PrD variants where asparagines were replaced with glutamine (N→Q) or where glutamines were replaced with asparagine (Q→N). Suppressors are shown in blue, and enhancers are shown in orange. (*C*) High-content microscopy analysis of SH-EP cells coexpressing Htt79Q and PrD modifiers. GIT1 (black) and PFN1 (light gray) are aggregation-enhancing and aggregation-suppressing controls, respectively. (*D*) Cell death and aggregation in HEK-293 cells coexpressing Htt72Q and PrD suppressors. Only the PrDs with high expression in this cell line were used for this analysis. *$P < 0.05$, **$P < 0.01$, and ***$P < 0.001$.

Reconciling Different Results from a Similar Screen. Very recently, an apparently similar yeast overexpression screen for modifiers of Htt103Q toxicity was reported (16). Of the 317 hits reported, none were among our suppressors, nor was there a bias for proteins containing prion-like sequences. We investigated three properties of the Mason et al. (16) screen that differed from our own and might account for the disparate findings: (*i*) a haploid yeast strain from a different genetic background was used; (*ii*) each ORF carried three C-terminal tags, HA, 6x His, and protein A; and (*iii*) both the Htt103Q expression construct and the ORF library were on high-copy 2μ plasmids. After reanalyzing their strongest suppressor, Gpx1, in a variety of strains (Fig. S1 and *SI Results*), we concluded that their suppressors were recovered due to an artifact of using two high-copy plasmids that both carried the galactose-regulated promoter (for the expression of both Htt103Q and the ORF library). Using a 2μ to express the ORF will create competition for limiting transcription factors and reduce the expression of Htt103Q. The variations in copy number that occur with 2μ libraries likely accounted for the apparent differences in suppression. We also note that while our manuscript was under review, another overexpression screen for modifiers of Htt103Q toxicity in yeast reported results highly consistent with our own (17).

PrDs Themselves Can Suppress Htt103Q Toxicity. The high percentage of proteins containing prion-like domains among our suppressors prompted us to examine whether the Q/N-rich PrDs might suppress toxicity on their own. First, we tested the PrD segments from four of the suppressors identified in our screen—Nup49, Pop2, Sup35, and Gts1 (see ref. 12 for the amino acid sequences of all PrDs), each expressed with a C-terminal EYFP fusion. Overexpression of just the PrDs of Nup49 and Pop2 did not suppress Htt103Q toxicity, indicating that it is not just Q-richness that determines suppression. It may be that the full-length protein or a longer fragment of the protein is required. [While our paper was under review, a slightly longer fragment of Pop2 was reported to suppress Htt103Q toxicity (17).] More importantly, the PrDs of both Sup35 (known as NM) and Gts1 were effective suppressors, demonstrating that some PrDs can modify Htt103Q toxicity on their own.

Next, we tested 38 previously reported N- or Q-rich PrDs (Table S1) (12). Of 20 Q-rich PrDs tested, 12 suppressed Htt103Q toxicity, whereas only 2 of 22 N-rich PrDs were capable of suppression. Both N-rich PrD suppressors also possessed Q-rich segments.

To more rigorously test the relationship between the suppression of toxicity and the enrichment for Q/N residues, we used two sets of PrD variants (Table S2). In one set, all glutamine residues were changed to asparagines (Q→N). In the second set, all asparagine residues were changed to glutamines

(N→Q). Each of the N→Q variants potently suppressed Htt103Q toxicity. In fact, the N→Q variants were much more potent than the wild-type PrDs and were stronger than any of the suppressors identified in the screen. The Q→N variants not only failed to suppress toxicity but in contrast often enhanced it (Fig. 1*B* and Fig. S2).

PrDs Can Also Reduce Htt Toxicity in Human Cells. The neurodegeneration caused by various polyQ expansion proteins is highly cell specific, despite the fact that these proteins are broadly expressed throughout the body. Thus, toxicity in any particular cell type must be influenced by the sequences flanking the polyQ segments and the unique proteomes of the susceptible cell types (5, 18, 19). We do not, therefore, suggest that our yeast suppressors are directly relevant to human disease. Nor would we expect them to behave in any particular mammalian cell type exactly as they do in yeast or another mammalian cell type. Rather, we consider them "proteome-modifying agents" and wondered if some of them are capable of modifying the aggregation and/or toxicity of polyQ-expanded Htt exon-1 in any human cell type.

First, we used a neuroblastoma-derived cell line (SH-EP) where the expression of polyQ expansion proteins is not toxic and examined changes in the aggregation state of Htt (20). We chose to limit this analysis to the prion domains in which we had exchanged all of the Qs or all of the Ns because these produced the strongest phenotypes. Cell cultures were cotransfected with Htt79Q (tagged with YFP) and our PrD modifiers (tagged with mCherry). The aggregation of Htt79Q in cells that expressed both proteins was scored 48 h posttransfection, using high-content fluorescence microscopy and an automated imaging system. This instrument assesses the mean intensity, area, and number of aggregates per cell, normalized to a neutral control (beta-glucuronidase from *Escherichia coli*, uidA). Two human proteins lacking PrDs—the GIT1 protein, which increases polyQ-expanded Htt exon-1 aggregation, and the PFN2 protein, which decreases it (21, 22)—were used as additional controls. In this cell line, the N-rich PrDs increased aggregation of Htt79Q, whereas most of the Q-rich variants had the opposite effect (Fig. 1*C* and Fig. S3).

To examine cells with a different tissue of origin and hence a different proteome, we used HEK293 cells. These cells are commonly used to study both the toxicity and aggregation of various disease-related proteins (23). We cotransfected cells with Htt72Q (tagged with GFP) and several of the yeast PrD modifiers (tagged with mCherry). After 48 h, we fixed the cells and scored them for aggregation of Htt72Q and cell death (Fig. 1*D* and Fig. S4). Only four of the PrDs were expressed at sufficient levels to include in the analysis (NM, $NM^{N→Q}$, $Ure2^{N→Q}$, and Gal11). The effects of these proteins on Htt72Q aggregation varied. NM had no visible effect, $NM^{N→Q}$ significantly decreased aggregation, and Gal11 and $Ure2^{N→Q}$ increased aggregation. Nevertheless, all four of these Q-rich PrDs suppressed Htt72Q toxicity. NM and $Ure2^{N→Q}$ reduced cell death by over 40%, whereas $NM^{N→Q}$ and Gal11 attenuated toxicity by ∼20%. Although we neither expected nor found identical outcomes in the two different human cell types and in yeast, clearly, the PrD modifiers can affect both the aggregation and the toxicity of polyQ-expanded Htt exon-1 in the context of human proteomes.

Paradoxically, PrD Suppressors Increase Htt103Q Protein Levels. To investigate further, we returned to the more tractable yeast cells. These cells provide genetically identical, genomically stable populations that are subject to only minor epigenetic modifications of gene activity in culture. Further, each and every cell carries an identical complement of inducible genes, either integrated in the genome or on a plasmid. This ensures more homogenous and controlled gene expression across the entire population.

We first asked if coexpression of PrD modifiers altered the amount of Htt103Q protein in the yeast cells. Western blotting with antibodies against GFP simultaneously revealed the Htt103Q protein and the PrD modifiers because both were modified with a GFP variant (Fig. 2*A*). Enhancers did not increase the level of Htt103Q protein (if anything, they decreased it). Even more surprisingly, suppressors of Htt103Q toxicity actually increased Htt103Q protein levels (Fig. 2*A*). Experiments in which cycloheximide was used to abruptly terminate all protein synthesis demonstrated that the half-life of the Htt103Q was dramatically increased by the presence of a PrD suppressor (Fig. 2*B*). Because coexpression of PrD suppressors does not decrease the amount of Htt103Q, they must (directly or indirectly) reduce its toxicity.

PrD Suppressors Form Large Coaggregates with Htt103Q. We turned to fluorescence microscopy to examine the relative localization of Htt103Q and the PrD modifiers in the yeast cells. In the absence of a modifier, the toxic Htt103Q protein formed irregular agglomerations of various sizes and shapes distributed throughout the cytoplasm (Fig. 3*A*). As expected, a coexpressed EYFP control (EYFP protein alone) was diffusely distributed in these cells. When cells coexpressed EYFP-tagged enhancers, the aggregation pattern of Htt103Q did not change in any obvious way, and the enhancer protein either remained diffuse or formed independent aggregates that excluded Htt103Q. In the presence of a suppressor, however, Htt103Q collected in only one or two large foci in the cytoplasm of each cell, where it colocalized with the suppressor protein (Fig. 3*A* and Fig. S5).

Cells with Suppressor/PrD Coaggregates Grow More Rapidly. To determine whether the formation of large Htt103Q foci was directly related to the suppression of toxicity, we used a PrD with only moderate suppressor activity (NM) and which colocalized with Htt103Q in many but not all cells. Time-lapse video microscopy of yeast in microfluidic chambers allowed us to both monitor protein aggregation within each cell and unambiguously track the lineages of the cells as they divided over the course of the experiment. Thus, any difference in the growth rates of cells with and without aggregates would be apparent.

As expected, some founder cells possessed colocalized foci of NM and Htt103Q. In others, the foci contained only Htt103Q but not the suppressor. As the colonies grew, cells descended from founders with colocalized foci often maintained that distribution and repeatedly divided, eventually taking over the entire field of view. Cells in which NM was not colocalized with Htt103Q grew poorly and soon died (Fig. 3*B*). Cells that initially possessed both colocalized and independent Htt103Q aggregates were particularly informative. In these, the focus in which NM and Htt103Q colocalized was occasionally lost. When this happened, it was quickly followed by cell death (Fig. 3*C*). In total, cells that did not inherit a colocalized focus (40% of deaths) and those that lost it (29% of deaths) constituted 69% of deaths.

Suppressor PrD/Htt103Q Coaggregates Accumulate at the IPOD. In eukaryotes, there are two cytoplasmic sites for the deposition of misfolded proteins: the insoluble protein deposit (IPOD) and the juxtanuclear quality control compartment (JUNQ) (24). The

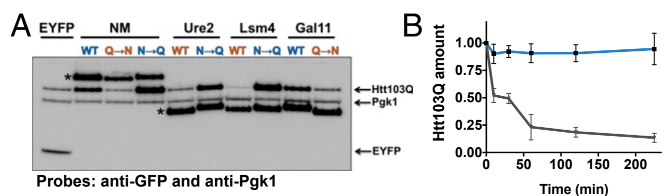

Fig. 2. Effect of PrD suppressors on Htt103Q protein levels. (*A*) Western blot for EGFP and Pgk1 reveals the protein levels of Htt103Q, the modifier, and Pgk1 (loading control) in cells grown overnight in 2% galactose. Bands corresponding to modifiers are marked with asterisks. (*B*) Htt103Q protein levels in cells expressing the suppressor $NM^{N→Q}$ (blue line) or a neutral protein (EYFP, gray line) as a function of time following inhibition of translation with cycloheximide.

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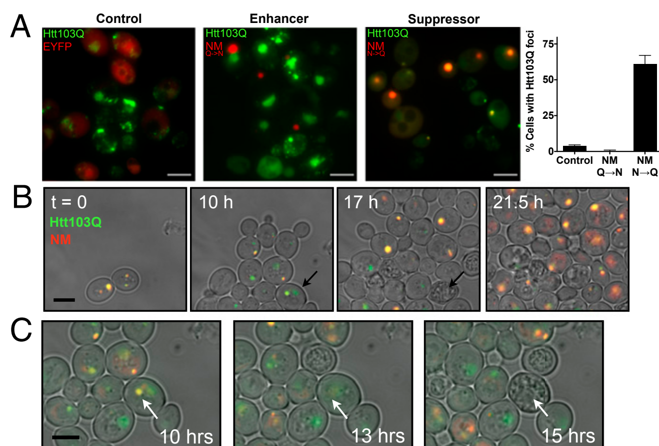

Fig. 3. PrD suppressors alter the intracellular localization of Htt103Q. (*A*) Strains expressing Htt103Q (green) along with a neutral control (EYFP) or an EYFP-tagged PrD enhancer of toxicity ($NM^{Q\rightarrow N}$, red) or an EYFP-tagged suppressor of toxicity ($NM^{N\rightarrow Q}$, red). Far right graph shows quantitation of the percentage of cells with Htt103Q aggregated in one or two foci. (*B*) Time course of a single microcolony coexpressing Htt103Q and NM. (*C*) The fate of the cell indicated by the black arrow in *B* is shown in greater time resolution. The white arrow indicates the location of a focus with colocalized Htt103Q and suppressor PrD. This focus was spontaneously lost between 12.5 h and 14.5 h, after which the cell died. (All scale bars: 5 μm.)

IPOD is located near the vacuole and serves as a site for the sequestration of aggregated proteins. The JUNQ is located adjacent to the nucleus and contains misfolded proteins that are destined for proteasomal degradation. To test whether Htt103Q localizes to either of these structures, we coexpressed Htt103Q and some of our PrD modifiers in three separate yeast strains carrying markers for different subcellular compartments. These labeled either the IPOD with Rnq1, the JUNQ with von Hippel-Lindau tumor suppressor (VHL), or the nucleus with NHP6a. Htt103Q formed many small puncta when expressed on its own or together with an enhancer. These aggregates were broadly distributed and often around, but not within, the nucleus. In the majority of cells (82 ± 9%), a small portion of Htt103Q was colocalized with VHL at the JUNQ (Fig. S6). However, much of the aggregated Htt103Q was outside the JUNQ and never localized to the IPOD (Fig. 4). In contrast, when Htt103Q was coexpressed with a suppressor PrD, both proteins consistently colocalized at the IPOD (Fig. 4).

Proteins localized to the IPOD characteristically have very low mobility (24). To determine if Htt103Q and suppressor proteins in the IPOD had these dynamics, we used fluorescence recovery after photobleaching (FRAP) to quantify the mobility of Htt103Q molecules inside and outside the foci. We photobleached a small region of the cell with a brief, intense laser pulse and then determined how quickly fluorescence was restored by the migration of unaffected proteins into this spot. In cells coexpressing Htt103Q and NM, photobleached regions outside of foci regained roughly 60% of their signal within a minute and eventually recovered more than 80% of their original fluorescence, indicating that the Htt103Q molecules outside of foci were highly mobile. In contrast, when we photobleached Htt103Q protein inside foci, recovery was negligible for at least 5 min (Fig. 5*A*). Thus, Htt protein localized to the IPOD is highly immobile.

PrD Suppressors Eliminate Diffusible Oligomers of Htt103Q. Small oligomers have been implicated as the causal agents in many proteinopathies. To monitor changes in the population of Htt103Q oligomers caused by our PrD enhancers and suppressors in yeast, we used fluorescence correlation spectroscopy (FCS) (25). To concentrate our analysis on the Htt103Q protein that was not localized to large aggregates, cell lysates were subjected to centrifugation to remove them. The supernatant was recovered and two-photon excitation was exploited to generate a very small excitation volume. We measured the fluctuations of fluorescence caused by the diffusion of single particles into, and out of, this volume. The brightness of these events (i.e., the number of fluorophores per diffusing particle) provides a measure of the oligomerization state of the Htt103Q. To limit artifacts from intermolecular quenching, which would result in lower fluorescence, we used mCherry tags on the PrD modifiers. We also measured the fluorescence intensity of the lysates to ensure that the number of fluorophores in the excitation volume was within acceptable limits. Because some cultures expressing moderate suppressors contained a mixed population of cells experiencing varying degrees of toxicity (see above for the example of NM), they were excluded from the analysis.

In lysates of cells expressing Htt103Q and a neutral protein (EYFP), we detected slowly diffusing particles of ECFP-tagged Htt103Q. The molecular brightness of these particles was much greater than monomeric fluorophores (i.e., that of ECFP without Htt103Q), consistent with an oligomeric species (Fig. 5*B*). In lysates of cells coexpressing Htt103Q and PrD enhancers, Htt particles had diffusion coefficients similar to those of cells expressing Htt103Q and the neutral control (Fig. S7). As determined by their molecular brightness, these particles were smaller on average but more broadly distributed in sizes. In lysates of cells coexpressing strong suppressors, Htt103Q particles had the fastest diffusion coefficients and molecular brightness comparable to that of monomeric fluorophores, indicating that Htt103Q was monomeric.

Discussion

Starting with an unbiased genome-wide screen, we discovered that glutamine (Q)-rich protein domains can act as potent suppressors of Htt103Q toxicity. These suppressors coaggregated with Htt103Q. The resulting Htt103Q aggregates were much less toxic, and small oligomers of Htt103Q were undetectable. Thus, interactions between polyQ-expanded disease proteins and other Q-rich proteins do not always contribute to pathology. Some of these interactions may instead have the beneficial effect of capturing the misfolded polyQ-expanded protein and preventing it from inactivating more essential proteins. The complexities such interactions are formidable, but understanding them may offer new therapeutic strategies.

What features of Q-rich domains might determine their capacity to suppress Htt103Q toxicity? Strikingly, this ability is inversely related to their capacity to form prions. Prion proteins have the unusual ability to convert into self-perpetuating amyloids, which can act as protein-based elements of inheritance (15). The majority of known prion proteins have a distinct prion-determining region (PrD) that is rich in N and Q residues. In

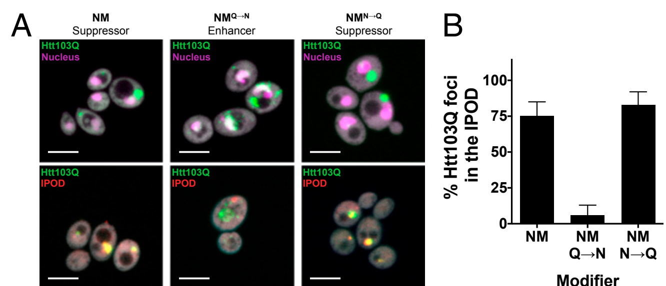

Fig. 4. Localization of Htt103Q in the presence of PrD modifiers in yeast. (*A*) The relative localization of Htt103Q (green) with the nucleus (magenta) or the insoluble protein deposit marker Rnq1 (red) upon coexpression with a PrD modifier. (*B*) Quantitation of the colocalization of Htt103Q and Rnq1 in the IPOD. (All scale bars: 5 μm.)

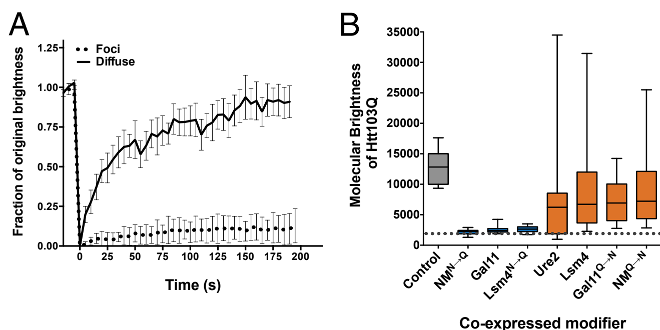

Fig. 5. Dynamics of Htt103Q foci. (*A*) FRAP traces of Htt103Q in foci (dashed line) and outside of foci (solid line) in cells expressing Htt103Q and the suppressor NM. (*B*) Brightness of Htt103Q-ECFP particles in lysates of cells expressing mCherry-tagged PrD modifiers or a neutral control (free EYFP). The brightness of free ECFP monomers is indicated by the dotted line.

a previous study unrelated to Htt toxicity, we investigated the consequences of altering the balance between these two amino acids (26). PrD variants in which all Q residues were replaced with N residues were much more likely to convert to the prion, amyloid form. In the present study, these variants enhanced the toxicity of Htt103Q. Variants in which all N residues were replaced with Q residues virtually never converted to the prion form. These variants suppressed the toxicity of Htt103Q.

Examining the properties of these proteins in vitro, we previously showed that Q→N PrDs efficiently self-assembled and formed highly stable amyloids, whereas N→Q variants aggregated much more slowly and rarely formed stable amyloids. When we tested the capacity of the aggregates formed by these PrD variants to seed the assembly of themselves and each other, only N→Q variants (which we identified as suppressors here) were effective in cross-seeding other sequences. Although these cross-seeded aggregates are often β-sheet–rich amyloids, Q/N-rich proteins can also form coiled coils (27). Cross-seeding by Q-rich PrDs could produce α-helical structures, especially when coaggregating with another protein that has α-helical propensity, such as polyQ-expanded Htt exon-1 (28). Although we do not yet know the structural details of the coaggregates, we suggest that the capacity of Q-rich PrDs to suppress Htt103Q toxicity is a direct consequence of their cross-seeding activity.

The large foci formed by coaggregated Htt103Q and the PrD suppressors resemble the inclusion bodies (IBs) found in the nervous system of human patients with HD. These foci and IBs may have similar biological roles. Although IBs were originally considered to be toxic, a growing compendium of findings supports a major reinterpretation, that IBs are protective (29). In support of this interpretation, IB formation often does not correlate with toxicity in yeast, fly, worm, and mouse models of polyQ toxicity (5, 30–32). In humans with HD, IBs are more commonly found in regions of the brain that are less affected by the disease and in less vulnerable cell types (33, 34). Long-term imaging and survival analysis of neuronal cultures expressing polyQ-expanded Htt provided a particularly strong argument for the protective nature of IBs, demonstrating that neurons that formed IBs survived longer than those that did not (35).

Our yeast PrD modifiers provided a unique opportunity to directly study the connection between toxicity and aggregation. Whether coexpressed with a neutral protein, an enhancer, or a suppressor, a portion of Htt103Q protein was always in an aggregated state. However, the different forms of aggregates elicited profoundly different toxicities. Toxic Htt103Q aggregates consisted of many small puncta, whereas protective Htt103Q aggregates consisted of large foci at the IPOD. In another report, the sequestration of Htt103Q into Sti1 foci, a juxtanuclear site distinct from the JUNQ and IPOD, also reduced toxicity (36). Thus, irrespective of their subcellular localization, the formation of large Htt103Q foci seems to be protective against toxicity.

As evidence for the protective nature of IBs has mounted, a consensus has emerged implicating small oligomeric particles as the toxic species. For polyQ-containing proteins, oligomers form before IBs, their formation is polyQ length-dependent, and their presence is well correlated with cell death (25, 37). Both chaperones that remodel oligomers and peptides that inhibit oligomer formation suppress toxicity (38, 39). In our yeast model, cells experiencing the greatest toxicity harbored many small oligomers. In cells experiencing the lowest toxicity, similar oligomers were undetectable. Because the suppressors greatly increased the total accumulation of Htt103Q, our PrD suppressors must prevent the formation of oligomers and/or promote their sequestration. PolyQ-expanded Htt exon-1, in vitro, forms an α-helical oligomer early in the aggregation process (40). It is possible that the suppressor PrDs intercalate into such α-helix–rich oligomers and promote their assembly into the large coaggregated foci.

When overexpressed separately from the rest of the protein, the PrDs of some of the suppressors recovered from our screen could not suppress Htt103Q toxicity. In some cases, the PrD and at least part of the rest of the protein must work together to relieve Htt103Q toxicity. It is notable that four of these particular suppressors—Sis1, Nup49, Bre5, and Upb3—fit logically into a nuclear trafficking and degradation pathway recently identified in yeast and implicated in Htt103Q toxicity (41, 42). In previous literature, most Q-rich proteins that modify Htt toxicity have been shown to be enhancers (7, 8, 10). Indeed, many of the PrDs we tested that had very strong suppressor activity on their own were not recovered as suppressors in our screen of the full-length proteins. The Q-rich segments, as well as the rest of the protein to which they are attached, can each influence Htt toxicity and can do so in different ways. Thus, the physical interaction of Q-rich PrDs with Htt103Q, although highly significant, is not the sole determinant of toxicity suppression or enhancement.

The interaction between Q-rich PrDs and the polyQ-expanded disease protein is not necessarily specific to a given cell type or even specific to Htt. The Sup35 PrD, NM, not only suppresses polyQ-expanded Htt exon-1 toxicity in yeast and human cells as shown in this report but also suppresses polyQ-expanded SCA3 toxicity in *Drosophila* (43). As noted above, interaction between Q-rich proteins and polyQ-expanded disease proteins frequently leads to enhanced toxicity, but clearly, there are examples of beneficial interactions like those reported here in yeast and previously in *C. elegans* (44). No doubt the phenotypic outcome will depend on the expression patterns of the Q-rich proteins, as well as their posttranslational modifications, in the context of a particular proteome. Variability in this interaction network must be a key contributor to the vulnerability of different cell types to different polyQ expansion proteins. The complexity of these effects is daunting. Nevertheless, learning to control these interactions might prove a valuable strategy in the treatment of polyQ expansion diseases.

Materials and Methods

Overexpression Screen and PrD Modifiers. The overexpression library consisted of 5,532 full-length, untagged, sequence-verified, galactose-inducible yeast ORFs in the plasmid pBY001 in a BY4741 yeast strain (14). PrD modifiers were cloned into Gateway destination vectors with C-terminal fluorescent fusion proteins and transformed into the BY4741 strain. These strains were individually mated with a [RNQ$^+$] w303 strain containing Htt103Q integrations of pRS303GAL-FLAG-Htt103Q-ECFP and pRS305GAL-FLAG-Htt103Q-DsRed (see *SI Materials and Methods* for more details).

HEK-293 Assays. Approximately 200 EGFP-Htt72Q and PrD-mCherry expressing cells were counted per modifier and assessed for cell death and aggregation. Nuclei were stained with 4′,6-diamidino-2-phenylindole, and those that showed morphology indicative of necrosis or apoptosis (for example, fragmentation or pyknosis) were considered dead. Each experiment was carried out in triplicate and performed at least twice. Thus, cell death and

aggregation are expressed in terms of odds ratio (see *SI Materials and Methods* for more details).

Epifluorescence, Time Lapse, and Confocal Imaging. For epifluorescence imaging, we used the original screening strain described above with EYFP-tagged PrD modifiers. The ECFP-tagged Htt103Q protein proved superior for fluorescence microscopy and was used as a general indicator of the fate of Htt103Q in our yeast cells. Cells were grown overnight in liquid culture, and images were acquired with a Nikon Plan Apo 100× oil objective (NA 1.4). Data from two biological replicates for enhancers and three for suppressors were quantitated.

The strains used for time-lapse and confocal imaging experiments were identical except that all modifiers were integrated into the genome at the *URA* locus. VHL was tagged with EYFP and expressed from a galactose-inducible vector integrated in the *URA* locus. Rnq1 and NHP6a were both endogenously tagged with iRFP. For time-lapse imaging, mKate2 was integrated into the *HO* locus to serve as a cytoplasmic marker. Time-lapse bright field and RFP images were captured every 15 min, and CFP and YFP channels were acquired every 30 min (see *SI Materials and Methods* for more details).

High-Content Microscopy. High-content microscopy of SH-EP cells coexpressing EYFP-tagged Htt79Q and mCherry-tagged PrD modifiers was performed as previously described (20).

FRAP. The Htt103Q strain coexpressing EYFP-tagged PrD modifiers growing in log phase was subjected to FRAP on an Andor Revolution spinning disk confocal microscope using a 100× 1.49 NA Nikon Plan Apo objective. ECFP-tagged Htt103Q molecules were bleached with a single 405-nm laser pulse with a dwell time of 600 μs at 15% of maximum power. Recovery was recorded with 2-s exposures of 405 nm excitation every 5 s. Little or no additional photobleaching occurred during these acquisitions. Data were analyzed with EasyFRAP analysis software (45).

FCS. All experiments were performed with the Htt103Q strain coexpressing mCherry-tagged PrD modifiers. Yeasts were spheroplasted and gently lysed with 2% Igepal at 4 °C and centrifuged for 30 min at 14,000 × *g* to remove large aggregates (see *SI Materials and Methods* for details).

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